

STIC-Biotech/ChemLib

82382

From: Schmidt, Mary
Sent: Sunday, December 15, 2002 5:40 PM
To: STIC-Biotech/ChemLib
Subject: sequence search request 09/121,239

Please search the following primer sequences, and please size limit the results to less than 100 bases:

SEQ ID NOS: 1, 5, 9, 13, 16, 22, 23, 26 and 27.

Thanks,
Melissa
mailboxes 11e12
art unit 1635

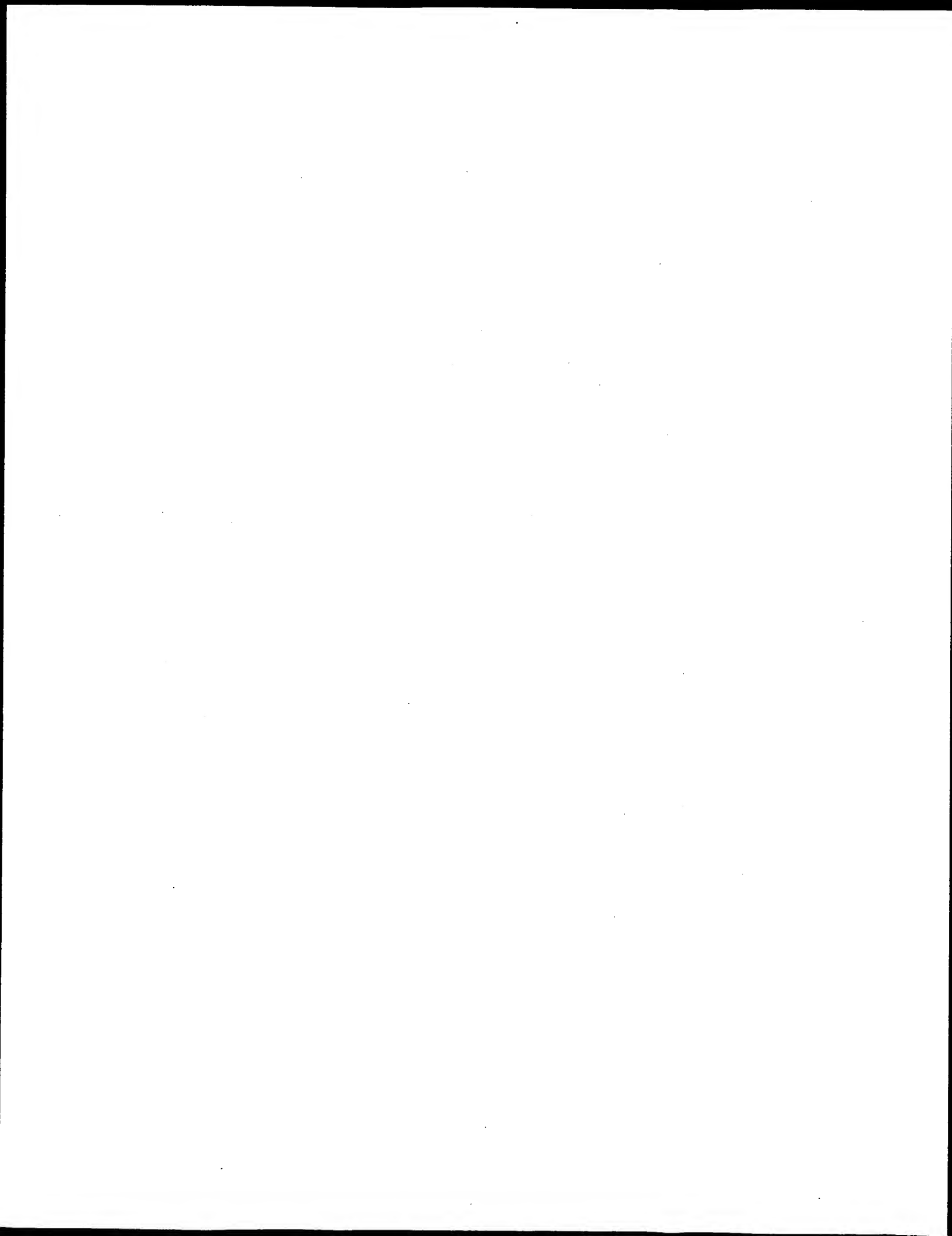
Priority July 23, 1997
(Prov.)

POINT OF CONTACT:
PAUL SCHULWITZ
TECHNICAL INFO. SPECIALIST
CM1 6B06 TEL. (703) 305-1954

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:00:32; Search time 185.363 Seconds
(without alignments)
656,052 Million cell updates/sec

Title: US-09-121-239-1

Sequence: 1 TAAATTAATACGACCTCACTA.....CCCTGAGCCTCAAGTCAGA 54

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

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23: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001.DAT.*
24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	54	21	AAZ60840
2	54	100.0	54	21	AAZ60841
3	54	100.0	54	21	AAZ60842
4	54	100.0	54	21	AAZ60843
5	49	90.7	50	16	AAO86626
6	49	90.7	50	17	AAZ42417
7	49	90.7	50	17	AAZ15571
8	49	90.7	50	19	AAV65349
9	49	90.7	50	20	AAZ3191

10	32	59.3	52	21	AAZ62310	Human prostate spe
11	32	59.3	54	21	AAZ6067	Human prostate spe
12	31.8	58.9	51	24	ABK53140	HIV-1 reverse tran
13	31.8	58.9	51	24	AAZ5502	HIV-1 pol gene RT
14	31	57.4	49	14	AAO52394	Sequence used in t
15	31	57.4	49	17	AAO70705	Oligonucleotide 1b
16	31	57.4	49	18	AAV00790	5' PCR primer 1b a
17	31	57.4	49	19	AAV14575	Sequence used in c
18	31	57.4	49	20	AAV79650	HIV RT DNA templ
19	31	57.4	49	21	AAAZ2750	High-affinity nucl
20	31	57.4	49	24	ABK61126	SELEX identified n
21	31	57.4	49	24	AAV14878	HIV RT candidate m
22	31	57.4	49	24	AAV79950	High-affinity nucl
23	31	57.4	49	24	AAV3050	SELEX process nucl
24	31	57.4	49	24	ABK61426	SELEX process nucl
25	30.8	57.0	49	17	AAZ62218	Coccioides limit
26	30.8	57.0	49	21	AAZ62218	Human prostate spe
27	30.2	55.9	52	21	AAZ6206	Human prostate spe
28	30.2	55.9	52	22	AAO57040	M. tuberculosis pr
29	30.2	55.9	52	15	AAO57040	Human prostate spe
30	30	55.6	49	21	AAV76205	Human prostate spe
31	30	55.6	50	21	AAV76205	HIV-1 reverse tran
32	30	55.6	55	24	ABK53145	HIV-1 pol gene RT
33	30	55.6	55	24	AAZ45507	Human prostate-spe
34	29.8	55.2	54	21	AAZ6220	7' (tag2) 118VN pr
35	29.8	55.2	51	22	AAV05775	Human CXK-chemok
36	29.6	54.8	53	19	AAV05775	Human CXK-chemok
37	29.6	54.8	55	21	AAZ38562	Human immunodef
38	29.4	54.4	50	16	AAO86614	Human immunodef
39	29.4	54.4	50	17	AAZ42406	HIV probe #3. Hum
40	29.4	54.4	50	17	AAZ42406	Human immunodef
41	29.4	54.4	50	17	AAZ15559	Human immunodef
42	29.4	54.4	50	19	AAZ6337	HIV region 3 prime
43	29.4	54.4	50	20	AAZ3179	Probe #1. Unident
44	29.4	54.4	50	22	AAZ6582	Human Interferon b
45	29.4	54.4	70	22	AAZ00081	

ALIGNMENTS

RESULT 1
ID AAZ60840 standard; DNA; 54 BP.
XX AAZ60840;
XX
XX 16-MAY-2000 (first entry)
XX
XX
XX Oligonucleotide used to detect bcr b3-abl fusion transcripts.
DE
XX Fusion transcript; translocation; bcr b3 region; abl gene;
XX amplification assay; detection assay; medical diagnosis;
XX clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX disease marker; cancer; leukemia; ss.
XX
XX Synthetic.
XX
XX WO200005418-A1.
XX
XX
XX 03-FEB-2000.
XX
XX
XX 23-JUL-1999; 99WO-0516832.
XX
XX 23-JUL-1998; 98US-0121339.
XX (GENP-) GEN-PROBE INC.
XX Harvey RC, Eastman PS;
XX
XX WPI: 2000-182730/16.
XX
XX Novel methods for preparing RNA from biological samples, used for the

CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC samples. The methods are useful in the human medical and veterinary
CC fields, for medical diagnoses and clinical monitoring of a patient's
CC response to therapy where a disease or medical condition is associated
CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associated with cancers,
CC particularly forms of leukemia.

XX Sequence 54 BP; 11 A; 11 C; 12 G; 20 T; 0 other;

Query Match 100.0%; Score 54; DB 21; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.8e-12;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAAATACGACTCTATAGGAGACCTGAGGCTCAAGTCA 54
DB 54 TAAATTAAATACGACTCTATAGGAGACCTGAGGCTCAAGTCA 1

RESULT 4

AAZ60843/C
ID AAZ60843 standard; RNA; 54 BP.

XX AAZ60843;

XX 16-MAY-2000 (first entry)

XX Oligonucleotide used to detect bcr b3-abl fusion transcripts.

XX Fusion transcript; translocation: bcr b3 region; abl gene;

XX amplification assay; detection assay; medical diagnosis;

XX clinical monitoring; chimeric RNA; fusion RNA; condition marker;

XX disease marker; cancer; leukemia; ss.

XX Synthetic.

XX WO200005418-A1.

XX 03-FEB-2000.

XX 23-JUL-1999; 99WO-US16832.

XX 23-JUL-1998; 98US-0121239.

XX (GENP-) GEN-PROBE INC.

XX Harvey RC, Eastman PS;

XX WPI; 2000-182730/16.

XX Novel methods for preparing RNA from biological samples, used for the
XX detection and measurement of nucleic acids and fusion nucleic acids

XX Claim 19; Page 40; 49pp; English.

CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation
CC between the bcr b3 region and the abl gene. The specification describes
CC a method for detecting a fusion nucleic acid (particularly chimeric RNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is
CC used for the simple and rapid preparation of RNA from a biological
CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC samples. The methods are useful in the human medical and veterinary
CC fields, for medical diagnoses and clinical monitoring of a patient's
CC response to therapy where a disease or medical condition is associated

CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associated with cancers,
CC particularly forms of leukemia.

XX Sequence 54 BP; 11 A; 11 C; 12 G; 20 T; 0 other;

Query Match 100.0%; Score 54; DB 21; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.8e-12;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAAATACGACTCTATAGGAGACCTGAGGCTCAAGTCA 54
DB 54 TAAATTAAATACGACTCTATAGGAGACCTGAGGCTCAAGTCA 1

RESULT 5

AAQ86626
ID AAQ86626 standard; DNA; 50 BP.

XX AAQ86626;

XX 15-NOV-1995 (first entry)

XX CML chromosomal translocation minus strand primer.

XX primer; autocatalytic; target; CML; translocation; ss.

XX Synthetic.

XX US5399491-A.

XX 21-MAR-1995.

XX 11-JUL-1989; 89US-0379501.

XX 11-JUL-1989; 89US-0379501.

XX 10-JUL-1990; 90US-050837.

XX 19-MAR-1992; 92US-0855732.

XX (GENP-) GEN-PROBE INC.

XX Fultz TJ, Kacian DL;

XX WPI; 1995-130686/17.

XX Amplification of nucleic acid targets - using a reverse
XX transcriptase with RNase H activity and a RNA polymerase at
XX constant temp.

XX Disclosure; Column 9; 58pp; English.

CC AAQ86626-28 are primers and a probe for the CML chromosomal;
CC translocation. They are used to produce autocatalytic
CC oligonucleotides which require no change in the experimental
CC conditions i.e. constant temperature, pH and ionic strength.
CC These sequences are useful in generating multiple copies of
CC specific nucleic acid target sequences.

XX Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;

Query Match 90.7%; Score 49; DB 16; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTAATACGACTCTATAGGAGACCTGAGGCTCAAGTCA 51
DB 2 AATTAATACGACTCTATAGGAGACCTGAGGCTCAAGTCA 50

RESULT 6

AA742417

49 9.0.2000

```

ID  AAT42417 standard; DNA: 50 BP.
XX
XX  AAT42417;
AC
XX  28-APR-1997 (first entry)
DT
XX  CML chromosomal translocation primer #1.
DE
XX  HIV; probe; primer; amplify; polymerase chain reaction; microorganism;
KM  BCL-2; PCR; hepatitis B virus; HBV; CML; ss.
XX
XX  Synthetic.
OS
XX  EP731175-A2.
PN
XX  11-SEP-1996.
PD
XX  10-JUL-1990; 90EP-0307503.
PF
XX  11-JUL-1989; 89US-0379501.
PR
XX  (GENP-) GEN-PROBE INC.
PA
XX  McDonough S;
PI
XX  WPI; 1996-403995/41.
DR
XX  Detection of HIV nucleic acids in samples - using new specific
PT  oligo-nucleotide(s) for the amplification and detection of target
PS  sequences.
XX  Disclosure; Page 8; 66pp; English.
XX
XX  AAT42417-T42419 represent primers and a probe for the CML chromosomal
CC  translocation t(9;22). These sequences can be used in modified versions
CC  of the kits of the invention. The kits of the invention, are for
CC  detecting the presence of HIV nucleic acid sequences in a sample. The
CC  kits comprise two amplification primers (such as AAT40182 and AAT40183),
CC  and a probe (such as AAT42404) for detection of the amplified sequence.
CC  By using these sequences, the amplification of HIV nucleic acid sequences
CC  is improved. The kits can also be used for the detection of other
CC  microorganisms, by using different probe sequences. Other sequences
CC  that can be detected using this method include those from HBV (using the
CC  sequences shown in AAT42410-T42412), and BCL-2 (using AAT42413-T42416).
CC  The samples can be clinical, environmental or forensic samples, and the
CC  method produces large amounts of the target sequence for a variety of
CC  uses. The method can also be used to produce multiple copies of a
CC  target sequence for use in cloning, and sequencing, and to produce probes
CC  for the target sequence.
XX
XX  Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;
XX
XX  Query Match 90.7%; Score 49; DB 17; Length 50;
XX  Best Local Similarity 100.0%; Pred. No. 2.9e-10;
XX  Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  3 AATTATACGACTACTATAGGAGACTCAGACCTCGAGCTCAAAAGTC 51
DB  2 AATTATACGACTACTATAGGAGACTCAGACCTCGAGCTCAAAAGTC 50
XX
XX
XX  RESULT 7
XX  AAT15571
XX  AAT15571 standard; DNA: 50 BP.
AC
XX  AAT15571;
XX
XX  17-JUL-1996 (first entry)
DT
XX  CML-2 chromosomal translocation major breakpoint t(9;22) (-) primer.
DE
XX  CML-2 chromosomal translocation major breakpoint; t(9;22); primer;
KM  auto-catalytic; synthesis; RNA target sequence; assay; detection;
XX

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XX  quantification; ss.
XX
XX  Synthetic.
OS
XX  US5480784-A.
PN
XX  02-JAN-1996.
PD
XX  11-JUL-1989; 89US-0379501.
PF
XX  10-JUL-1990; 90US-0550837.
PR  11-JUL-1989; 89US-0379501.
XX  (GENP-) GEN-PROBE INC.
PA
XX  Fultz TJ, Kacian DL;
PI
XX  WPI; 1996-068248/07.
DR
XX  Auto-catalytic synthesis of multiple copies of an RNA target
PT  sequence - uses cooperative action of a DNA and RNA polymerase in
PT  presence of RNase H, useful for detection of target sequence e.g. in
PS  clinical or environmental sample
XX  Example; Columns 9-10; 51pp; English.
XX
XX  The present sequence is a primer for the CML-2 chromosomal
CC  translocation major breakpoint t(9;22), which was used to
CC  demonstrate an improved method for synthesizing multiple copies of
CC  a RNA target sequence. The method comprises combining the target
CC  target, a promoter which hybridises to the 3'-terminal portion of the
CC  DNA primer extension prod., reverse transcriptase, RNase H and
CC  and/or quantitate specific target sequences in clinical
CC  and/or environmental or forensic samples. It also has the advantages of
CC  being autocatalytic, using the cooperative action of a DNA
CC  polymerase, e.g. a reverse transcriptase and avoids repetitive
CC  manipulations of reaction conditions, e.g. temp., ionic strength
CC  and pH.
XX
XX  Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;
XX
XX  Query Match 90.7%; Score 49; DB 17; Length 50;
XX  Best Local Similarity 100.0%; Pred. No. 2.9e-10;
XX  Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  3 AATTATACGACTACTATAGGAGACTCAGACCTCGAGCTCAAAAGTC 51
DB  2 AATTATACGACTACTATAGGAGACTCAGACCTCGAGCTCAAAAGTC 50
XX
XX
XX  RESULT 8
XX  AAV66349
XX  AAV66349 standard; DNA: 50 BP.
AC
XX  AAV66349;
XX
XX  06-JAN-1999 (first entry)
DT
XX  CML-2 chromosomal translocation t(9;22) primer.
DE
XX  CML-2 chromosomal translocation t(9;22); block splice template;
KM  autocatalytic RNA amplification; primer; ss.
XX
XX  Synthetic.
OS
XX  US5824518-A.
PN
XX  20-OCT-1998.
PD
XX  06-JUN-1995; 95US-0469067.
PF
XX

```


CC and the primers and probes of the invention are able to detect the
CC abnormal presence of mRNA expressed by their coding sequences in tissues
CC other than the prostate. This enables the presence of cancer to be
CC perceived and aids in the detection of metastases.

SO Sequence 52 BP; 18 A; 9 C; 12 G; 13 T; 0 other;

Query Match 59.3%; Score 32; DB 21; Length 52;
Best Local Similarity 79.2%; Pred. No. 0.0021;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 TAAATTAATAGCAGCTACTATAGGAGAGACCTGAGGCTCTCAA 48
1 TAAATTAATAGCAGCTACTATAGGAGAGACCTGCTTCAAGATGAAA 48

RESULT 11

AAA76067
ID AAA76067 standard; DNA; 54 BP.

AAA76067;

25-JAN-2001 (first entry)

Human prostate specific antigen PCR primer SEQ ID NO: 29.

Prostate specific antigen; PSA; prostate-specific membrane antigen; PSMA;
glandular kallikrein-2; hK2; prostate cancer; breast cancer; probe;
PCR primer; ss.

Homo sapiens.

W0200044940-A2.

03-AUG-2000.

28-JAN-2000; 2000WO-US022270.

28-JAN-1999; 99US-0117640.

(GENP-) GEN-PROBE INC.

Harvey RC, Clark TJ;

WPI; 2000-505986/45.

Detecting prostate-specific antigen (PSA), prostate specific membrane
antigen (PSMA) or human kallikrein 2 (hK2) nucleic acids in samples
using probe molecules, useful for the diagnosis of prostate and breast
cancers

Claim 1; Page 12; 77pp; English.

The present invention is concerned with the detection of nucleic acid
markers for prostate and breast cancer, and PCR primers and probes which
are able to detect and quantify these markers. Prostate specific antigen
(PSA), prostate-specific membrane antigen (PSMA) and glandular
kallikrein-2 (hK2) have all been linked to prostate and breast cancers,
and the primers and probes of the invention are able to detect the
abnormal presence of mRNA expressed by their coding sequences in tissues
other than the prostate. This enables the presence of cancer to be
perceived and aids in the detection of metastases.

Sequence 54 BP; 16 A; 13 C; 11 G; 14 T; 0 other;

Query Match 59.3%; Score 32; DB 21; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAATAGCAGCTACTATAGGAGAGACTCA 32
1 TAAATTAATAGCAGCTACTATAGGAGAGACTCA 32

RESULT 12

ABK53140
ID ABK53140 standard; DNA; 51 BP.

ABK53140;

12-AUG-2002 (first entry)

HIV-1 reverse transcriptase gene specific oligonucleotide primer #11.

HIV; human immunodeficiency virus; ss; primer; gag; pol;
protease; reverse transcriptase; infection; PCR.

Human immunodeficiency virus type 1.

US2002055095-A1.

09-MAY-2002.

31-AUG-2001; 2001US-0944036.

01-SEP-2000; 2000US-229790P.

(YANG/) YANG Y Y.

(BREN/) BRENTANO S T.

(BARO/) BAROLA O.

(TRAN/) TRAN N.

(VERN/) VERNET G.

Yang Y, Brentano ST, Barola O, Tran N, Vernet G;

WPI; 2002-462902/49.

Claim 1; Page 25; 37pp; English.

This invention relates to a series of nucleic acid oligomers for
amplifying and detecting a nucleotide sequence of human immunodeficiency
virus type 1 (HIV-1). The invention also comprises a labeled
oligonucleotide that specifically hybridises to an HIV-1 sequence
derived from gag or pol sequences, having one of the sequences fully
defined in the specification, and a method for detecting HIV-1 in a
biological sample, comprising mixing the sample with two or more of the
amplification oligomers that specifically amplify at least one HIV-1
target sequence within gag and a pol sequence which is a protease or
reverse transcriptase sequence, amplifying the target, and detecting the
diagnose HIV-1 infection. The oligonucleotides of the invention may be used to
primer used to amplify the HIV-1 reverse transcriptase gene in the HIV
detection method or the invention.

Sequence 51 BP; 17 A; 11 C; 8 G; 15 T; 0 other;

Query Match 58.9%; Score 31.8; DB 24; Length 51;
Best Local Similarity 76.5%; Pred. No. 0.0025;
Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2 AAATTAATAGCAGCTACTATAGGAGAGACTCAGACCTGAGGCTCAAGTCA 52
1 AAATTAATAGCAGCTACTATAGGAGAGACTCAGACCTGAGGCTCAAGTCA 51

RESULT 13

ABL45502
ID ABL45502 standard; DNA; 51 BP.

ABL45502;

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:00:32 ; Search time 82.3837 Seconds
(without alignments)
656.052 Million cell updates/sec

Title: US-09-121-239-5
Perfect score: 24
Sequence: 1 GACCACTGCTGTGTAACCTCA 24

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapept 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	24	100.0	24	16	AA086635	Modified non-prom
2	24	100.0	24	19	AAV66353	CML-2 chromosomal
3	24	100.0	24	20	AAV63985	bcf-abl sense prim
4	24	100.0	24	20	AAV63204	CML t(14; 18) non-
5	24	100.0	24	21	AAV60844	oligonucleotide us
6	24	100.0	24	21	AAV60845	oligonucleotide us
7	24	100.0	24	21	AAV60846	oligonucleotide us
8	24	100.0	24	21	AAV60847	oligonucleotide us
9	21	87.5	40	13	AA066789	L6 bcr exon 2/abl

10	20	83.3	20	14	AA051829	bcr mRNA ribozyme
11	19	79.2	47	18	AAV91751	primer BB232 for b
12	17	70.8	47	18	AAV91749	primer BB232 for b
13	16	66.7	22	24	AB092608	Human Leukemia ch
14	16	66.7	40	19	AAV58775	forward primer for
15	15	62.5	47	17	AAV03636	3SR primer 325. S
16	15	62.5	47	18	AAV91753	Human BB325 for b
17	15	62.5	51	21	AAV76855	Human clone G93940
18	14.6	60.8	51	22	AAV29108	Human SNP oligonuc
19	14.4	60.0	20	20	AAV97409	primer used to amp
20	14.4	60.0	60	24	AAV34009	Human spliced tran
21	14.4	60.0	60	24	AAV58313	Mouse spliced tran
22	14	58.3	33	17	AAV31737	Escherichia coli t
23	14	58.3	38	20	AAV84137	PCR primer for Ara
24	14	58.3	60	24	AAV33510	Human spliced tran
25	14	58.3	60	24	AAV36796	Human spliced tran
26	14	58.3	65	24	AAV53882	Mouse spliced tran
27	14	58.3	65	24	AAV54134	Human spliced tran
28	13.8	57.5	60	24	AAV33655	Human spliced tran
29	13.8	57.5	60	24	AAV44873	Downstream sequenc
30	13.8	57.5	76	13	AAV33613	Flaviviral hybrid
31	13.6	56.7	76	13	AAV33613	Rat galanin recept
32	13.6	56.7	46	24	AAV35843	Human ERG ambery
33	13.6	56.7	46	24	AAV35843	Human ERG ambery
34	13.6	56.7	48	24	AAV21959	Human spliced tran
35	13.6	56.7	51	22	AAV33807	Human spliced tran
36	13.6	56.7	60	24	AAV45501	Human spliced tran
37	13.6	56.7	60	24	AAV45501	Human spliced tran
38	13.6	56.7	65	24	AAV30666	Rat spliced transc
39	13.6	56.7	69	21	AAV14815	DNA encoding a wil
40	13.4	55.8	32	18	AAV88367	Primer for chicken
41	13.4	55.8	51	21	AAV76854	Human clone G93940
42	13.4	55.8	60	24	AAV58935	Human spliced tran
43	13.4	55.8	80	20	AAV30013	Oligonucleotide IF
44	13.4	55.8	80	20	AAV30014	Oligonucleotide IF
45	13.4	55.8	80	20	AAV35329	Oligonucleotide us

ALIGNMENTS

RESULT 1
AA086635 standard; DNA; 24 BP.
AA086635:
16-NOV-1995 (first entry)
Modified non-promoter primer for the CML major breakpoint region.
Primer: autocatalytic; PCR; target; sequence; ss.
Synthetic.
US5399491-A.
21-MAR-1995.
11-JUL-1989; 89US-0379501.
11-JUL-1989; 89US-0379501.
10-JUL-1990; 90US-0550837.
19-MAR-1992; 92US-0855732.
(GENP-) GEN-PROBE INC.
Fultz TJ, Kactan DL;
WPI: 1995-130686/17.
Amplification of nucleic acid targets - using a Reverse
transcriptase with RNase H activity and a RNA polymerase at

PT constant temp.
 XX
 PS Example 18; Column 47; 58pp; English.
 CC
 CC The oligonucleotide AA086635 is a non-promoter primer for the CML
 CC major breakpoint amplification region. It is used to illustrate
 CC that small changes in the NA sequence result in large changes in
 CC the amplification efficiency. AA086635 is capable of serving as a
 CC primer for the synthesis of autocatalytic oligonucleotides which
 CC require no change in the PCR conditions i.e. constant temperature,
 CC pH and ionic strength. This sequence is useful in generating
 CC multiple copies of specific nucleic acid target sequences.
 SQ Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 other;
 QY
 Query Match 100.0%; Score 24; DB 16; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 GACCAACTGCTGTGGAACCTCA 24
 1 GACCAACTGCTGTGGAACCTCA 24
 RESULT 2
 AA066353
 ID AA066353 standard; DNA; 24 BP.
 XX
 AC AA066353;
 XX
 DT 06-JAN-1999 (first entry)
 DE CML-2 chromosomal translocation major breakpoint non-promoter primer.
 XX
 KM CML-2 chromosomal translocation t(14;18) major breakpoint;
 KM block splice template; autocatalytic RNA amplification; primer; ss.
 XX
 OS Synthetic.
 XX
 PN US5824518-A.
 PD 20-OCT-1998.
 XX
 PF 06-JUN-1995; 95US-0469067.
 XX
 PR 10-JUL-1990; 90US-0550837.
 PR 11-JUL-1989; 89US-0379501.
 PR 06-JUN-1995; 95US-0469067.
 XX
 XX (GENP-) GEN-PROBE INC.
 XX
 PI Pultz TJ, Kacian DL;
 XX
 DR WPI; 1998-582557/49.
 XX
 PT Block splice template useful for amplification of nucleic acids -
 PT comprises two nucleic acid regions, the first region located 3' of
 PT the second region and blocked at its 3' terminus to inhibit primer
 PT extension by a DNA polymerase
 XX
 PS Example 18; Column 43; 51pp; English.
 XX
 CC AA066352-55 represent CML-2 chromosomal translocation t(14;18) major
 CC breakpoint amplification region non-promoter primers. The primers
 CC are used to exemplify the invention. The specification describes
 CC methods of synthesizing multiple copies of a target nucleic acid
 CC sequence autocatalytically under conditions of substantially
 CC constant temperature, ionic strength and pH are provided in which
 CC multiple RNA copies of the target sequence autocatalytically
 CC generate additional copies. The target sequence is a block splice
 CC template which comprises two nucleic acid regions. The first region is
 CC located 3' of the second region and is blocked at its 3' terminus to
 CC inhibit primer extension by a DNA polymerase, and the second region

CC comprises a promoter sequence recognised by an RNA polymerase. The
 CC methods are used to amplify nucleic acids, especially RNA, for
 CC analysis, cloning or probe production.
 CC
 SQ Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 other;
 QY
 Query Match 100.0%; Score 24; DB 19; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 GACCAACTGCTGTGGAACCTCA 24
 1 GACCAACTGCTGTGGAACCTCA 24
 RESULT 3
 AA083985
 ID AA083985 standard; DNA; 24 BP.
 XX
 AC AA083985;
 XX
 DT 08-SEP-1999 (first entry)
 DE bcr-abl sense primer.
 XX
 KM Reverse transcription PCR: oligonucleotide-immobilised microplate;
 KM polypropylene; thermal cycle; solid phase; cell lysate; research;
 KM gene expression analysis; diagnostic; drug screening; primer; ss.
 XX
 OS Synthetic.
 XX
 PN W09932654-A1.
 PD 01-JUL-1999.
 XX
 PF 22-DEC-1998; 98WO-US27293.
 XX
 PR 16-JAN-1998; 98US-0071627.
 PR 22-DEC-1997; 97US-0068394.
 XX
 PA (HITB) HITACHI CHEM CO LTD.
 PA (HITB) HITACHI CHEM RES CENT INC.
 XX
 PI Mitsuhashi M;
 XX
 DR WPI; 1999-418942/35.
 XX
 PT Using oligonucleotide-immobilized microplates in polymerase chain
 PT reactions
 XX
 PS Example; Page 9; 34pp; English.
 XX
 CC The present invention describes the use of oligonucleotide-immobilized
 CC microplates having heat-stability for thermal cycles of reverse
 CC transcription-polymerase chain reaction (RT-PCR). The method of RT-PCR
 CC comprises: (a) preparing cell lysate of a target cell; (b) transferring
 CC the cell lysate to an oligonucleotide-immobilized microplate having
 CC wells to which oligonucleotides are securely immobilized, the microplate
 CC having heat-stability for thermal cycles of PCR, the oligonucleotides
 CC having nucleic acid sequences specifically complementary to mRNA of
 CC interest present in the cell lysate; (c) capturing mRNA by the
 CC oligonucleotides of the microplate; (d) conducting RT-PCR on the same
 CC microplate, using an appropriate buffer; and (e) detecting PCR products
 CC of interest. The method is used for gene expression analysis. The
 CC multiple PCR system is useful in basic research, diagnostics and drug
 CC screening, with potential application to future automation. The method
 CC simplifies the process of RT-PCR. cDNA synthesized from mRNA captured by
 CC immobilized oligonucleotide on the PCR microplates can be used more than
 CC once, thus amplifying several times different or same portions of the
 CC cDNA by using appropriate primers. The method also drastically
 CC simplifies the preparation of cell lysate and significantly stabilizes
 CC the yield of recovered cytosolic RNA. The present sequence represents a
 CC primer used in an example from the present invention.

```

XX Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 other;
SQ
Query Match      100.0%; Score 24; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACCAACTGCTGTGGAACCTCCA 24
   |||
DB 1 GACCAACTGCTGTGGAACCTCCA 24

RESULT 4
AAZ3204
ID AAZ3204 standard; DNA; 24 BP.
AC AAZ3204;
XX
XX 11-JUN-1999 (first entry)
DT
XX CML t(14; 18) non-promoter primer #2.
XX
XX Autocatalytic amplification; transcription-based amplification; CML;
XX thermal cycling; diagnostic; environmental testing; probe; detection;
XX genetic disease; infectious disease; microorganism; food; forensic;
XX paternity; primer; ss.
XX
XX Synthetic.
XX
XX US588779-A.
XX
XX 30-MAR-1999.
XX
XX 05-JUN-1995; 950S-0461654.
XX
XX 10-JUL-1990; 90US-0550837.
XX
XX 11-JUL-1989; 89US-0379501.
XX
XX 05-JUN-1995; 95US-0461654.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Fultz TJ, Kacian DL;
XX
XX WPI; 1999-253231/21.
XX
XX Kit for autocatalytic amplification of RNA targets
XX
XX Example 18; Column 43; 51pp; English.
XX
XX This invention describes a novel method for the autocatalytic
XX amplification of an RNA target in a transcription-based amplification
XX system without thermal cycling. The method generates oligonucleotides for
XX diagnostic or environmental testing, for use e.g., as probes and in
XX cloning. Typical applications are the detection of genetic or infectious
XX diseases, the monitoring of responses to therapy, the quantitation or
XX detection of microorganisms in foods, forensic studies and the
XX establishment of paternity. Kits containing the products of the invention
XX provide many copies of selected RNA targets under conditions of constant
XX temperature, ionic strength and pH. Specific amplification of RNA targets
XX increases sensitivity, convenience, accuracy and the reliability of
XX assays.
XX
XX Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 other;
SQ
Query Match      100.0%; Score 24; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACCAACTGCTGTGGAACCTCCA 24
   |||
DB 1 GACCAACTGCTGTGGAACCTCCA 24

RESULT 5
AAZ60844
ID AAZ60844 standard; DNA; 24 BP.
AC AAZ60844;
XX
XX 16-MAY-2000 (first entry)
DT
XX
XX Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX
XX DE Fusion transcript; translocation; bcr b3 region; abl gene;
XX
XX KW amplification assay; detection assay; medical diagnosis;
XX
XX KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX
XX KW disease marker; cancer; leukemia; ss.
XX
XX Synthetic.
XX
XX WO200005418-A1.
XX
XX 03-FEB-2000.
XX
XX 23-JUL-1999; 99WO-US16832.
XX
XX 23-JUL-1998; 98US-0121239.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Harvey RC, Eastman PS;
XX
XX WPI; 2000-182730/16.
XX
XX Novel methods for preparing RNA from biological samples, used for the
XX detection and measurement of nucleic acids and fusion nucleic acids
XX
XX Claim 19; Page 40; 49pp; English.
XX
XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
XX the invention to detect fusion transcripts produced from a translocation
XX between the bcr b3 region and the abl gene. The specification describes
XX a method for detecting a fusion nucleic acid (particularly chimeric mRNA
XX species), in a biological sample. The method comprises contacting a
XX sample of fusion nucleic acid with primers, amplifying the hybridized
XX fusion nucleic acid, and detecting the target hybrid. The method is
XX used for the simple and rapid preparation of RNA from a biological
XX sample, particularly from the cytoplasm of eukaryotic cells, which is
XX suitable for use in an amplification and detection assay. The methods
XX are used for the analysis and detection of nucleic acids in biological
XX samples. The methods are useful in the human medical and veterinary
XX fields, for medical diagnoses and clinical monitoring of a patient's
XX response to therapy where a disease or medical condition is associated
XX with a particular type and/or level of mRNA present in the sample. The
XX methods are also useful for detecting or quantifying fusion or chimeric
XX RNA species, and for detecting a translocation as a marker for a given
XX condition or disease, e.g. translocations associate with cancers,
XX particularly forms of leukemia.
XX
XX Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 other;
SQ
Query Match      100.0%; Score 24; DB 21; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACCAACTGCTGTGGAACCTCCA 24
   |||
DB 1 GACCAACTGCTGTGGAACCTCCA 24

RESULT 6
AAZ60845
ID AAZ60845 standard; RNA; 24 BP.
AC AAZ60845;
XX
XX
XX

```

DT	16-MAY-2000	(first entry)
xx	Oligonucleotide used to detect bcr b3-abl fusion transcripts.	
DE	Fusion transcript; translocation; bcr b3 region; abl gene;	
KW	amplification assay; detection assay; medical diagnosis;	
KM	clinical monitoring; chimeric RNA; fusion RNA; condition marker;	
KW	disease marker; cancer; leukemia; ss.	
xx	Synthetic.	
OS	WO200005418-A1.	
PN	03-FEB-2000.	
xx	23-JUL-1999; 99WO-US16832.	
PF	23-JUL-1998; 98US-0121239.	
PR	(GENP-) GEN-PROBE INC.	
xx	Harvey RC, Eastman PS;	
PA	WPI; 2000-182730/16.	
xx	Novel methods for preparing RNA from biological samples, used for the	
PT	detection and measurement of nucleic acids and fusion nucleic acids -	
xx	Claim 19; Page 40; 49pp; English.	
PS	Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of	
xx	the invention to detect fusion transcripts produced from a translocation	
CC	between the bcr b3 region and the abl gene. The specification describes	
CC	a method for detecting a fusion nucleic acid (particularly chimeric mRNA	
CC	species), in a biological sample. The method comprises contacting a	
CC	sample of fusion nucleic acid with primers, amplifying the hybridized	
CC	fusion nucleic acid, and detecting the target hybrid. The method is	
CC	used for the simple and rapid preparation of RNA from a biological	
CC	sample, particularly from the cytoplasm of eukaryotic cells, which is	
CC	suitable for use in an amplification and detection assay. The methods	
CC	are used for the analysis and detection of nucleic acids in biological	
CC	samples. The methods are useful in the human medical and veterinary	
CC	fields, for medical diagnoses and clinical monitoring of a patient's	
CC	response to therapy where a disease or medical condition is associated	
CC	with a particular type and/or level of mRNA present in the sample. The	
CC	methods are also useful for detecting or quantifying fusion or chimeric	
CC	RNA species, and for detecting a translocation as a marker for a given	
CC	condition or disease, e.g. translocations associate with cancers,	
CC	particularly forms of leukemia.	
xx	Sequence 24 BP; 7 A; 7 C; 5 G; 5 U; 0 other;	
QY	Query Match 100.0%; Score 24; DB 21; Length 24;	
Db	Best Local Similarity 79.2%; Pred. No. 0.022; Mismatches 0; Indels 0; Gaps 0	
Matches	19; Conservative 5; Mismatches 0; Indels 0; Gaps 0	
1	GACCAACTGCTGTGTTAAACTCA 24	
	T T T T T T	
1	GACCACUCUGUGUGAACAUCUCA 24	
RESULT 7	AAZ60846/c	
ID	AAZ60846 standard; DNA; 24 BP.	
AC	AAZ60846;	
xx	16-MAY-2000 (first entry)	
DE	Oligonucleotide used to detect bcr b3-abl fusion transcripts.	
KW	Fusion transcript; translocation; bcr b3 region; abl gene;	
KM	amplification assay; detection assay; medical diagnosis;	

[illegible]

XX 03-FEB-2000.
 PD 23-JUL-1999; 99WO-US16832.
 XX 23-JUL-1998; 98US-0121239.
 PR (GENE-) GEN-PROBE INC.
 PA Harvey KC, Eastman PS;
 PI WPI; 2000-182730/16.
 DR Novel methods for preparing RNA from biological samples, used for the
 XX detection and measurement of nucleic acids and fusion nucleic acids -
 XX Claim 19, Page 41; 49pp; English.
 CC Oligonucleotides AA260840-62 and AA260865-66 are used in the method of
 CC the invention to detect fusion transcripts produced from a translocation
 CC between the bcr b3 region and the abl gene. The specification describes
 CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
 CC species), in a biological sample. The method comprises contacting a
 CC sample of fusion nucleic acid with primers, amplifying the hybridized
 CC fusion nucleic acid, and detecting the target hybrid. The method is
 CC used for the simple and rapid preparation of RNA from a biological
 CC sample, particularly from the cytoplasm of eukaryotic cells, which is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC samples. The methods are useful in the human medical and veterinary
 CC fields, for medical diagnoses and clinical monitoring of a patient's
 CC response to therapy where a disease or medical condition is associated
 CC with a particular type and/or level of mRNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associated with cancers,
 CC particularly forms of leukemia.
 SO Sequence 24 BP; 5 A; 5 C; 7 G; 7 U; 0 other;
 Query Match 100.0%; Score 24; DB 21; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.022; 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GACCACTCGTGTGTAACCTCA 24
 DB 24 GACCACTCGTGTGTAACCTCA 1
 RESULT 9
 AA066789
 ID AA066789 standard; RNA; 40 BP.
 AC AA066789;
 AC 10-FEB-1995 (first entry)
 DT L6 bcr exon 2/abl exon 2 cloning 5' primer.
 XX DE
 XX L6 bcr exon 2/abl exon 2 cloning 5' primer.
 XX FUSION mRNA; L6; hematopoietic cells; chronic myelogenous leukaemia;
 KW CML; acute lymphocytic leukaemia; ALL; exon 2; abl; bcr; exon 3; K28;
 KW translocation; chromosome 9; chromosome 22; tyrosine kinase; cleavage;
 KW ribozymes; nucleation; anchor sequence; follicular lymphomas; ss.
 XX OS Synthetic.
 XX PN WO9413793-A.
 XX PD 23-JUN-1994.
 XX PF 16-NOV-1993; 93WO-US11144.
 XX PR 04-DEC-1992; 92US-0989652.

XX (APOL-) APOLLON INC.
 PA Coney LR, Oakes FT, Pachuk CJ;
 PI WPI; 1994-217873/26.
 DR Ribozymes comprising catalytic sequence, two legs and anchor
 XX sequence(s) complementary to substrate mRNA - is used for treatment
 XX of chronic myelogenous leukaemia and acute lymphoblastic leukaemia
 XX Disclosure; Page 26; 67pp; English.
 CC The sequences given in AA066789-95 are primers which were used in the
 CC cloning of fragments of the L6 and K28 fusion mRNAs. These mRNAs are
 CC expressed by some of the hematopoietic cells of some chronic myelogenous
 CC leukemia (CML) and acute lymphocytic leukaemia (ALL) patients. In the
 CC L6-mRNA, abl exon 2 is linked to bcr exon 2, and in K28 abl exon 2 is
 CC linked to bcr exon 3. This is caused by a translocation between
 CC chromosomes 9 and 22. The L6 and K28 mRNAs encode a protein with
 CC aberrant tyrosine kinase activity which is unique to CML cells and which
 CC is thought to play a key role in the establishment of CML. The
 CC ribozymes of the invention are specifically targeted to the L6 and K28
 CC mRNAs. Non-contiguous regions of the substrate RNA can be utilised for
 CC the separate events of ribozyme nucleation and ribozyme cleavage. The
 CC ribozymes are targeted to the L6 bcr-abl RNA via an anchor sequence
 CC which is proximal to the bcr-abl junction. Cleavage by these ribozymes
 CC occurs at a downstream site located within an abl specific sequence in
 CC the fusion mRNA. Normal abl and bcr substrates are not cleaved.
 CC Ribozymes such as these are useful in treating diseases involving
 CC translocations eg. CML, ALL and follicular lymphomas. See also
 CC AA066774-96.
 SO Sequence 40 BP; 12 A; 7 C; 9 G; 12 T; 0 other;
 Query Match 87.5%; Score 21; DB 15; Length 40;
 Best Local Similarity 100.0%; Pred. No. 0.72;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 4 CAACCTCGTGTGTAACCTCA 24
 DB 20 CAACCTCGTGTGTAACCTCA 40
 RESULT 10
 AA051829
 ID AA051829 standard; RNA; 20 BP.
 AC AA051829;
 AC 26-MAY-1994 (first entry)
 DT bcr mRNA ribozyme cleavable nucleotide 3245.
 XX DE
 XX Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
 KW resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
 KW actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
 KW adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
 KW human; chronic myelogenous leukemia; CML; follicular lymphoma;
 KW B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
 KW neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
 KW halpin; hepatitis delta virus; group I intron; RNaseP; ss.
 XX OS Homo sapiens.
 XX PN WO9323057-A.
 XX PD 25-NOV-1993.
 XX PF 13-MAY-1993; 93WO-US04573.
 XX PR 14-MAY-1992; 92US-0882822.
 XX PR 14-MAY-1992; 92US-0882865.

PR 26-AUG-1992; 92US-0936110.
 PR 26-AUG-1992; 92US-0936421.
 PR 26-AUG-1992; 92US-0936422.
 PR 26-AUG-1992; 92US-0936531.
 PR 26-AUG-1992; 92US-0936532.
 PR 07-DEC-1992; 92US-0987131.
 PR 19-JAN-1993; 93US-0006122.
 PR 19-JAN-1993; 93US-0008910.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Draper KG, Thompson JD;
 XX
 DR WPI; 1993-386203/48.
 XX
 PT New enzymatic RNA molecules (ribozymes) - which cleave mRNA
 PT associated with tumours or mRNA expressed from gene encoding
 PT multiple drug resistance
 XX
 PS Claim 3; Fig 3; 69pp; English.

CC The sequences given in AA051825-2266 represent areas of mRNAs
 CC associated with development or maintenance of chronic myelogenous
 CC leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or
 CC acute lymphocytic leukemia, follicular lymphoma, B-cell acute
 CC lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma
 CC and lung cancer. The full length mRNAs containing these target
 CC sequences, encode aberrant cellular proteins which are able to control
 CC cellular proliferation and are directly linked to a leukemic
 CC phenotype. These target sequences are identified by the ribozyme of
 CC the invention. The ribozymes is formed in a hammerhead motif, but may
 CC also be formed in the motif of a hairpin, hepatitis delta virus, group
 CC I intron or RNaseP-like RNA. These ribozymes may be used to inhibit
 CC the development or expression of a transformed phenotype in man and
 CC other animals by modulating expression of the corresponding gene.
 CC Cleavage of target mRNAs expressed in pre-neoplastic and transformed
 CC cells elicits inhibition of the transformed state. Multiple drug
 CC resistance (mdr-1) mRNA specific ribozymes remove the mechanism of
 CC drug resistance used by transformed cells and thus enhances drug
 CC therapies for tumours. The ribozymes may also be used to study
 CC genetic drift and mutations within cells.
 XX
 SQ Sequence 20 BP; 5 A; 6 C; 4 G; 5 U; 0 other;

Query Match 83.3%; Score 20; DB 14; Length 20;
 Best Local Similarity 75.0%; Pred. No. 2;
 Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 4 CAACCTGCTGTGAACTCC 23
 DB 1 CAACUCGUGUGAACAUC 20

RESULT 11

AAT91751
 ID AAT91751 standard; DNA; 47 BP.

AC AAT91751;

DT 08-JAN-1998 (first entry)

DE Primer BB326 for bcr2-ab12 and bcr3-ab12 translocation regions.

XX PCR; primer; amplify; polymerase chain reaction; haematopoietic cell;
 KW chronic myelogenous leukaemia; human; bcr2-ab12; translocation region;
 KW cytogenetic remission; ph chromosome; bcr3-ab12; CML cell;
 KW acute lymphotrophic leukaemia; ss.
 XX
 OS Synthetic.

XX W09708339-A1.
 PN
 XX
 PD 06-MAR-1997.

XX 28-AUG-1995; 95WO-US10919.
 PE
 XX 25-AUG-1995; 95US-0296258.
 PR
 XX (DADE-) DADE INT INC.
 PA
 XX Brown J, Lockhart-bruce C;
 PI
 DR WPI; 1997-179294/16.
 XX
 PT Detection of chronic myelogenous leukemia cells - by amplification
 PT of RNA from haematopoietic cells with primers for the bcr2-ab12 and
 PT bcr3-ab12 trans-location regions
 XX
 PS Claim 3; Page 11; 79pp; English.

CC AAT91749-T91763, and AAT91765-T91792 are primers used in the method of
 CC the invention. AAT91754-T91759 can also be used as capture
 CC oligonucleotides (ON), while AAT91760-T91763, AAT91791 and AAT91792 can
 CC also be used as detector agents. The method of the invention is for
 CC detecting or monitoring chronic myelogenous leukaemia (CML) cells in a
 CC human patient. The method comprises obtaining RNA from haematopoietic
 CC cells of the patient, and amplifying it using a pair of primers that
 CC amplify both the bcr2-ab12 and bcr3-ab12 translocation regions. The
 CC amplified sequence is contacted with a capture agent comprising a capture
 CC ON and a binding ligand to form a capture mixture. The capture ON is
 CC specific for the bcr2-ab12 and bcr3-ab12 translocation regions. The
 CC mixture is contacted with a solid phase coupled to a receptor specific
 CC for the binding ligand. The solid phase is washed, then contacted with a
 CC detector agent comprising a detector ON specific for the bcr2-ab12 or
 CC bcr3-ab12 translocation regions and a label. The amount of labelled
 CC detector ON bound to the solid phase is then correlated with the presence
 CC or quantity of CML cells in the patient. The method is to detect or
 CC monitor CML cells in patients. It can also be used prognostically to
 CC assess cytogenetic remission in patients with CML. The method detects
 CC both the bcr2-ab12 and the bcr3-ab12 translocations associated with CML.
 CC The assay does not detect CML in the absence of the ph chromosome, nor
 CC does it detect acute lymphotrophic leukaemia (ALL) even if the ALL
 CC patient has the ph chromosome.

SQ Sequence 47 BP; 16 A; 9 C; 10 G; 12 T; 0 other;

Query Match 79.2%; Score 19; DB 18; Length 47;
 Best Local Similarity 100.0%; Pred. No. 7.2;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GACCAACTGCTGTGAAA 19
 DB 29 GACCAACTGCTGTGAAA 47

RESULT 12

AAT91749
 ID AAT91749 standard; DNA; 47 BP.

AC AAT91749;

DT 08-JAN-1998 (first entry)

DE Primer BB332 for bcr2-ab12 and bcr3-ab12 translocation regions.

XX PCR; primer; amplify; polymerase chain reaction; haematopoietic cell;
 KW chronic myelogenous leukaemia; human; bcr2-ab12; translocation region;
 KW cytogenetic remission; ph chromosome; bcr3-ab12; CML cell;
 KW acute lymphotrophic leukaemia; ss.
 XX
 OS Synthetic.

XX W09708339-A1.
 PN
 XX
 PD 06-MAR-1997.

PR 28-AUG-1995; 95MO-US10919.
 XX
 ER 25-AUG-1995; 95US-0296258.
 XX
 PA (DADE-) DADE INT INC.
 XX
 PI Brown J, Lockhart-bruce C;
 XX WPI: 1997-179294/16.
 DR
 XX
 PT Detection of chronic myelogenous leukaemia cells - by amplification
 PT of RNA from haematopoietic cells with primers for the bcr2-abl2 and
 PT bcr3-abl2 trans-location regions
 PS Claim 3; Page 11; 79pp; English.
 XX
 XX AAT91749-T91763, and AAT91765-T91792 are primers used in the method of
 CC the invention AAT91754-T91759 can also be used as capture
 CC oligonucleotides (ON), while AAT91760-T91763, AAT91791 and AAT91792 can
 CC also be used as detector agents. The method of the invention is for
 CC detecting or monitoring chronic myelogenous leukaemia (CML) cells in a
 CC human patient. The method comprises obtaining RNA from haematopoietic
 CC cells of the patient, and amplifying it using a pair of primers that
 CC amplify both the bcr2-abl2 and bcr3-abl2 translocation regions. The
 CC ON and a binding ligand to form a capture mixture. The capture ON is
 CC specific for the bcr2-abl2 and bcr3-abl2 translocation regions. The
 CC mixture is contacted with a solid phase coupled to a receptor specific
 CC for the binding ligand. The solid phase is washed, then contacted with a
 CC detector agent comprising a detector ON specific for the bcr2-abl2 or
 CC bcr3-abl2 translocation regions and a label. The amount of labelled
 CC detector ON bound to the solid phase is then correlated with the presence
 CC or quantity of CML cells in the patient. The method is to detect or
 CC monitor CML cells in patients. It can also be used prognostically to
 CC assess cytogenetic remission in patients with CML. The method detects
 CC both the bcr2-abl2 and the bcr3-abl2 translocations associated with CML.
 CC The assay does not detect CML in the absence of the Ph chromosome, nor
 CC does it detect acute lymphoblastic leukaemia (ALL) even if the ALL
 CC patient has the Ph chromosome.
 XX
 SO Sequence 47 BP; 15 A; 9 C; 10 G; 13 T; 0 other;
 Query Match 70.8%; Score 17; DB 18; Length 47;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GACCAACTCGTGTGTA 17
 DB 31 GACCAACTCGTGTGTA 47
 RESULT 13
 ABQ92608
 ID ABQ92608 standard; DNA; 22 BP.
 XX
 AC ABQ92608;
 XX
 DT 08-OCT-2002 (first entry)
 XX
 DE Human leukaemia chimera gene Major bcr/abl forward PCR primer.
 XX
 KW Human: PCR: primer; ss; leukaemia; Major-bcr/abl; minor-bcr/abl;
 KM PML/RARalpha; AML1/MTG8; Micro-bcr/abl; TEL/MML1; E2A/PBX1; MLL/AF4;
 KN CBFBeta/MYH11; MLL/AF9; WTI; GAPDH.
 XX
 OS Homo sapiens.
 XX
 PN JP002136300-A.
 XX
 PD 14-MAY-2002.
 XX
 PE 12-DEC-2000; 2000JP-0377325.
 XX

PR 25-AUG-2000; 2000JP-0255570.
 XX
 PA (SAKA) OTSUKA PHARM CO LTD.
 XX
 DR WPI: 2002-532069/57.
 XX
 PT A method for detection of leukemia chimera genes of Major-bcr/abl,
 PT minor-bcr/abl, PML/RARalpha and AML1/MTG8 with their specific primer
 PT sets and probes for the diagnosis
 PS Example 1; Page 9; 20pp; Japanese.
 XX
 XX The invention relates to a novel screening and diagnostic system for
 CC detection of leukaemia chimera genes. Included in the disclosure is a
 CC polymerase chain reaction (PCR) method for real time detection of
 CC leukaemia chimera genes of Major-bcr/abl, minor-bcr/abl, PML/RARalpha and
 CC AML1/MTG8 with their specific primer sets and probes so as to
 CC simultaneously give PCR amplified product including regions capable of
 CC detection of the genes. The sequences shown in ABQ92608-ABQ92652
 CC represent the primer sets and probes used in the invention.
 XX
 SO Sequence 22 BP; 4 A; 5 C; 7 G; 6 T; 0 other;
 Query Match 66.7%; Score 16; DB 24; Length 22;
 Best Local Similarity 100.0%; Pred. No. 24+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GACCAACTCGTGTGTG 16
 DB 7 GACCAACTCGTGTGTG 22
 RESULT 14
 AAV58775
 ID AAV58775 standard; DNA; 40 BP.
 XX
 AC AAV58775;
 XX
 DT 10-DEC-1998 (first entry)
 XX
 DE Forward primer for BCR/ABL type chimera mRNA.
 XX
 KW PCR primer: BCR/ABL type chimera; chimera detection; Major-bcr;
 KW nucleic acid strand based amplification; NASBA method; ss.
 XX
 OS Synthetic.
 XX
 PN JP10229899-A.
 XX
 PD 02-SEP-1998.
 XX
 PE 21-FEB-1997; 97JP-0054092.
 XX
 PR 21-FEB-1997; 97JP-0054092.
 XX
 PA (SRLS-) SRL KK.
 PA (TOYO) TOYOBO KK.
 XX
 DR WPI: 1998-524294/45.
 XX
 PT Forward side primer and reverse side primer - used for detection of
 PT BCR/ABL type chimera mRNA easily with high sensitivity
 PS Claim 1; Page 6; 8pp; Japanese.
 XX
 XX This sequence represents a primer of the invention used for the detection
 CC of a BCR/ABL type chimera mRNA with a cleavage point in Major-bcr by a
 CC nucleic acid strand based amplification (NASBA) method. The primers can
 CC be used to detect BCR/ABL type chimera mRNA easily with high sensitivity.
 XX
 SO Sequence 40 BP; 9 A; 13 C; 9 G; 9 T; 0 other;
 Query Match 66.7%; Score 16; DB 19; Length 40;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 CGTGTGTAAGTCCA 24
| | | | | | | | | |
DB 1 CGTGTGTAAGTCCA 16

RESULT 15

AAT03636
ID AAT03636 standard; DNA; 47 BP.

XX
AC AAT03636;

DT 02-SEP-1996 (first entry)

XX
DE 3SR primer 325.

XX Self-sustained sequence replication; 3SR; primer; amplification;
KW K562 cell; RNA purification; DNA purification;
KV chronic myelogenous leukaemia; ss.

XX
OS Synthetic.

XX
PN WO9600228-A1.

XX
PD 04-JAN-1996.

XX
PF 23-JUN-1995; 95WO-US07940.

XX
PR 23-JUN-1994; 94US-0264556.

XX
PA (DADE-) DADE INT INC.

XX
PI Brown JT;

XX
DR WPI; 1996-068821/07.

XX
PT Isolating intact nucleic acid from biological samples - using a
PT lysing buffer contg. an ionic detergent, ppty. protein and then
PT ppty. and sepg. nucleic acid

XX
PS Example 3; Page 18; 46pp; English.

XX
CC Primers 325 (AAT03636) and 329 (AAT03637) were used for the 3SR
CC amplification of RNA from K562 cells obtd. from a chronic
CC myelogenous leukaemia (CML) patient. The RNA was obtd. using a
CC novel rapid isolation method that involved use of a lysing buffer
CC contg. ionic detergent, ppty. protein, and then ppty. and sepg.
CC the RNA. A probe (AAT03638) complementary to the junction sequence
CC of the bcr2-abl2 translocation characteristic of CML was used to
CC detect 3SR products, demonstrating that the isolated RNA was a
CC suitable template for 3SR amplification.

XX
SQ Sequence 47 BP; 15 A; 9 C; 10 G; 13 T; 0 other;

Query Match 62.5%; Score 15; DB 17; Length 47;

Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GACCAACTGCTGTGT 15
| | | | | | | | | |
DB 33 GACCAACTGCTGTGT 47

Search completed: December 21, 2002, 11:54:31
Job time : 86.3837 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:00:32 ; Search time 85.8163 Seconds
(without alignments) 656.052 Million cell updates/sec

Title: US-09-121-239-9

Perfect score: 25
Sequence: 1 GACGTCCACAGCATTCCTGACAC 25

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /SID2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SID2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SID2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
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24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	25	100.0	25	AAZ60848
2	25	100.0	25	AAZ60849
3	25	100.0	25	AAZ60850
4	25	100.0	25	AAZ60851
5	25	100.0	25	AAZ60852
6	25	100.0	25	AAZ60853
7	25	100.0	25	AAZ60854
8	25	100.0	25	AAZ60855
9	25	100.0	25	AAZ60856

C	10	18.8	75.2	39	20	AAZ60848
C	11	18.8	72.0	22	14	AAZ60849
C	12	18.8	72.0	22	14	AAZ60850
C	13	18.8	72.0	22	14	AAZ60851
C	14	18.8	72.0	22	14	AAZ60852
C	15	18.8	72.0	22	14	AAZ60853
C	16	18.8	72.0	22	14	AAZ60854
C	17	18.8	72.0	22	14	AAZ60855
C	18	18.8	72.0	22	14	AAZ60856
C	19	18.8	72.0	22	14	AAZ60857
C	20	18.8	72.0	22	14	AAZ60858
C	21	18.8	72.0	22	14	AAZ60859
C	22	18.8	72.0	22	14	AAZ60860
C	23	18.8	72.0	22	14	AAZ60861
C	24	18.8	72.0	22	14	AAZ60862
C	25	18.8	72.0	22	14	AAZ60863
C	26	18.8	72.0	22	14	AAZ60864
C	27	18.8	72.0	22	14	AAZ60865
C	28	18.8	72.0	22	14	AAZ60866
C	29	18.8	72.0	22	14	AAZ60867
C	30	18.8	72.0	22	14	AAZ60868
C	31	18.8	72.0	22	14	AAZ60869
C	32	18.8	72.0	22	14	AAZ60870
C	33	18.8	72.0	22	14	AAZ60871
C	34	18.8	72.0	22	14	AAZ60872
C	35	18.8	72.0	22	14	AAZ60873
C	36	18.8	72.0	22	14	AAZ60874
C	37	18.8	72.0	22	14	AAZ60875
C	38	18.8	72.0	22	14	AAZ60876
C	39	18.8	72.0	22	14	AAZ60877
C	40	18.8	72.0	22	14	AAZ60878
C	41	18.8	72.0	22	14	AAZ60879
C	42	18.8	72.0	22	14	AAZ60880
C	43	18.8	72.0	22	14	AAZ60881
C	44	18.8	72.0	22	14	AAZ60882
C	45	18.8	72.0	22	14	AAZ60883

ALIGNMENTS

AAZ60848	16-MAY-2000 (first entry)
AAZ60849	16-MAY-2000 (first entry)
AAZ60850	16-MAY-2000 (first entry)
AAZ60851	16-MAY-2000 (first entry)
AAZ60852	16-MAY-2000 (first entry)
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AAZ60859	16-MAY-2000 (first entry)
AAZ60860	16-MAY-2000 (first entry)
AAZ60861	16-MAY-2000 (first entry)
AAZ60862	16-MAY-2000 (first entry)
AAZ60863	16-MAY-2000 (first entry)
AAZ60864	16-MAY-2000 (first entry)
AAZ60865	16-MAY-2000 (first entry)
AAZ60866	16-MAY-2000 (first entry)
AAZ60867	16-MAY-2000 (first entry)
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AAZ60869	16-MAY-2000 (first entry)
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AAZ60998	16-MAY-2000 (first entry)
AAZ60999	16-MAY-2000 (first entry)
AAZ61000	16-MAY-2000 (first entry)

Probe used to isolate Human bcr exon 3 5' L6(131) ribozyme s L6(131) ribozyme. PCR primer for bcr Chronic myeloid le Biotin labeled DN Probe #19309 for g Human brain expres Human bone marrow Probe #17924 for g Human spliced tran Sequence of oligo Rat spliced transc Mouse spliced tran Human spliced tran Human spliced tran Human spliced tran Rat spliced transc PCR primer #2 for IL-4 2'NH2 RNA 119 IL-4 2'NH2 RNA 119 Human map-related Human spliced tran Mouse spliced tran Mouse spliced tran Nucleotide sequenc Human BCR exon 1 5 Forward primer for Human coding sequ Human spliced tran

PT detection and measurement of nucleic acids and fusion nucleic acids
 XX
 XX Claim 19; Page 41; 49pp; English.
 PS
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
 CC the invention to detect fusion transcripts produced from a translocation
 CC between the bcr b3 region and the abl gene. The specification describes
 CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
 CC species), in a biological sample. The method comprises contacting a
 CC sample of fusion nucleic acid with primers, amplifying the hybridized
 CC fusion nucleic acid, and detecting the target hybrid. The method is
 CC used for the simple and rapid preparation of RNA from a biological
 CC sample, particularly from the cytoplasm of eukaryotic cells, which is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC fields, for medical diagnoses and clinical monitoring of a patients
 CC response to therapy where a disease or medical condition is associated
 CC with a particular type and/or level of mRNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associate with cancers,
 CC particularly forms of leukemia.
 CC
 SQ Sequence 25 BP; 5 A; 10 C; 5 G; 5 T; 0 other;
 Query Match 100.0%; Score 25; DB 21; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GACTGTCACAGCATTCGGCTGACC 25
 |||:|||||:|||||:|||||
 Db 1 GACTGTCACAGCATTCGGCTGACC 25
 RESULT 2
 ID AAZ60849 standard; RNA; 25 BP.
 AC
 XX AAZ60849;
 DT 16-MAY-2000 (first entry)
 KW Oligonucleotide used to detect bcr b3-abl fusion transcripts.
 KW Fusion transcript; translocation; bcr b3 region; abl gene;
 KW amplification assay; detection assay; medical diagnosis;
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
 KW disease marker; cancer; leukemia; ss.
 XX
 OS Synthetic.
 PN WO200005418-A1.
 PD 03-FEB-2000.
 PF 23-JUL-1999; 99WO-US16832.
 PR 23-JUL-1998; 98US-0121239.
 XX
 PA (GENP-) GEN-PROBE INC.
 PI Harvey RC, Eastman PS;
 XX
 DR WPI; 2000-182730/16.
 XX
 PT Novel methods for preparing RNA from biological samples, used for the
 PT detection and measurement of nucleic acids and fusion nucleic acids
 XX
 PS Claim 19; Page 41; 49pp; English.
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
 CC the invention to detect fusion transcripts produced from a translocation

CC between the bcr b3 region and the abl gene. The specification describes
 CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
 CC species), in a biological sample. The method comprises contacting a
 CC sample of fusion nucleic acid with primers, amplifying the hybridized
 CC fusion nucleic acid, and detecting the target hybrid. The method is
 CC used for the simple and rapid preparation of RNA from a biological
 CC sample, particularly from the cytoplasm of eukaryotic cells, which is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC fields, for medical diagnoses and clinical monitoring of a patients
 CC response to therapy where a disease or medical condition is associated
 CC with a particular type and/or level of mRNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associate with cancers,
 CC particularly forms of leukemia.
 CC
 SQ Sequence 25 BP; 5 A; 10 C; 5 G; 5 U; 0 other;
 Query Match 100.0%; Score 25; DB 21; Length 25;
 Best Local Similarity 80.0%; Pred. No. 0.032;
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GACTGTCACAGCATTCGGCTGACC 25
 |||:|||||:|||||:|||||
 Db 1 GACUGGCACAGCAUUCGCCUGACC 25
 RESULT 3
 ID AAZ60850/c
 AC AAZ60850 standard; DNA; 25 BP.
 XX
 XX AAZ60850;
 DT 16-MAY-2000 (first entry)
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.
 XX
 KW Fusion transcript; translocation; bcr b3 region; abl gene;
 KW amplification assay; detection assay; medical diagnosis;
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
 KW disease marker; cancer; leukemia; ss.
 XX
 OS Synthetic.
 PN WO200005418-A1.
 PD 03-FEB-2000.
 PF 23-JUL-1999; 99WO-US16832.
 PR 23-JUL-1998; 98US-0121239.
 XX
 PA (GENP-) GEN-PROBE INC.
 PI Harvey RC, Eastman PS;
 XX
 DR WPI; 2000-182730/16.
 XX
 PT Novel methods for preparing RNA from biological samples, used for the
 PT detection and measurement of nucleic acids and fusion nucleic acids
 XX
 PS Claim 19; Page 41; 49pp; English.
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
 CC the invention to detect fusion transcripts produced from a translocation
 CC between the bcr b3 region and the abl gene. The specification describes
 CC a method for detecting a fusion nucleic acid (particularly chimeric
 CC species), in a biological sample. The method comprises contacting a
 CC sample of fusion nucleic acid with primers, amplifying the hybridized
 CC fusion nucleic acid, and detecting the target hybrid. The method is
 CC used for the simple and rapid preparation of RNA from a biological

CC sample, particularly from the cytoplasm of eukaryotic cells, which is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC samples. The methods are useful in the human medical and veterinary
 CC fields, for medical diagnoses and clinical monitoring of a patient's
 CC response to therapy where a disease or medical condition is associated
 CC with a particular type and/or level of mRNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associated with cancers,
 CC particularly forms of leukemia.

SO Sequence 25 BP; 5 A; 5 C; 10 G; 5 T; 0 other;

QY Query Match 100.0%; Score 25; DB 21; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.032; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0;

DB 1 GACTGTCCACGACGATTCGCTGACC 25
 25 GACTGTCCACGACGATTCGCTGACC 1

RESULT 4
 AA60851/C
 ID AA60851 standard; RNA; 25 BP.
 XX
 AC AA60851;
 XX
 DT 16-MAY-2000 (first entry)
 XX
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.
 XX
 KW Fusion transcript; translocation; bcr b3 region; abl gene;
 KW amplification assay; detection assay; medical diagnosis;
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
 KW disease marker; cancer; leukemia; ss.
 XX
 OS Synthetic.
 XX
 PN WO200005418-A1.
 XX
 PD 03-FEB-2000.
 XX
 PF 23-JUL-1999; 99WO-US16832.
 XX
 PR 23-JUL-1998; 98US-0121239.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Harvey RC, Eastman PS;
 XX
 DR WPI; 2000-182730/16.
 XX
 PT Novel methods for preparing RNA from biological samples, used for the
 PT detection and measurement of nucleic acids and fusion nucleic acids
 XX
 PS Claim 19; Page 41; 49pp; English.

CC Oligonucleotides AA60840-62 and AA60865-66 are used in the method of
 CC the invention to detect fusion transcripts produced from a translocation
 CC between the bcr b3 region and the abl gene. The specification describes
 CC a method for detecting a fusion nucleic acid (particularly chimeric RNA
 CC species), in a biological sample. The method comprises contacting a
 CC sample of fusion nucleic acid with primers, amplifying the hybridized
 CC fusion nucleic acid, and detecting the target hybrid. The method is
 CC used for the simple and rapid preparation of eukaryotic cells, which is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC samples. The methods are useful in the human medical and veterinary
 CC fields, for medical diagnoses and clinical monitoring of a patient's
 CC response to therapy where a disease or medical condition is associated

CC with a particular type and/or level of mRNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associated with cancers,
 CC particularly forms of leukemia.

SO Sequence 25 BP; 5 A; 5 C; 10 G; 5 U; 0 other;

QY Query Match 100.0%; Score 25; DB 21; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.032; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0;

DB 1 GACTGTCCACGACGATTCGCTGACC 25
 25 GACTGTCCACGACGATTCGCTGACC 1

RESULT 5
 AA046951
 ID AA046951 standard; DNA; 56 BP.
 XX
 AC AA046951;
 XX
 DT 21-JAN-1994 (first entry)
 XX
 DE Blanked probe to CMLb translocation region of chromosome 22.
 XX
 KW Chronic myelogenous leukemia; CMLb; abl region;
 KW acute lymphocytic leukemia; ALL; genetic translocation;
 KW chromosome 22; target sequence; universal detection oligomer;
 KW branched probe; chemiluminescent acridinium ester; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..40
 FT /tag- a
 FT /note- "complementary to region of chromosome 22
 FT associated with CMLb translocation"
 FT misc_feature 41..56
 FT /tag- b
 FT /note- "complementary to nucleotides 16-1 of
 FT universal detection probe AA046949"

XX
 PN EP552931-A.
 XX
 PD 28-JUL-1993.
 XX
 PF 20-JAN-1993; 93EP-0300377.
 XX
 PR 22-JAN-1992; 92US-0827021.
 XX
 PA (GENP-) GEN PROBE INC.
 XX
 PI Arnold LJ, Bezerkov R, Hogan JT, Nelson NC;
 XX
 DR WPI; 1993-236606/30.
 XX
 PT Nucleic acid molecules which hybridise in presence of target
 PT nucleic acid - are used as probes in hybridisation assays or as
 PT therapeutic agents for diseases
 XX
 PS Example 6; Fig 12B; 58pp; English.

CC Chimeric targets were synthesised homologous to 3 different
 CC genetic translocations between a constant abl region of chromosome
 CC 9 and various regions of chromosome 22; two are the most common
 CC translocations associated with chronic myelogenous leukemia (CMLa
 CC and CMLb) and the other is associated with acute lymphocytic
 CC leukemia (ALL). An AE-labelled universal detection oligomer (AA046949)
 CC specific for the abl region was synthesised. Three different
 CC strands were designed to contain a probe region specific for one of
 CC the translocated chromosome 22 regions as well as an arm region

CC complementary to part of the universal probe (AA046950-2). The probe
CC mixes were found to detect only the correct chimeric targets and
CC did not cross-react significantly with the other targets.

XX
SQ Sequence 56 BP; 18 A; 18 C; 9 G; 11 T; 0 other;

Query Match 100.0%; Score 25; DB 14; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGAC 25
|||||
DB 3 GACTGTCCACAGCATTCGCTGAC 27

RESULT 6
AA051830
ID AA051830 standard; RNA; 26 BP.

XX
AC AA051830;
XX
DT 26-MAY-1994 (first entry)

XX
DE bcr mRNA ribozyme cleavable nucleotide 3264.

XX Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
XX resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
XX actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
XX adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
XX human; chronic myelogenous leukemia; CML; follicular lymphoma;
XX B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
XX neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
XX hairpin; hepatitis delta virus; group I intron; RNaseP; ss.

OS Homo sapiens.

XX
PN W09323057-A.

XX
PD 25-NOV-1993.

XX
PF 13-MAY-1993; 93WO-US04573.

XX
PR 14-MAY-1992; 92US-0882822.

XX
PR 14-MAY-1992; 92US-0882885.

XX
PR 26-AUG-1992; 92US-0936110.

XX
PR 26-AUG-1992; 92US-0936421.

XX
PR 26-AUG-1992; 92US-0936422.

XX
PR 26-AUG-1992; 92US-0936531.

XX
PR 26-AUG-1992; 92US-0936532.

XX
PR 07-DEC-1992; 92US-0987131.

XX
PR 19-JAN-1993; 93US-0006122.

XX
PR 19-JAN-1993; 93US-0008910.

XX
PA (RIBO-) RIBOZYME PHARM INC.

XX
PI Draper KG, Thompson JD;

XX
PT WPI; 1993-386203/48.

XX
PS Claim 3; Fig 3; 69pp; English.

CC The sequences given in AA051825-2266 represent areas of mRNAs
CC associated with development or maintenance of chronic myelogenous
CC leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or
CC acute lymphocytic leukemia, follicular lymphoma, B-cell acute
CC lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma
CC and lung cancer. The full length mRNAs containing these target
CC sequences, encode aberrant cellular proteins which are able to control
CC cellular proliferation and are directly linked to a leukemic

CC phenotype. These target sequences are identified by the ribozyme of
CC the invention. The ribozymes is formed in a hammerhead motif, but may
CC also be formed in the motif of a hairpin, hepatitis delta virus, group
CC I intron or RNaseP-like RNA. These ribozymes may be used to inhibit
CC the development or expression of a transformed phenotype in man and
CC other animals by modulating expression of the corresponding gene.
CC Cleavage of target mRNAs expressed in pre-neoplastic and transformed
CC cells elicits inhibition of the transformed state. Multiple drug
CC resistance (mdr-1) mRNA specific ribozymes remove the mechanism of
CC drug resistance used by transformed cells and thus enhances drug
CC therapies for tumours. The ribozymes may also be used to study
CC genetic drift and mutations within cells.

XX Sequence 26 BP; 6 A; 10 C; 5 G; 5 U; 0 other;

Query Match 96.0%; Score 24; DB 14; Length 26;
Best Local Similarity 79.2%; Pred. No. 0.095;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGAC 24
|||||
DB 3 GACTGTCCACAGCATTCGCTGAC 26

RESULT 7
AAV58775
ID AAV58775 standard; DNA; 40 BP.

XX
AC AAV58775;

XX
DT 10-DEC-1998 (first entry)

XX
DE Forward primer for BCR/ABL type chimera mRNA.

XX
KM PCR primer; BCR/ABL type chimera; chimera detection; Major-bcr;
XX nucleic acid strand based amplification; NASBA method; ss.

OS Synthetic.

XX
PN JP10229899-A.

XX
PD 02-SEP-1998.

XX
PF 21-FEB-1997; 97JP-0054092.

XX
PR 21-FEB-1997; 97JP-0054092.

XX
PA (SRLS-) SRL KK.

XX
PA (TOYM) TOYOBO KK.

XX
DR WPI; 1998-524294/45.

XX
PT Forward side primer and reverse side primer - used for detection of
XX BCR/ABL type chimera mRNA easily with high sensitivity

XX
PS Claim 1; Page 6; 8pp; Japanese.

CC This sequence represents a primer of the invention used for the detection
CC of a BCR/ABL type chimera mRNA with a cleavage point in Major-bcr by a
CC nucleic acid strand based amplification (NASBA) method. The primers can
CC be used to detect BCR/ABL type chimera mRNA easily with high sensitivity.

XX
SQ Sequence 40 BP; 9 A; 13 C; 9 G; 9 T; 0 other;

Query Match 96.0%; Score 24; DB 19; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGAC 24
|||||
DB 17 GACTGTCCACAGCATTCGCTGAC 40

```

RESULT 8
AAAT91761/C
ID AAAT91761 standard; DNA: 20 BP.
XX
XX AAAT91761;
AC
XX 08-JAN-1998 (first entry)
XX
XX Primer DERT350 for bcr2-ab12 and bcr3-ab12 translocation regions.
DE
XX PCR; primer: amplify; polymerase chain reaction; haematopoietic cell;
XX chronic myelogenous leukaemia; human; bcr2-ab12; translocation region;
XX cytogenetic remission; Ph chromosome; bcr3-ab12; CML cell;
XX acute lymphotrophic leukaemia; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
XX modified_base 20 /*tag= a
XX /note= "amidated"
XX
XX WO9708339-A1.
XX
XX 06-MAR-1997.
XX
XX 28-AUG-1995; 95WO-US10919.
XX
XX 25-AUG-1995; 95US-0296258.
XX
XX (DADE-) DADE INT INC.
XX
XX Brown J, Lockhart-bruce C;
XX
XX WPI: 1997-179294/16.
XX
XX Detection of chronic myelogenous leukaemia cells - by amplification
XX of RNA from haematopoietic cells with primers for the bcr2-ab12 and
XX bcr3-ab12 trans-location regions
XX
XX Claim 11: Page 12: 79pp; English.
XX
XX AAAT91749-T91763, and AAAT91765-T91792 are primers used in the method of
XX the invention. AAAT91754-T91759 can also be used as capture
XX oligonucleotides (ON), while AAAT91760-T91763, AAAT91791 and AAAT91792 can
XX also be used as detector agents. The method of the invention is for
XX detecting or monitoring chronic myelogenous leukaemia (CML) cells in a
XX human patient. The method comprises obtaining RNA from haematopoietic
XX cells of the patient, and amplifying it using a pair of primers that
XX amplify both the bcr2-ab12 and bcr3-ab12 translocation regions. The
XX amplified sequence is contacted with a capture agent comprising a capture
XX ON and a binding ligand to form a capture mixture. The capture ON is
XX specific for the bcr2-ab12 and bcr3-ab12 translocation regions. The
XX mixture is contacted with a solid phase coupled to a receptor specific
XX for the binding ligand. The solid phase is washed, then contacted with a
XX detector agent comprising a detector ON specific for the bcr2-ab12 or
XX bcr3-ab12 translocation regions and a label. The amount of labelled
XX detector ON bound to the solid phase is then correlated with the presence
XX or quantity of CML cells in the patient. The method is to detect or
XX monitor CML cells in patients. It can also be used prognostically to
XX assess cytogenetic remission in patients with CML. The method detects
XX both the bcr2-ab12 and the bcr3-ab12 translocations associated with CML.
XX The assay does not detect CML in the absence of the Ph chromosome, nor
XX does it detect acute lymphotrophic leukaemia (ALL) even if the ALL
XX patient has the Ph chromosome.
XX
XX Sequence 20 BP: 4 A; 3 C; 9 G; 4 T; 0 other;
XX
XX Query Match 80.0%; Score 20; DB 18; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 6.6;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 6 TCCACAGCATTCGCTGACC 25

```

```

Db 20 TCCACAGCATTCGCTGACC 1
XXXXXXXXXXXXXXXXXXXX
RESULT 9
AAAT91782
ID AAAT91782 standard; DNA: 45 BP.
XX
XX AAAT91782;
AC
XX 08-JAN-1998 (first entry)
XX
XX Primer BB316 for bcr2-ab12 and bcr3-ab12 translocation regions.
DE
XX PCR; primer: amplify; polymerase chain reaction; haematopoietic cell;
XX chronic myelogenous leukaemia; human; bcr2-ab12; translocation region;
XX cytogenetic remission; Ph chromosome; bcr3-ab12; CML cell;
XX acute lymphotrophic leukaemia; ss.
XX
XX Synthetic.
OS
XX
XX WO9708339-A1.
XX
XX 06-MAR-1997.
XX
XX 28-AUG-1995; 95WO-US10919.
XX
XX 25-AUG-1995; 95US-0296258.
XX
XX (DADE-) DADE INT INC.
XX
XX Brown J, Lockhart-bruce C;
XX
XX WPI: 1997-179294/16.
XX
XX Detection of chronic myelogenous leukaemia cells - by amplification
XX of RNA from haematopoietic cells with primers for the bcr2-ab12 and
XX bcr3-ab12 trans-location regions
XX
XX Example 1: Page 11: 79pp; English.
XX
XX AAAT91749-T91763, and AAAT91765-T91792 are primers used in the method of
XX the invention. AAAT91754-T91759 can also be used as capture
XX oligonucleotides (ON), while AAAT91760-T91763, AAAT91791 and AAAT91792 can
XX also be used as detector agents. The method of the invention is for
XX detecting or monitoring chronic myelogenous leukaemia (CML) cells in a
XX human patient. The method comprises obtaining RNA from haematopoietic
XX cells of the patient, and amplifying it using a pair of primers that
XX amplify both the bcr2-ab12 and bcr3-ab12 translocation regions. The
XX amplified sequence is contacted with a capture agent comprising a capture
XX ON and a binding ligand to form a capture mixture. The capture ON is
XX specific for the bcr2-ab12 and bcr3-ab12 translocation regions. The
XX mixture is contacted with a solid phase coupled to a receptor specific
XX for the binding ligand. The solid phase is washed, then contacted with a
XX detector agent comprising a detector ON specific for the bcr2-ab12 or
XX bcr3-ab12 translocation regions and a label. The amount of labelled
XX detector ON bound to the solid phase is then correlated with the presence
XX or quantity of CML cells in the patient. The method is to detect or
XX monitor CML cells in patients. It can also be used prognostically to
XX assess cytogenetic remission in patients with CML. The method detects
XX both the bcr2-ab12 and the bcr3-ab12 translocations associated with CML.
XX The assay does not detect CML in the absence of the Ph chromosome, nor
XX does it detect acute lymphotrophic leukaemia (ALL) even if the ALL
XX patient has the Ph chromosome.
XX
XX Sequence 45 BP: 15 A; 11 C; 8 G; 11 T; 0 other;
XX
XX Query Match 76.0%; Score 19; DB 18; Length 45;
XX Best Local Similarity 100.0%; Pred. No. 21;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GACTGTCCACAGCATTCG 19
XXXXXXXXXXXXXXXXXXXX

```

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DB      27 GACTGTCCACAGCATTCGG 45

RESULT 10
AAx81653/C
ID   AAx81653 standard; DNA; 39 BP.
XX
XX
AC   AAx81653;
XX
DE   26-AUG-1999 (first entry)
XX
DE   Probe used to isolate erythrovirus V9 nucleotide sequences.
XX
KW   Erythrovirus V9; differential diagnosis; parvovirus; infection;
KW   erythrovirus screening; typing; immunoassay; probe; ss.
XX
OS   Synthetic.
XX   Erythrovirus.
XX
PN   FR2771751-A1.
XX
PD   04-JUN-1999.
XX
PF   03-DEC-1997; 97FR-0015197.
XX
PR   03-DEC-1997; 97FR-0015197.
PA   (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
PI   Auguste V, Garbarg CA, Nguyen QT;
XX
DR   WPI, 1999-349543/30.
XX
PT   Erythrovirus V9 and its nucleic acid sequences - can be used in the
PS   diagnosis of its infections
XX
XX   Claim 3; Page 38; 80pp; French.
XX
CC   AAX81630-x81666 represent probes used to isolate erythrovirus V9
CC   polynucleotide sequences. Probes and primers derived from erythrovirus
CC   V9 polynucleotide sequences (AAX81580) can be used for differential
CC   diagnosis of erythrovirus (parvovirus) infections by a combination
CC   of amplification and hybridisation assay. The probes can also be
CC   used to assess susceptibility to erythrovirus infection and for
CC   erythrovirus screening and typing. The antibodies can be used in
CC   immunoassays for diagnosis of erythrovirus V9 infections.
XX
SQ   Sequence 39 BP; 8 A; 11 C; 13 G; 7 T; 0 other;
    Query Match          75.2%; Score 18.8; DB 20; Length 39;
    Best Local Similarity 90.9%; Pred. No. 26;
    Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY     2 ACTGTCACAGCATTCCGCTGA 23
       |||
Db      33 ACTGTCACAGCATTCGTGGGA 12
       |||

RESULT 11
AAQ34635
ID   AAQ34635 standard; cDNA; 22 BP.
XX
XX   AAQ34635;
XX
DT   10-MAY-1993 (first entry)
XX
DE   Human bcr exon 3 5' PCR primer.
XX
DE   Leukaemia; treatment; blast crisis; specific; CMV; translocation;
KW   Philadelphia chromosome; chronic myeloid; chronic myelogenous;
KW   leukemia; polymerase chain reaction; ss.
XX
OS   Synthetic.
```

[illegible]

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XX  . MO9413793-A.
XX  23-JUN-1994.
XX  16-NOV-1993; 93WO-US11144.
XX  04-DEC-1992; 92US-0989852.
XX  (APOL-) APOLLON INC.
XX  Coney LR, Oakes FT, Pachuk CJ;
XX  WPI; 1994-217873/26.
XX  Ribozymes comprising catalytic sequence, two legs and anchor
XX  sequence(s) complementary to substrate mRNA - is used for treatment
XX  of chronic myelogenous leukaemia and acute lymphoblastic leukaemia
XX  Example 1; Page 31; 67pp; English.
XX  This sequence represents a portion of the fusion mRNA L6 which is
XX  expressed by some of the hematopoietic cells of some chronic
XX  myelogenous leukaemia (CML) and acute lymphocytic leukaemia (ALL)
XX  patients. In the L-6 mRNA, abl exon 2 is linked to bcr exon 2. This
XX  is caused by a translocation between chromosomes 9 and 22. The L6
XX  mRNA encodes a protein with aberrant tyrosine kinase activity which is
XX  unique to CML cells and which is thought to play a key role in the
XX  establishment of CML. The ribozymes of the invention are specifically
XX  targeted to the L6, and related K28, mRNAs. Non-contiguous regions of
XX  the substrate RNA can be utilised for the separate events of ribozyme
XX  cleavage and ribozyme cleavage. The ribozymes are targeted to the L6
XX  bcr-abl RNA via an anchor sequence which is proximal to the bcr-abl
XX  junction. Cleavage by these ribozymes occurs at a downstream site
XX  located within an abl specific sequence in the fusion mRNA. Normal abl
XX  and bcr substrates are not cleaved. Ribozymes such as these are useful
XX  in treating diseases involving translocations eg. CML, ALL and
XX  follicular lymphomas. See also AA066774-96.
XX  Sequence 62 BP; 18 A; 19 C; 13 G; 12 U; 0 other:
XX  Query Match 72.0%; Score 18; DB 15; Length 62;
XX  Best Local Similarity 73.3%; Pred. No. 65;
XX  Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX  QY 8 CACAGCATTCGCGTGACC 25
XX  1 CACAGCAUUCGCGTGACC 18
XX  Db
XX  RESULT 13
XX  AA066775/c
XX  ID AA066775 standard; RNA; 81 BP.
XX  AC AA066775;
XX  DT 10-FEB-1995 (first entry)
XX  DE L6(1)31 ribozyme.
XX  KW Fusion mRNA; L6; hematopoietic cells; chronic myelogenous leukaemia;
XX  CML; acute lymphocytic leukaemia; ALL; exon 2; abl; bcr; exon 3; K28;
XX  translocation; chromosome 9; chromosome 22; tyrosine kinase; cleavage;
XX  ribozymes; nucleation; anchor sequence; follicular lymphomas; ss.
XX  OS Homo sapiens.
XX  Key 1.37 Location/Qualifiers
XX  FT misc_RNA /tag= a
XX  FT 10..31 /note= "Complementary to abl exon 2"
XX  FT /tag= b

```

```

FT  . MO9413793-A.
FT  23-JUN-1994.
FT  16-NOV-1993; 93WO-US11144.
FT  04-DEC-1992; 92US-0989852.
FT  (APOL-) APOLLON INC.
FT  Coney LR, Oakes FT, Pachuk CJ;
FT  WPI; 1994-217873/26.
FT  Ribozymes comprising catalytic sequence, two legs and anchor
FT  sequence(s) complementary to substrate mRNA - is used for treatment
FT  of chronic myelogenous leukaemia and acute lymphoblastic leukaemia
FT  Claim 17; Fig 2; 67pp; English.
FT  This sequence represents a ribozyme which binds to and cleaves,
FT  a portion of the fusion mRNA L6 which is expressed by some of the
FT  hematopoietic cells of some chronic myelogenous leukaemia (CML) and
FT  acute lymphocytic leukaemia (ALL) patients. In the L-6 mRNA, abl
FT  exon 2 is linked to bcr exon 2, this is caused by a translocation
FT  between chromosomes 9 and 22. The L6 mRNA encodes a protein with
FT  aberrant tyrosine kinase activity which is unique to CML cells and
FT  which is thought to play a key role in the establishment of CML.
FT  Ribozymes such as this are specifically targeted to the L6, and
FT  related K28, mRNAs. Non-contiguous regions of the substrate RNA can
FT  be utilised for the separate events of ribozyme nucleation and
FT  ribozyme cleavage. The ribozymes are targeted to the L6 bcr-abl
FT  RNA via an anchor sequence which is proximal to the bcr-abl
FT  junction. Cleavage by these ribozymes occurs at a downstream site
FT  located within an abl specific sequence in the fusion mRNA. Normal abl
FT  and bcr substrates are not cleaved. Ribozymes such as these are useful
FT  in treating diseases involving translocations eg. CML, ALL and
FT  follicular lymphomas. See also AA066774-96.
FT  Sequence 81 BP; 23 A; 17 C; 23 G; 18 U; 0 other:
FT  Query Match 72.0%; Score 18; DB 15; Length 81;
FT  Best Local Similarity 100.0%; Pred. No. 67;
FT  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT  QY 8 CACAGCATTCGCGTGACC 25
FT  81 CACAGCAUUCGCGTGACC 64
FT  Db
FT  RESULT 14
FT  AA291685
FT  ID AA291685 standard; DNA; 20 BP.
FT  AC AA291685;
FT  DT 19-MAY-2000 (first entry)
FT  DE PCR primer for bcr-abl sequence.
FT  KW PCR primer; bcr-abl gene; chromosomal aberration; BCR gene; ABL gene;
FT  breakpoint cluster region; aberration region; ALL; CML; diagnosis;
FT  acute lymphocytic leukaemia; chronic myelogenous leukaemia; ss.

```

OS Homo sapiens.
 XX
 PN US6025126-A.
 XX
 PD 15-FEB-2000.
 XX
 PF 28-OCT-1991; 91US-0784222.
 XX
 PR 28-OCT-1991; 91US-0784222.
 XX
 PA (ARCH-) ARCH DEV CORP.
 XX
 PI Westbrook CA;
 XX
 DR WPI; 2000-181800/16.
 XX
 PT Composition comprising two labeled probes hybridizing to different ends
 of a chromosome, useful for diagnosis of acute lymphocytic leukaemia
 (ALL) and/or chronic myelogenous leukaemia (CML) -
 XX
 PS Example 3; Column 19; 18pp; English.
 XX
 CC This sequence represents a PCR primer for the bcr-abl sequence. The
 CC invention relates to a composition comprising at least 2 labeled probes
 CC for detecting a chromosomal aberration involving the BCR (breakpoint
 CC cluster region) and ABL genes, where one probe hybridises to the ABL side
 CC of the chromosomal aberration and the other to the BCR side of the
 CC chromosomal aberration. The probes are long enough to be specifically
 CC detected in cytogenetic analysis. The composition is useful for
 CC diagnosing acute lymphocytic leukaemia (ALL) and/or chronic myelogenous
 CC leukaemia (CML).
 XX
 SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 other;
 QY Query Match 68.0%; Score 17; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 ACAGCATTCGCTGACC 17

RESULT 15
 AAT29713
 ID AAT29713 standard; mRNA; 60 BP.
 XX
 AC AAT29713;
 XX
 DT 17-DEC-1996 (first entry)
 XX
 DE Chronic myeloid leukaemia b2a2-type bcr-abl junction mRNA.
 XX
 KW Chronic myeloid leukaemia; Philadelphia chromosome; bcr-abl junction;
 KW chromosomal translocation; CD34 antigen; b2a2 type junction; I6;
 KW inhibition; ex vivo treatment; therapy; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_recomb 30..31
 FT /*tag= a
 FT /label= junction
 FT note= "site where exon 2 of bcr gene is joined to
 exon 2 of abl gene"

W09612803-A1.
 XX
 PD 02-MAY-1996.
 XX
 PF 23-OCT-1995; 95WO-FR01398.
 XX
 PR 24-OCT-1994; 94FR-0012673.

XX
 PA (GENO) GENSET.
 XX
 PI Blumenfeld M;
 XX
 DR WPI; 1996-230604/23.
 XX
 PT Ex vivo treatment of chronic myeloid leukaemia - by treating
 PT isolated CD34 cells with anti-sense oligo:nucleotide specific for
 the bcr-abl junction
 XX
 PS Disclosure; Fig 1; 40pp; French.
 XX
 CC In a novel ex vivo treatment for chronic myeloid leukaemia (CML),
 CC cells which express the CD34 antigen are selected from amongst the
 CC mononuclear cells of a patient in the chronic phase of CML; the CD34+
 CC cells are then treated with an antisense oligonucleotide which is
 CC complementary to the bcr-abl junction and which prevents expression
 CC of the junction region. The present sequence is that of mRNA from
 CC the region around the b2a2-type bcr-abl junction, one of the two
 CC aberrant junctions found in CML sufferers.
 XX
 SQ Sequence 60 BP; 18 A; 18 C; 13 G; 11 U; 0 other;
 QY Query Match 68.0%; Score 17; DB 17; Length 60;
 Best Local Similarity 82.4%; Pred. No. 1.9e+02;
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 DB 1 ACAGCAUUCGCGUGACC 17

Search completed: December 21, 2002, 11:54:34
 Job time : 88.8163 secs

PT detection and measurement of nucleic acids and fusion nucleic acids -
PS Claim 19; Page 42; 49pp; English.
XX
XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation
CC between the bcr b3 region and the abl gene. The specification describes
CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is
CC used for the simple and rapid preparation of RNA from a biological
CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC samples. The methods are useful in the human medical and veterinary
CC fields, for medical diagnoses and clinical monitoring of a patient's
CC response to therapy where a disease or medical condition is associated
CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia.
XX

SQ Sequence 20 BP; 9 A; 2 C; 9 G; 0 U; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAAAGCAGCAGGAGAGAGG 20
DB 1 CAAAGCAGCAGGAGAGAGG 20

RESULT 2

AAZ60853/c
ID AAZ60853 standard; DNA; 20 BP.

XX
XX AAZ60853;

DT 16-MAY-2000 (first entry)

DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.

XX
XX Fusion transcript; translocation; bcr b3 region; abl gene;

KW amplification assay; detection assay; medical diagnosis;

KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;

KW disease marker; cancer; leukemia; ss.

XX
XX Synthetic.

PN WO200005418-A1.

XX
XX 03-FEB-2000.

PD 23-JUL-1999; 99WO-US16832

XX
XX 23-JUL-1998; 98US-0121239.

PR (GENP-) GEN-PROBE INC.

PA Harvey RC, Eastman PS;

PI
XX WPI; 2000-182730/16.

XX
XX Novel methods for preparing RNA from biological samples, used for the
PT detection and measurement of nucleic acids and fusion nucleic acids -
PS Claim 19; Page 42; 49pp; English.

CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation

CC between the bcr b3 region and the abl gene. The specification describes
CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is
CC used for the simple and rapid preparation of RNA from a biological
CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC samples. The methods are useful in the human medical and veterinary
CC fields, for medical diagnoses and clinical monitoring of a patient's
CC response to therapy where a disease or medical condition is associated
CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia.
XX

SQ Sequence 20 BP; 0 A; 9 C; 2 G; 9 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAAAGCAGCAGGAGAGAGG 20
DB 20 CAAAGCAGCAGGAGAGAGG 1

RESULT 3

AAZ60854/c
ID AAZ60854 standard; RNA; 20 BP.

XX
XX AAZ60854;

DT 16-MAY-2000 (first entry)

DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.

XX
XX Fusion transcript; translocation; bcr b3 region; abl gene;

KW amplification assay; detection assay; medical diagnosis;

KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;

KW disease marker; cancer; leukemia; ss.

XX
XX Synthetic.

PN WO200005418-A1.

XX
XX 03-FEB-2000.

PD 23-JUL-1999; 99WO-US16832

XX
XX 23-JUL-1998; 98US-0121239.

PR (GENP-) GEN-PROBE INC.

PA Harvey RC, Eastman PS;

PI
XX WPI; 2000-182730/16.

XX
XX Novel methods for preparing RNA from biological samples, used for the
PT detection and measurement of nucleic acids and fusion nucleic acids -
PS Claim 19; Page 42; 49pp; English.

CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation
CC between the bcr b3 region and the abl gene. The specification describes
CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is
CC used for the simple and rapid preparation of RNA from a biological

50 Sequence: 78 BP; 28 A; 12 C; 31 G; 7 T; 0 other; 0;
Query Match 87.0%; Score 17.4; DB 21; Length 78;
Best Local Similarity 94.7%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CY 1 CAAAGGAGCAGCGAAGAG 19
|||||
DB 19 CAAAGGAGCAGCGAAGAG 37
RESULT 5
AA115289
ID AA115289 standard; cDNA, 96 BP.
AC AA115289.
XX
XX
XX 28-OCT-1996 (first entry)
XX
XX cDNA encoding human prepro-TRH peptide having CRF activity.
XX
XX TRH; thyrotropin release factor; Cushing's disease; anxiety;
XX corticotropin release inhibiting factor; CRF; depression; obesity;
XX anorexia nervosa; withdrawal; hypocortisolism; colitis; autoimmune;
XX arthritis; premenstrual syndrome; inflammatory; obsessive compulsive;
XX disorder; ss.
XX
XX Homo sapiens.
XX
XX OS
XX
XX Key Location/Qualifiers
XX CDS 1..96 /tag= a
XX CDS /note= "no start or stop codon"
XX
XX
XX W09608265-A1.
XX
XX 21-MAR-1996.
XX
XX PD
XX 08-SEP-1995; 95MO-US11455.
XX
XX PF
XX 12-SEP-1994; 94US-0304383.
XX
XX PR
XX
XX PA
XX (TYPE-) UNIV PENNSYLVANIA.
XX
XX
XX A1rd F, Redel E;
XX
XX
XX WPI: 1996-1/9720/18.
XX
XX DR
XX P-PSDB; AAR95846.
XX
XX
XX New isolated corticotropin release inhibiting factor peptide(s)
XX used to develop prods. for the diagnosis and treatment of CRF
XX related disorders, e.g. stress responses or inflammation
XX
XX
XX Claim 16; Page 40; 66pp; English.
XX
XX
XX AA115289 is a human cDNA sequence encoding a portion of the prepro-TRH
XX (thyrotropin releasing hormone) protein positioned between the
XX fourth and fifth TRH sequences (amino acids 158-183). The peptide
XX encoded has CRF (corticotropin release inhibiting factor) activity
XX and may be used for the diagnosis and treatment of CRF related
XX disorders. Such disorders include Cushing's disease, anxiety, anorexia
XX nervosa, depression, obesity, withdrawal from drug or alcoholic
XX dependence, some cancers, hypocortisolism, ACTH (adrenocorticotropin)
XX deficiency; premenstrual syndrome, inflammatory conditions e.g.
XX colitis and autoimmune disease e.g. arthritis. Peptides with CRF
XX activity may also be used to enhance immune responses and to increase
XX the efficacy of immunity to vaccines.
XX
XX
XX Sequence 96 BP; 34 A; 18 C; 37 G; 7 T; 0 other;
XX
XX
XX Query Match 87.0%; Score 17.4; DB 17; Length 96;
XX Best Local Similarity 94.7%; Pred. No. 1.1e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX

QY 1 CAAAGGAGCAGGAGAGAG 19
 |||||
 Db 37 CAAAGGAGCTGGGAGAGAG 55

RESULT 6
 ID AAA07233
 AC AAA07233 standard; DNA; 96 BP.

XX
 AC AAA07233;

DT 22-JUN-2000 (first entry)

XX Human CRIF coding sequence fragment.

XX Corticotropin release inhibitory factor; CRIF; behavioural symptom;
 KW anxiety disorder; thyrotropin releasing hormone; TRH sequence; human;
 KW general anxiety disorder; panic disorder; obsessive compulsive disorder;
 KW post-traumatic stress disorder; therapy; ss.

XX Homo sapiens.

XX US6039956-A.

XX 21-MAR-2000.

PF 07-JUN-1996; 96US-0660561.

XX 12-SEP-1994; 94US-0304383.

PR 08-SEP-1995; 95US-0523125.

XX (UNPE-) UNIV PENNSYLVANIA.

PI McGivenn RF, Rittenhouse PA, Aird F, Redel E;

DR WPI: 2000-270120/23.

PT Treating behavioural symptoms including panic disorder, post-traumatic
 stress disorder and obsessive compulsive disorder in humans, involves
 PT administering corticotropin release inhibiting factor -

PS Disclosure; Column 3; 43pp; English.

XX This sequence encodes a human corticotropin release inhibitory factor
 CC (CRIF) fragment. The invention relates to a method for treating (1)
 CC behavioural symptoms in an anxiety disorder in a human, comprising
 CC administering CRIF which comprises 3 contiguous amino acids contained
 CC within the amino acid sequence positioned between the fourth and fifth
 CC thyrotropin releasing hormone (TRH) sequence on a prepro-TRH protein. (1)
 CC is useful for treating behavioural symptoms in an anxiety disorder which
 CC includes general anxiety disorder, panic disorder, obsessive compulsive
 CC disorder and post-traumatic stress disorder. Peripheral administration of
 CC CRIF is capable of crossing the blood-brain barrier.

XX Sequence 96 BP; 34 A; 18 C; 37 G; 7 T; 0 other;

Query Match 87.0%; Score 17.4; DB 21; Length 96;

Best Local Similarity 94.7%; Pred. No. 1.9e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGAGAGAG 19
 |||||
 Db 37 CAAAGGAGCTGGGAGAGAG 55

RESULT 7
 ID AAI72555 standard; cDNA; 96 BP.

XX AAI72555;

DT 21-MAY-2002 (first entry)

XX Human CRIF coding sequence.

DE Rat; human; mouse; gene; corticotropin release inhibiting factor;
 KW CRIF; ACTH; adrenocorticotropin; TRH; prepro; behavioural disorder;
 KW thyrotropin releasing hormone; Cushing's disease; panic disorder;
 KW obsessive compulsive disorder; anorexia nervosa; depression; anxiety;
 KW obesity; alcohol dependence; drug dependence; premenstrual syndrome;
 KW chronic stress related syndrome; autoimmune disease; cancer;
 KW chronic fatigue syndrome; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT 19..96
 FT /*tag= a
 CDS /note= "Encodes prepro human TRH 158-183"

XX US6348571-B1.

XX 19-FEB-2002.

PF 03-AUG-1999; 99US-0366627.

XX 12-SEP-1994; 94US-0304383.

PR 08-SEP-1995; 95US-0523125.

XX 07-JUN-1996; 96US-0660561.

PA (NCUN) UNIV NORTHWESTERN.
 (UNPE-) UNIV PENNSYLVANIA.

PI Redel E, Aird F;

DR WPI: 2002-237138/29.

DR P-P-SDB; AAB47924.

PT A corticotropin release inhibiting factor peptide, useful for treating
 behavioural disorders in mammals, particularly humans e.g. anxiety
 disorders, depression, anorexia and drug withdrawal -

PS Disclosure; Fig 10; 24pp; English.

XX The sequences given in AAI72554-56 encode rat, human and mouse
 CC corticotropin release inhibiting factor (CRIF), respectively. CRIF
 CC peptides regulate ACTH (adrenocorticotropin) production. The CRIF
 CC peptide of the invention consists of 3-21 residues positioned within
 CC the amino acids sequence positioned between the fourth and fifth TRH
 CC sequence on a prepro-TRH protein (preprothyrotropin releasing hormone).
 CC The CRIF peptide is useful for treating behavioural disorders in
 CC mammals, especially humans, including Cushing's disease, anxiety
 CC disorders (e.g. panic disorder, obsessive compulsive disorder),
 CC anorexia nervosa, depression, obesity, withdrawal from alcohol and drug
 CC dependence, chronic stress related syndromes, autoimmune disease,
 CC chronic fatigue syndrome, premenstrual syndrome, and some cancers
 CC (those where an enhanced autoimmune response reduces the severity of
 CC the disease).

XX Sequence 96 BP; 34 A; 18 C; 37 G; 7 T; 0 other;

Query Match 87.0%; Score 17.4; DB 24; Length 96;

Best Local Similarity 94.7%; Pred. No. 1.9e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGAGAGAG 19
 |||||
 Db 37 CAAAGGAGCTGGGAGAGAG 55

RESULT 8
 ID AAA76522/c
 AC AAA76522 standard; cDNA; 51 BP.

XX AAA76522;

```

XX 16-NOV-2000 (first entry)
XX Human clone cg20723460 polymorphic site, SEQ ID NO:205.
XX
XX Human; single nucleotide polymorphism; SNP;
XX detection; identification; gene therapy; ss.
XX
XX Homo sapiens.
XX
XX Key location/Qualifiers
XX variation replace (26,T)
XX /*tag- a
XX
XX WO200029623-A2.
XX
XX 25-MAY-2000.
XX
XX 17-NOV-1999; 99WO-US27293.
XX
XX 17-NOV-1998; 98US-0109024.
XX
XX 16-NOV-1999; 99US-0109024.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinkets RA, Leach MD;
XX
XX WPI: 2000-387826/33.
XX
XX Human nucleic acids containing single nucleotide polymorphisms, useful
XX for treating a subject suffering, or at risk from a pathology due to
XX the presence of a sequence polymorphism -
XX
XX Claim 1; Page 220; 543pp; English.
XX
XX Sequences AAAT6318-A77509 represent 1192 human nucleic acid sequences
XX which contain single nucleotide polymorphisms (SNPs). Sequences 1 to
XX 1112 (AAAT6318-A77429) are consecutive pairs of nucleotides which
XX contain silent SNPs. Sequences 1113 to 1192 (AAAT7430-A77509) are
XX consecutive pairs of nucleotides containing SNPs which result in changes
XX in the corresponding amino acid sequences (AAB1749-B11828). The SNPs in
XX sequences 1113 to 1128 (AAAT7430-A77445) lead to conservative amino acid
XX changes, while those in sequences 1129 to 1186 (AAAT7446-A77503) result
XX in non-conservative changes. The SNPs in sequences 1187 to 1192
XX (AAAT7504-A77509) generate frameshift mutations. The invention also
XX relates to a method of detecting a polymorphic site in a nucleic acid and
XX a method of determining the relatedness of two nucleic acids. It also
XX encompasses peptides containing polymorphic sites, antibodies raised
XX against such peptides, and a method of detecting polymorphic
XX proteins/peptides using the antibodies. The nucleic acids are useful for
XX gene therapy of an individual having, suspected of having, or at risk of
XX developing a pathological condition due to the presence of a sequence
XX polymorphism. Such treatment would comprise administration of the
XX wild-type nucleic acid sequence. Antibodies raised against polymorphic
XX peptides can also be used in the treatment of such individuals.
XX
XX Sequence 51 BP; 10 A; 24 C; 2 G; 15 T; 0 other;
XX
XX Query Match 79.0%; Score 15.8; DB 21; Length 51;
XX Best Local Similarity 89.5%; Pred. No. 8.9e+02;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 2 AAAGGACGCGAGGAGAGG 20
XX 11111111111111111111
XX 47 AAAGGCGCAAGGAGAGAGG 29
XX
XX RESULT 9
XX AAAT6523/C
XX ID AAAT6523 standard; cDNA; 51 BP.
XX
XX AC AAAT6523;
XX

```

```

DT 16-NOV-2000 (first entry)
DT Human clone cg20723460 polymorphic site, SEQ ID NO:206.
DT
DT Human; single nucleotide polymorphism; SNP;
DT detection; identification; gene therapy; ss.
DT
DT Homo sapiens.
DT
DT Key location/Qualifiers
DT variation replace (26,C)
DT /*tag- a
DT
DT WO200029623-A2.
DT
DT 25-MAY-2000.
DT
DT 17-NOV-1999; 99WO-US27293.
DT
DT 17-NOV-1998; 98US-0109024.
DT
DT 16-NOV-1999; 99US-0109024.
DT
DT (CURA-) CURAGEN CORP.
DT
DT Shinkets RA, Leach MD;
DT
DT WPI: 2000-387826/33.
DT
DT Human nucleic acids containing single nucleotide polymorphisms, useful
DT for treating a subject suffering, or at risk from a pathology due to
DT the presence of a sequence polymorphism -
DT
DT Claim 1; Page 220; 543pp; English.
DT
DT Sequences AAAT6318-A77509 represent 1192 human nucleic acid sequences
DT which contain single nucleotide polymorphisms (SNPs). Sequences 1 to
DT 1112 (AAAT6318-A77429) are consecutive pairs of nucleotides which
DT contain silent SNPs. Sequences 1113 to 1192 (AAAT7430-A77509) are
DT consecutive pairs of nucleotides containing SNPs which result in changes
DT in the corresponding amino acid sequences (AAB1749-B11828). The SNPs in
DT sequences 1113 to 1128 (AAAT7430-A77445) lead to conservative amino acid
DT changes, while those in sequences 1129 to 1186 (AAAT7446-A77503) result
DT in non-conservative changes. The SNPs in sequences 1187 to 1192
DT (AAAT7504-A77509) generate frameshift mutations. The invention also
DT relates to a method of detecting a polymorphic site in a nucleic acid and
DT a method of determining the relatedness of two nucleic acids. It also
DT encompasses peptides containing polymorphic sites, antibodies raised
DT against such peptides, and a method of detecting polymorphic
DT proteins/peptides using the antibodies. The nucleic acids are useful for
DT gene therapy of an individual having, suspected of having, or at risk of
DT developing a pathological condition due to the presence of a sequence
DT polymorphism. Such treatment would comprise administration of the
DT wild-type nucleic acid sequence. Antibodies raised against polymorphic
DT peptides can also be used in the treatment of such individuals.
DT
DT Sequence 51 BP; 10 A; 23 C; 2 G; 16 T; 0 other;
DT
DT Query Match 79.0%; Score 15.8; DB 21; Length 51;
DT Best Local Similarity 89.5%; Pred. No. 8.9e+02;
DT Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DT
DT 2 AAAGGACGCGAGGAGAGG 20
DT 11111111111111111111
DT 47 AAAGGCGCAAGGAGAGAGG 29
DT
DT RESULT 10
DT AAAT5110
DT ID AAAT5110 standard; DNA; 41 BP.
DT
DT AC AAAT5110;
DT
DT DT 11-JAN-1999 (first entry)
DT

```

```

XX Maize polymorphic marker S28G5/G6-3 DNA.
DE Polymorphic marker; allele-specific; primer; probe; amplification;
XX hybridisation; plant; hybrid certification; genetic contribution;
KM progeny; back-cross; hybrid; ancestry; maize; ss.
XX
XX Zea mays.
OS
XX
XX Key Location/Qualifiers
FH 21
FT variation
FT /*tag= a
FT /replace= "a"
FT /note= "polymorphism"
XX
XX W09824796-A1.
PN
XX
XX 11-JUN-1998.
PD
XX
XX 01-DEC-1997; 97WO-US21782.
PE
XX
XX 07-MAR-1997; 97US-0813507.
PR
XX 02-DEC-1996; 96US-0032069.
XX
XX (AFPPY-) AFFYMETRIX INC.
PA
XX Landry BS, Lemieux B, Murgineux A, Sapolsky RJ;
PI WPI; 1998-333252/29.
DR
XX
XX Brassica species allele-specific oligonucleotide probes and primers
PT - useful for plant breeding
XX
XX Claim 1; Page 46; 65pp; English.
XX
XX This DNA sequence is a region of a Zea mays genome which contains a
CC polymorphic marker. This sequence can be used in the construction of
CC allele-specific primers and probes for amplification or hybridisation,
CC e.g. to determine common or disparate ancestry between 2 or more plants,
CC to monitor the genetic contribution of an ancestral plant, to trace the
CC progeny of proprietary plants, in certification of a hybrid plant or to
CC identify the progeny of a back-crossed plant with an ancestral plant.
XX
XX Sequence 41 BP; 12 A; 7 C; 19 G; 3 T; 0 other;
SQ
XX
XX Query Match 76.0%; Score 15.2; DB 19; Length 41;
XX Best Local Similarity 85.0%; Pred. No. 1.6e+03;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 CAAAGGACGACGAGGAAGG 20
DB 6 CCATGACGACGAGGAAGG 25
XX
XX RESULT 11
XX AAV47858
XX ID AAV47858 standard; DNA: 41 BP.
XX
XX AAV47858;
XX
XX 14-OCV-1998 (first entry)
XX
XX Maize polymorphic site oligonucleotide marker UMC21-G5/G6-3.
DE
XX
XX Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;
KM polymorphic site; corn; gramineae species; ss.
XX
XX Synthetic.
OS
XX
XX Zea sp.
PN W09830717-A2.
XX
XX 16-JUL-1998.
PD

```

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XX
XX 02-DEC-1997; 97WO-EP07134.
PE
XX
XX 02-DEC-1996; 96US-0032069.
PR
XX
XX (BIOC-) BIOCEM SA.
PA
XX
XX Murgineux A;
PI WPI; 1998-399160/34.
DR
XX
XX Vegetal sequences including single nucleotide polymorphism - useful,
PT e.g. to determine polymorphisms in plants, determine strain in plant
XX breeding and to correlate polymorphisms with phenotypic traits
XX
XX Claim 2; Page 14; 32pp; English.
XX
XX The present invention describes a nucleic acid segment comprising at
CC least 10 contiguous nucleotides from a vegetal sequence including a
CC polymorphic site which is a single nucleotide polymorphism (SNP), or the
CC complement of the segment. Also described are: (1) an allele-specific
CC oligonucleotide hybridising to segment, or their complements, and (2) a
CC method of analysing nucleic acids from a subject, by determining if a
CC base is occupying any one (or a set) of polymorphic sites in 261
CC sequences derived from six maize lines (see AAV47701 to AAV47961). The
CC segments are useful in fingerprint analysis in plants to determine which
CC polymorphisms are present, which strain a plant belongs to and to
CC distinguish between strains. The polymorphisms may correlate with
CC phenotypic traits (e.g. plant growth rate or crop yield), and the
CC segments are useful to determine the presence/absence of specific
CC polymorphisms correlating with the existence/absence of particular
CC traits. The segments are also useful in marker assisted back-cross
CC techniques to select plants with a higher percentage of recurrent parent
CC in a back-cross population. Segments incorporate SNPs which occur more
CC frequently than other polymorphism types and are therefore more likely
CC to be located close to genetic loci of interest; different forms of
CC characterised SNPs are also often easier to detect than other
XX polymorphism types.
XX
XX Sequence 41 BP; 12 A; 7 C; 18 G; 3 T; 1 other;
SQ
XX
XX Query Match 74.0%; Score 14.8; DB 19; Length 41;
XX Best Local Similarity 80.0%; Pred. No. 2.4e+03;
XX Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 CAAAGGACGACGAGGAAGG 20
DB 6 CCATGACGACGAGGAAGG 25
XX
XX RESULT 12
XX AAA07230
XX ID AAA07230 standard; DNA: 66 BP.
XX
XX AAA07230;
XX
XX 22-JUN-2000 (first entry)
XX
XX Rat CRTR coding sequence fragment.
XX
XX Corticotropin release inhibitory factor; CRIF; behavioural symptom;
KM anxiety disorder; thyrotropin releasing hormone; TRH sequence; rat;
KM general anxiety disorder; panic disorder; obsessive compulsive disorder;
KM post-traumatic stress disorder; therapy; ss.
XX
XX Rattus sp.
OS
XX
XX US6039956-A.
PN
XX
XX 21-MAR-2000.
PD
XX
XX 07-JUN-1996; 96US-0660561.
XX

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PR 12-SEP-1994; 94US-0304383.
PR 08-SEP-1995; 95US-0523125.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Mcgovern RF, Rittenhouse PA, Aird F, Redel E;
XX
XX WPI: 2000-270120/23.
XX
XX P-PSDB; AAY81902.
XX
XX Treating behavioural symptoms including panic disorder, post-traumatic
XX stress disorder and obsessive compulsive disorder in humans, involves
XX administering corticotropin release inhibiting factor
XX
XX Disclosure; Column 2: 43pp; English.
XX
XX This sequence encodes a rat corticotropin release inhibitory factor
XX (CRIF) fragment. The invention relates to a method for treating (1)
XX behavioural symptoms in an anxiety disorder in a human, comprising
XX administering CRIF which comprises 3 contiguous amino acids contained
XX within the amino acid sequence positioned between the fourth and fifth
XX thyrotropin releasing hormone (TRH) sequence on a prepro-TRH protein. (1)
XX is useful for treating behavioural symptoms in an anxiety disorder which
XX includes general anxiety disorder, panic disorder, obsessive compulsive
XX disorder and post-traumatic stress disorder. Peripheral administration of
XX CRIF is capable of crossing the blood-brain barrier.
XX
XX Sequence 66 BP; 22 A; 11 C; 21 G; 12 T; 0 other;
XX
XX Query Match 74.0%; Score 14.8; DB 21; Length 66;
XX Best Local Similarity 88.9%; Pred. No. 2.4e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 CAAGGAGCAGGAGAGA 18
DB 19 CAAGAAGCTCGGAGAGA 36
XX
XX RESULT 13
XX AAA07231
XX AAA07231 standard; DNA; 69 BP.
XX
XX AAA07231;
XX
XX 22-JUN-2000 (first entry)
XX
XX Mouse CRIF coding sequence fragment.
XX
XX Corticotropin release inhibitory factor; CRIF; behavioural symptom;
XX anxiety disorder; thyrotropin releasing hormone; TRH sequence; mouse;
XX general anxiety disorder; panic disorder; obsessive compulsive disorder;
XX post-traumatic stress disorder; therapy; ss.
XX
XX Mus sp.
XX
XX US6039956-A.
XX
XX 21-MAR-2000.
XX
XX 07-JUN-1996; 96US-0660561.
XX
XX 12-SEP-1994; 94US-0304383.
XX
XX 08-SEP-1995; 95US-0523125.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Mcgovern RF, Rittenhouse PA, Aird F, Redel E;
XX
XX WPI: 2000-270120/23.
XX
XX P-PSDB; AAY81903.
XX
XX Treating behavioural symptoms including panic disorder, post-traumatic
XX stress disorder and obsessive compulsive disorder in humans, involves
XX

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PT administering corticotropin release inhibiting factor
XX
XX Disclosure; Column 2: 43pp; English.
XX
XX This sequence encodes a mouse corticotropin release inhibitory factor
XX (CRIF) fragment. The invention relates to a method for treating (1)
XX behavioural symptoms in an anxiety disorder in a human, comprising
XX administering CRIF which comprises 3 contiguous amino acids contained
XX within the amino acid sequence positioned between the fourth and fifth
XX thyrotropin releasing hormone (TRH) sequence on a prepro-TRH protein. (1)
XX is useful for treating behavioural symptoms in an anxiety disorder which
XX includes general anxiety disorder, panic disorder, obsessive compulsive
XX disorder and post-traumatic stress disorder. Peripheral administration of
XX CRIF is capable of crossing the blood-brain barrier.
XX
XX Sequence 69 BP; 22 A; 11 C; 24 G; 12 T; 0 other;
XX
XX Query Match 74.0%; Score 14.8; DB 21; Length 69;
XX Best Local Similarity 88.9%; Pred. No. 2.4e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 CAAGGAGCAGGAGAGA 18
DB 19 CAAGAAGCTCGGAGAGA 36
XX
XX RESULT 14
XX AAT15288
XX AAT15288 standard; CDNA; 84 BP.
XX
XX AAT15288;
XX
XX 28-OCT-1996 (first entry)
XX
XX CDNA encoding rat prepro-TRH peptide having CRIF activity.
XX
XX TRH; thyrotropin release factor; Cushing's disease; anxiety;
XX corticotropin release inhibiting factor; CRIF; depression; obesity;
XX anorexia nervosa; withdrawal; hypocortisolism; colitis; autoimmune;
XX arthritis; premenstrual syndrome; inflammatory; obsessive compulsive;
XX disorder; ss.
XX
XX Rattus rattus.
XX
XX Key Location/Qualifiers
XX FT 1..84
XX CDS /*tag= a
XX FT /note= "no start or stop codon"
XX
XX WC9608265-A1.
XX
XX 21-MAR-1996.
XX
XX 08-SEP-1995; 95WO-US11455.
XX
XX 12-SEP-1994; 94US-0304383.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Aird F, Redel E;
XX
XX WPI: 1996-179720/18.
XX
XX P-PSDB; AAR95845.
XX
XX New isolated corticotropin release inhibiting factor peptide(s)
XX used to develop prods. for the diagnosis and treatment of CRIF
XX related disorders, e.g. stress responses or inflammation
XX
XX Claim 14; Fig 10; 66pp; English.
XX
XX AAT15288 is a rat CDNA sequence encoding a portion of the prepro-TRH
XX (thyrotropin releasing hormone) protein positioned between the
XX fourth and fifth TRH sequences (amino acids 178-199). The peptide
XX

```

CC encoded has CRIF (corticotropin release inhibiting factor) activity
 CC and may be used for the diagnosis and treatment of CRIF related
 CC disorders. Such disorders include Cushing's disease, anxiety, anorexia
 CC nervosa, depression, obesity, withdrawal from drug or alcoholic
 CC dependence, some cancers, hypercortisolism, ACHN (adrenocorticotropin)
 CC deficiency, premenstrual syndrome, inflammatory conditions e.g.
 CC colitis and autoimmune disease e.g. arthritis. Peptides with CRIF
 CC activity may also be used to enhance immune responses and to increase
 CC the efficacy of immunity to vaccines.
 XX
 SQ Sequence 84 BP; 27 A; 17 C; 27 G; 13 T; 0 other;

Query Match 74.0%; Score 14.8; DB 17; Length 84;
 Best Local Similarity 88.9%; Pred. No. 2.5e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAAGAGCAGGAGAGAA 18
 ||||| |||||
 DB 37 CAAAGAGCTGGAGAGAA 54

RESULT 15

AAA07232
 ID AAA07232 standard; DNA; 84 BP.

XX
 AC AAA07232;

XX
 DT 22-JUN-2000 (first entry)

XX
 DE Rat CRIF coding sequence fragment.

XX Corticotropin release inhibitory factor; CRIF; behavioural symptom;
 KW anxiety disorder; thyrotropin releasing hormone; TRH sequence; rat;
 KW general anxiety disorder; panic disorder; obsessive compulsive disorder;
 KW post-traumatic stress disorder; therapy; ss.
 XX

OS Rattus sp.

XX
 PN US6039956-A.

XX
 PD 21-MAR-2000.

XX
 PF 07-JUN-1996; 96US-0660561.

XX
 PR 12-SEP-1994; 94US-0304383.

XX
 PR 08-SEP-1995; 95US-0523125.

XX
 PA (UYPE-) UNIV PENNSYLVANIA.

XX
 PI McGovern RF, Rittenhouse PA, Aird F, Redei E;

XX
 DR WPI; 2000-270120/23.

XX Treating behavioural symptoms including panic disorder, post-traumatic
 PT stress disorder and obsessive compulsive disorder in humans, involves
 PT administering corticotropin release inhibiting factor
 XX
 PS Disclosure: Column 3; 43pp; English.
 XX

XX This sequence encodes a rat corticotropin release inhibitory factor
 CC (CRIF) fragment. The invention relates to a method for treating (I)
 CC behavioural symptoms in an anxiety disorder in a human, comprising
 CC administering CRIF which comprises 3 contiguous amino acids contained
 CC within the amino acid sequence positioned between the fourth and fifth
 CC thyrotropin releasing hormone (TRH) sequence on a prepro-TRH protein. (I)
 CC is useful for treating behavioural symptoms in an anxiety disorder which
 CC includes general anxiety disorder, panic disorder, obsessive compulsive
 CC disorder and post-traumatic stress disorder. Peripheral administration of
 CC CRIF is capable of crossing the blood-brain barrier.
 XX

SQ Sequence 84 BP; 27 A; 17 C; 27 G; 13 T; 0 other;

Query Match 74.0%; Score 14.8; DB 21; Length 84;

Best Local Similarity 88.9%; Pred. No. 2.5e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAAGAGCAGGAGAGAA 18
 ||||| |||||
 DB 37 CAAAGAGCTGGAGAGAA 54

Search completed: December 21, 2002, 11:54:37
 Job time : 71.6531 secs

PT detection and measurement of nucleic acids and fusion nucleic acids -
XX Claim 19; Page 43; 49pp; English.
XX
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation
CC between the bcr b3 region and the abl gene. The specification describes
CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is
CC used for the simple and rapid preparation of RNA from a biological
CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC fields. The methods are useful in the human medical and veterinary
CC response to therapy where a disease or medical condition is associated
CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia.

SQ Sequence 27 BP; 9 A; 8 C; 6 G; 4 T; 0 other;

Query Match 100.0%; Score 27; DB 21; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27
DB 27 TCTGACTTTGAGCCTCAGGCTCTGAGT 1

RESULT 2
AAZ60860/c
ID AAZ60860 standard; RNA; 27 BP.

XX AAZ60860;

DT 16-MAY-2000 (first entry)

XX Oligonucleotide used to detect bcr b3-abl fusion transcripts.

XX Fusion transcript; translocation; bcr b3 region; abl gene;

XX amplification assay; detection assay; medical diagnosis;

XX clinical monitoring; chimeric RNA; fusion RNA; condition marker;

XX disease marker; cancer; leukemia; ss.

XX Synthetic.

XX WO200005418-A1.

XX 03-FEB-2000.

XX 23-JUL-1999; 99WO-US16832.

XX 23-JUL-1998; 98US-0121239.

XX (GENP-) GEN-PROBE INC.

XX Harvey RC, Eastman PS;

XX WPI; 2000-182730/16.

XX Novel methods for preparing RNA from biological samples, used for the
XX detection and measurement of nucleic acids and fusion nucleic acids -
XX Claim 19; Page 43; 49pp; English.
XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
XX the invention to detect fusion transcripts produced from a translocation

CC between the bcr b3 region and the abl gene. The specification describes
CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is
CC used for the simple and rapid preparation of RNA from a biological
CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC fields. The methods are useful in the human medical and veterinary
CC response to therapy where a disease or medical condition is associated
CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia.

SQ Sequence 27 BP; 9 A; 8 C; 6 G; 4 T; 0 other;

Query Match 100.0%; Score 27; DB 21; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27
DB 27 TCTGACTTTGAGCCTCAGGCTCTGAGT 1

RESULT 3
AAZ60861
ID AAZ60861 standard; DNA; 27 BP.

XX AAZ60861;

DT 16-MAY-2000 (first entry)

XX Oligonucleotide used to detect bcr b3-abl fusion transcripts.

XX Fusion transcript; translocation; bcr b3 region; abl gene;

XX amplification assay; detection assay; medical diagnosis;

XX clinical monitoring; chimeric RNA; fusion RNA; condition marker;

XX disease marker; cancer; leukemia; ss.

XX Synthetic.

XX WO200005418-A1.

XX 03-FEB-2000.

XX 23-JUL-1999; 99WO-US16832.

XX 23-JUL-1998; 98US-0121239.

XX (GENP-) GEN-PROBE INC.

XX Harvey RC, Eastman PS;

XX WPI; 2000-182730/16.

XX Novel methods for preparing RNA from biological samples, used for the
XX detection and measurement of nucleic acids and fusion nucleic acids -
XX Claim 19; Page 43; 49pp; English.
XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
XX the invention to detect fusion transcripts produced from a translocation
XX between the bcr b3 region and the abl gene. The specification describes
XX a method for detecting a fusion nucleic acid (particularly chimeric mRNA
XX species), in a biological sample. The method comprises contacting a
XX sample of fusion nucleic acid with primers, amplifying the hybridized
XX fusion nucleic acid, and detecting the target hybrid. The method is
XX used for the simple and rapid preparation of RNA from a biological

CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC samples. The methods are useful in the human medical and veterinary
CC fields for medical diagnoses and clinical monitoring of a patient's
CC response to therapy where a disease or medical condition is associated
CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia.

SO Sequence 27 BP; 4 A; 6 C; 8 G; 9 T; 0 other;

Query Match 100.0%; Score 27; DB 21; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCTCAGGCTGTGAGT 27
Db 1 TCTGACTTTGAGCTCAGGCTGTGAGT 27

RESULT 4

AAZ60862 ID AAZ60862 standard; RNA; 27 BP.

AC AAZ60862;

DT 16-MAY-2000 (first entry)

DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.

XX Fusion transcript; translocation; bcr b3 region; abl gene;

KW amplification assay; detection assay; medical diagnosis;

KM clinical monitoring; chimeric RNA; fusion RNA; condition marker;

OS disease marker; cancer; leukemia; ss.

XX Synthetic.

PN WO200005418-A1.

XX 03-FEB-2000.

PF 23-JUL-1999; 99WO-US16832.

XX 23-JUL-1998; 98US-0121239.

PA (GENP-) GEN-PROBE INC.

PI Harvey RC, Eastman PS;

XX WPI: 2000-182730/16.

PT Novel methods for preparing RNA from biological samples, used for the

XX detection and measurement of nucleic acids and fusion nucleic acids -

Claim 19; Page 44; 49pp; English.
Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
the invention to detect fusion transcripts produced from a translocation
between the bcr b3 region and the abl gene. The specification describes
a method for detecting a fusion nucleic acid (particularly chimeric RNA
species), in a biological sample. The method comprises contacting a
sample of fusion nucleic acid with primers, amplifying the hybridized
fusion nucleic acid, and detecting the target hybrid. The method is
used for the simple and rapid preparation of RNA from a biological
sample, particularly from the cytoplasm of eukaryotic cells, which is
suitable for use in an amplification and detection assay. The methods
are used for the analysis and detection of nucleic acids in biological
samples. The methods are useful in the human medical and veterinary
fields, for medical diagnoses and clinical monitoring of a patient's
response to therapy where a disease or medical condition is associated

CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia.

SO Sequence 27 BP; 4 A; 6 C; 8 G; 9 U; 0 other;

Query Match 100.0%; Score 27; DB 21; Length 27;
Best Local Similarity 66.7%; Pred. No. 0.013;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCTCAGGCTGTGAGT 27
Db 1 UCUGACUUUGAGCCUCAGGUCUGAGU 27

RESULT 5

AAZ60840/C ID AAZ60840 standard; DNA; 54 BP.

AC AAZ60840;

DT 16-MAY-2000 (first entry)

DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.

XX Fusion transcript; translocation; bcr b3 region; abl gene;

KW amplification assay; detection assay; medical diagnosis;

KM clinical monitoring; chimeric RNA; fusion RNA; condition marker;

OS disease marker; cancer; leukemia; ss.

XX Synthetic.

PN WO200005418-A1.

XX 03-FEB-2000.

PF 23-JUL-1999; 99WO-US16832.

XX 23-JUL-1998; 98US-0121239.

PA (GENP-) GEN-PROBE INC.

PI Harvey RC, Eastman PS;

XX WPI: 2000-182730/16.

PT Novel methods for preparing RNA from biological samples, used for the

XX detection and measurement of nucleic acids and fusion nucleic acids -

Claim 19; Page 39; 49pp; English.
Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
the invention to detect fusion transcripts produced from a translocation
between the bcr b3 region and the abl gene. The specification describes
a method for detecting a fusion nucleic acid (particularly chimeric RNA
species), in a biological sample. The method comprises contacting a
sample of fusion nucleic acid with primers, amplifying the hybridized
fusion nucleic acid, and detecting the target hybrid. The method is
used for the simple and rapid preparation of RNA from a biological
sample, particularly from the cytoplasm of eukaryotic cells, which is
suitable for use in an amplification and detection assay. The methods
are used for the analysis and detection of nucleic acids in biological
samples. The methods are useful in the human medical and veterinary
fields, for medical diagnoses and clinical monitoring of a patient's
response to therapy where a disease or medical condition is associated
with a particular type and/or level of mRNA present in the sample. The
methods are also useful for detecting or quantifying fusion or chimeric
RNA species, and for detecting a translocation as a marker for a given
condition or disease, e.g. translocations associate with cancers,
particularly forms of leukemia.

SQ Sequence 54 BP; 20 A; 12 C; 11 G; 11 T; 0 other;
 Query Match 100.0%; Score 27; DB 21; Length 54;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 TCTGACTTTGAGCCTCAGGCTGTGAGT 27
 ID 1 TCTGACTTTGAGCCTCAGGCTGTGAGT 27
 DB 54 TCTGACTTTGAGCCTCAGGCTGTGAGT 28

RESULT 6
 AAZ60841/C
 ID AAZ60841 standard; RNA; 54 BP.

AC AAZ60841;
 DT 16-MAY-2000 (first entry)
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.
 KW Fusion transcript; translocation; bcr b3 region; abl gene;
 KW amplification assay; detection assay; medical diagnosis;
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
 KW disease marker; cancer; leukemia; ss.

OS Synthetic.
 PN WO200005418-A1.
 PD 03-FEB-2000.
 PF 23-JUL-1999; 99WO-US16832.
 PR 23-JUL-1998; 98US-0121239.
 PA (GENP-) GEN-PROBE INC.
 PI Harvey RC, Eastman PS;
 DR WPI: 2000-182730/16.

Novel methods for preparing RNA from biological samples, used for the detection and measurement of nucleic acids and fusion nucleic acids -
 Claim 19; Page 40; 49pp; English.

Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of the invention to detect fusion transcripts produced from a translocation between the bcr b3 region and the abl gene. The specification describes a method for detecting a fusion nucleic acid (particularly chimeric mRNA species), in a biological sample. The method comprises contacting a sample of fusion nucleic acid with primers, amplifying the hybridized fusion nucleic acid, and detecting the target hybrid. The method is used for the simple and rapid preparation of RNA from a biological sample, particularly from the cytoplasm of eukaryotic cells, which is suitable for use in an amplification and detection assay. The methods are used for the analysis and detection of nucleic acids in biological samples. The methods are useful in the human medical and veterinary fields, for medical diagnoses and clinical monitoring of a patient's response to therapy where a disease or medical condition is associated with a particular type and/or level of mRNA present in the sample. The methods are also useful for detecting or quantifying fusion or chimeric RNA species, and for detecting a translocation as a marker for a given condition or disease, e.g. translocations associate with cancers, particularly forms of leukemia.

Sequence 54 BP; 20 A; 12 C; 11 G; 11 U; 0 other;

Query Match 100.0%; Score 27; DB 21; Length 54;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGCTGTGAGT 27
 ID 1 TCTGACTTTGAGCCTCAGGCTGTGAGT 27
 DB 54 TCTGACTTTGAGCCTCAGGCTGTGAGT 28

RESULT 7
 AAZ60842
 ID AAZ60842 standard; DNA; 54 BP.

AC AAZ60842;
 DT 16-MAY-2000 (first entry)
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.
 KW Fusion transcript; translocation; bcr b3 region; abl gene;
 KW amplification assay; detection assay; medical diagnosis;
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
 KW disease marker; cancer; leukemia; ss.

OS Synthetic.
 PN WO200005418-A1.
 PD 03-FEB-2000.
 PF 23-JUL-1999; 99WO-US16832.
 PR 23-JUL-1998; 98US-0121239.
 PA (GENP-) GEN-PROBE INC.
 PI Harvey RC, Eastman PS;
 DR WPI: 2000-182730/16.

Novel methods for preparing RNA from biological samples, used for the detection and measurement of nucleic acids and fusion nucleic acids -
 Claim 19; Page 40; 49pp; English.

Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of the invention to detect fusion transcripts produced from a translocation between the bcr b3 region and the abl gene. The specification describes a method for detecting a fusion nucleic acid (particularly chimeric mRNA species), in a biological sample. The method comprises contacting a sample of fusion nucleic acid with primers, amplifying the hybridized fusion nucleic acid, and detecting the target hybrid. The method is used for the simple and rapid preparation of RNA from a biological sample, particularly from the cytoplasm of eukaryotic cells, which is suitable for use in an amplification and detection assay. The methods are used for the analysis and detection of nucleic acids in biological samples. The methods are useful in the human medical and veterinary fields, for medical diagnoses and clinical monitoring of a patient's response to therapy where a disease or medical condition is associated with a particular type and/or level of mRNA present in the sample. The methods are also useful for detecting or quantifying fusion or chimeric RNA species, and for detecting a translocation as a marker for a given condition or disease, e.g. translocations associate with cancers, particularly forms of leukemia.

Sequence 54 BP; 11 A; 11 C; 12 G; 20 T; 0 other;

Query Match 100.0%; Score 27; DB 21; Length 54;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGCTGTGAGT 27
 ID 1 TCTGACTTTGAGCCTCAGGCTGTGAGT 27
 DB 1 TCTGACTTTGAGCCTCAGGCTGTGAGT 27

RESULT 8

AAZ60843
ID AAZ60843 standard; RNA; 54 BP.
XX
AC AAZ60843;
XX
XX 16-MAY-2000 (first entry)
XX
XX Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX
XX Fusion transcript; translocation; bcr b3 region; abl gene;
XX amplification assay; detection assay; medical diagnosis;
XX clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX disease marker; cancer; leukemia; ss.
XX
XX Synthetic.
XX
XX W0200005418-A1.
XX
XX 03-FEB-2000.
XX
XX 23-JUL-1999; 99WO-US16832.
XX
XX 23-JUL-1998; 98US-0121239.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Harvey RC, Eastman PS;
XX
XX WPI: 2000-182730/16.
XX
XX Novel methods for preparing RNA from biological samples, used for the
XX detection and measurement of nucleic acids and fusion nucleic acids
XX
XX Claim 19, Page 40; 49pp: English.
XX
XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
XX the invention to detect fusion transcripts produced from a translocation
XX between the bcr b3 region and the abl gene. The specification describes
XX a method for detecting a fusion nucleic acid (particularly chimeric mRNA
XX species), in a biological sample. The method comprises contacting a
XX sample of fusion nucleic acid with primers, amplifying the hybridized
XX fusion nucleic acid, and detecting the target hybrid. The method is
XX used for the simple and rapid preparation of RNA from a biological
XX sample, particularly from the cytoplasm of eukaryotic cells, which is
XX suitable for use in an amplification and detection assay. The methods
XX are used for the analysis and detection of nucleic acids in biological
XX samples. The methods are useful in the human medical and veterinary
XX fields, for medical diagnoses and clinical monitoring of a patient's
XX response to therapy where a disease or medical condition is associated
XX with a particular type and/or level of mRNA present in the sample. The
XX methods are also useful for detecting or quantifying fusion or chimeric
XX RNA species, and for detecting a translocation as a marker for a given
XX condition or disease, e.g. translocations associate with cancers,
XX particularly forms of leukemia.
XX
XX Sequence 54 BP; 11 A; 11 C; 12 G; 20 U; 0 other;
XX
XX
XX Query Match 100.0%; Score 27; DB 21; Length 54;
XX Best Local Similarity 66.7%; Pred. No. 0.015;
XX Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27
XX :|||||:|||||:|||||:|||||:
XX 1 UCUGACUUGAGCCUCAGGCUUGAGU 27

RESULT 9
AAQ34631
ID AAQ34631 standard; cDNA; 80 BP.
XX
AC AAQ34631;
XX
XX 10-MAY-1993 (first entry)

XX
XX Human Ph1-positive cell line bcr-abl junction.
XX
XX Leukemia; treatment; blast crisis; specific; CML; translocation;
XX Philadelphia chromosome; chronic myeloid; chronic myelogenous;
XX leukemia; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Key 33..40
XX misc-feature /tag= a
XX /note= "bcr-abl breakpoint"
XX misc-feature 31..32
XX /tag= b
XX /note= "breakpoint junction target sequence"
XX
XX W09222303-A.
XX
XX 23-DEC-1992.
XX
XX 15-JUN-1992; 92WO-US05035.
XX
XX 18-JUN-1991; 91US-0718302.
XX
XX 14-APR-1992; 92US-0869911.
XX
XX (UTEM) UNIV TEMPLE.
XX
XX Calabretta B, Gewirtz AM;
XX
XX WPI: 1993-017893/02.
XX
XX Treating Ph1-positive leukemia(s) using bcr-abl anti-sense oligo-
XX nucleotide(s) - to selectively inhibit leukemic cell proliferation
XX without adversely affecting normal hematopoiesis
XX
XX Disclosure; Fig 5; 74pp: English.
XX
XX This is the sequence around the bcr-abl junction derived from the
XX cells of a Ph1 positive cell line. The bcr derived portion of the
XX sequence lies upstream from the breakpoint. The junction is formed
XX by the fusion of bcr exon 1 to c-abl exon 2.
XX
XX Sequence 80 BP; 16 A; 22 C; 27 G; 15 T; 0 other;
XX
XX
XX Query Match 96.3%; Score 26; DB 14; Length 80;
XX Best Local Similarity 100.0%; Pred. No. 0.042;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TCTGACTTTGAGCCTCAGGCTCTGAG 26
XX :|||||:|||||:|||||:|||||:
XX 55 TCTGACTTTGAGCCTCAGGCTCTGAG 80

RESULT 10
AAV20460
ID AAV20460 standard; DNA; 80 BP.
XX
AC AAV20460;
XX
XX 17-JUN-1998 (first entry)
XX
XX Human bcr-abl oncogene b1a2 genotype.
XX
XX Human; oncogene; proto-oncogene; neoplastic disease; anticancer;
XX cancer; antisense oligonucleotide; bcr-abl; ds.
XX
XX Homo sapiens.
XX
XX US5734039-A.
XX
XX 31-MAR-1998.

PF 15-SEP-1994; 94US-0306691.
 XX
 PR 15-SEP-1994; 94US-0306691.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Calabretta B, Skorski T;
 XX
 DR WPI; 1998-229882/20.
 XX
 PT Anticancer composition comprising two anti-sense oligo:nucleotide(s)
 XX - targeting cytoplasmic and nuclear oncogene(s)
 XX
 PS Claim 1: Column 109-110; 92pp; English.
 XX
 CC The present sequence represents an oncogene from the present invention.
 CC The present invention describes a composition which comprises two
 CC antisense oligonucleotides. The first oligonucleotide is specific for a
 CC cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1,
 CC c-fms, c-fos, c-kit, c-met, c-trk, c-src, c-abl, bcr-abl, c-fgr and
 CC c-yes. The second oligonucleotide is specific for a nuclear oncogene or
 CC proto-oncogene selected from myc, jun, c-ets, c-fos, c-myd, B-myd,
 CC c-rel, c-vav, c-ski, c-spl, cyclin D1, PML/RAR alpha, AML1/MF8,
 CC E2A/p1 and ALL-1/AF-4. The composition is used for treating cancer.
 CC The combination of antisense oligonucleotides has synergistically
 CC enhanced ability to inhibit growth of cancer cells.
 CC
 XX
 SO Sequence 80 BP; 16 A; 22 C; 27 G; 15 T; 0 other;
 XX
 Query Match 96.3%; Score 26; DB 19; Length 80;
 Best Local Similarity 100.0%; Pred. No. 0.042;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 OY 1 TCTGACTTTGAGCCTCAGGCTCTGAG 26
 Db 55 TCTGACTTTGAGCCTCAGGCTCTGAG 80
 XX
 RESULT 11
 ID AA086626/c
 XX AA086626 standard; DNA; 50 BP.
 XX
 AC AA086626;
 XX
 DT 15-NOV-1995 (first entry)
 XX
 DE CML chromosomal translocation minus strand primer.
 OS Primer; autocatalytic; target; CML; translocation; ss.
 XX
 OS Synthetic.
 XX
 PN US5399491-A.
 XX
 PD 21-MAR-1995.
 XX
 PF 11-JUL-1989; 89US-0379501.
 XX
 PR 11-JUL-1989; 89US-0379501.
 XX
 PR 10-JUL-1990; 90US-0550837.
 XX
 PR 19-MAR-1992; 92US-0855732.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Fultz TJ, Kacian DL;
 XX
 DR WPI; 1995-130686/17.
 XX
 PT Amplification of nucleic acid targets - using a reverse
 XX transcriptase with RNase H activity and a RNA polymerase at
 XX constant temp.
 PS Disclosure; Column 9; 58pp; English.

XX
 CC AA086626-28 are primers and a probe for the CML chromosomal
 CC translocation. They are used to produce autocatalytic
 CC oligonucleotides which require no change in the experimental
 CC conditions i.e. constant temperature, pH and ionic strength.
 CC These sequences are useful in generating multiple copies of
 CC specific nucleic acid target sequences.
 CC
 XX
 SO Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;
 XX
 Query Match 88.9%; Score 24; DB 16; Length 50;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 OY 4 GACTTTGAGCCTCAGGCTCTGAGT 27
 Db 50 GACTTTGAGCCTCAGGCTCTGAGT 27
 XX
 RESULT 12
 ID AAT42417/c
 XX AAT42417 standard; DNA; 50 BP.
 XX
 AC AAT42417;
 XX
 DT 28-APR-1997 (first entry)
 XX
 DE CML chromosomal translocation primer #1.
 XX
 KW HIV; probe; primer; amplify; polymerase chain reaction; microorganism;
 XX BCL-2; PCR; hepatitis B virus; HBV; CML; ss.
 XX
 OS Synthetic.
 XX
 PN BP731175-A2.
 XX
 PD 11-SEP-1996.
 XX
 PF 10-JUL-1990; 90EP-0307503.
 XX
 PR 11-JUL-1989; 89US-0379501.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI McDonough S;
 XX
 DR WPI; 1996-403995/41.
 XX
 PT Detection of HIV nucleic acids in samples - using new specific
 XX oligo-nucleotide(s) for the amplification and detection of target
 XX sequences.
 PS Disclosure; Page 8; 66pp; English.
 XX
 CC AAT42417-T42419 represent primers and a probe for the CML chromosomal
 CC translocation t(9;22). These sequences can be used in modified versions
 CC of the kits of the invention. The kits of the invention are for
 CC detecting the presence of HIV nucleic acid sequences in a sample. The
 CC kits comprise two amplification primers (such as AAT40182 and AAT40183),
 CC and a probe (such as AAT42404) for detection of the amplified sequence.
 CC By using these sequences, the amplification of HIV nucleic acid sequences
 CC is improved. The kits can also be used for the detection of other
 CC microorganisms, by using different probe sequences. Other sequences
 CC that can be detected using this method include those from HBV (using the
 CC sequences shown in AAT42410-T42412) and BCL-2 (using AAT42413-T42416).
 CC The samples can be clinical, environmental or forensic samples, and the
 CC method produces large amounts of the target sequence for a variety of
 CC uses. The method can also be used to produce multiple copies of a
 CC target sequence for use in cloning, and sequencing, and to produce probes
 CC for the target sequence.
 XX
 SO Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;

Query Match 88.9%; Score 24; DB 17; Length 50;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACTTGGAGCCTCAGGCTGAGT 27
 ||||||||||||||||||
 DB 50 GACTTGGAGCCTCAGGCTGAGT 27

RESULT 13

AAV15571/C
 ID AAV15571 standard; DNA; 50 BP.

AC AAV15571;

DT 17-JUL-1996 (first entry)

XX CML-2 chromosomal translocation major breakpoint t(9;22) (-) primer.

XX CML-2 chromosomal translocation major breakpoint; t(9;22); primer;
 auto-catalytic; synthesis; RNA target sequence; assay; detection;
 quantification; ss.

OS Synthetic.

XX US5480784-A.

PN 02-JAN-1996.

PD 11-JUL-1989; 89US-0379501.

PP 10-JUL-1990; 90US-0550837.

PR 11-JUL-1989; 89US-0379501.

XX (GENP-) GEN-PROBE INC.

XX Fultz TJ, Kacian DL;

XX WPI: 1996-068248/07.

XX Auto-catalytic synthesis of multiple copies of an RNA target
 sequence - uses cooperative action of a DNA and RNA polymerase in
 presence of RNase H, useful for detection of target sequence e.g. in
 clinical or environmental sample

XX Example; Columns 9-10; 51pp; English.

XX The present sequence is a primer for the CML-2 chromosomal
 translocation major breakpoint t(9;22), which was used to
 demonstrate an improved method for synthesising multiple copies of
 a RNA target sequence. The method comprises combining the target
 with a primer which hybridises to the 3'-terminal portion of the
 target, a promoter primer which hybridises with a portion of the
 DNA primer extension prod., reverse transcriptase, RNase H and
 transcriptase. It can be used as a component of an assay to detect
 and/or quantitate specific target sequences in clinical,
 environmental or forensic samples. It also has the advantages of
 being autocatalytic, using the cooperative action of a DNA
 polymerase e.g. a reverse transcriptase and avoids repetitive
 manipulations of reaction conditions, e.g. temp., ionic strength
 and pH.

XX Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;

XX Query Match 88.9%; Score 24; DB 17; Length 50;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACTTGGAGCCTCAGGCTGAGT 27
 ||||||||||||||||||
 DB 50 GACTTGGAGCCTCAGGCTGAGT 27

RESULT 14
 AAV6349/C
 ID AAV6349 standard; DNA; 50 BP.

AC AAV6349;

DT 06-JAN-1999 (first entry)

XX CML-2 chromosomal translocation t(9;22) primer.

XX CML-2 chromosomal translocation t(9;22); block splice template;
 autocatalytic RNA amplification; primer; ss.

OS Synthetic.

XX US5824518-A.

PN 20-OCT-1998.

PD 06-JUN-1995; 95US-0469067.

PP 10-JUL-1990; 90US-0550837.

PR 11-JUL-1989; 89US-0379501.

XX 06-JUN-1995; 95US-0469067.

XX (GENP-) GEN-PROBE INC.

XX Fultz TJ, Kacian DL;

XX WPI: 1998-582557/49.

XX Block splice template useful for amplification of nucleic acids -
 comprises two nucleic acid regions, the first region located 3' of
 the second region and blocked at its 3' terminus to inhibit primer
 extension by a DNA polymerase

XX Example 15; Column 9; 51pp; English.

XX AAV6349-50 represent CML-2 chromosomal translocation t(9;22) primers,
 for the (+) and (-) strands respectively. The primers are used to
 exemplify the invention, together with probe AAV6351. The specification
 describes methods of synthesising multiple copies of a target nucleic
 acid sequence autocatalytically under conditions of substantially
 constant temperature, ionic strength and pH are provided in which
 multiple RNA copies of the target sequence autocatalytically
 generate additional copies. The target sequence is a block splice
 template which comprises two nucleic acid regions. The first region is
 located 3' of the second region and is blocked at its 3' terminus to
 inhibit primer extension by a DNA polymerase, and the second region
 comprises a promoter sequence recognised by an RNA polymerase. The
 methods are used to amplify nucleic acids, especially RNA, for
 analysis, cloning or probe production.

XX Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;

XX Query Match 88.9%; Score 24; DB 19; Length 50;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACTTGGAGCCTCAGGCTGAGT 27
 ||||||||||||||||||
 DB 50 GACTTGGAGCCTCAGGCTGAGT 27

RESULT 15

AAV23191/C
 ID AAV23191 standard; DNA; 50 BP.

AC AAV23191;

DT 11-JUN-1999 (first entry)

XX CML chromosomal translocation t(9;22) primer #1.

XX Autocatalytic amplification; transcription-based amplification; CMU;
 KW thermalcycling; diagnostic; environmental testing; probe; detection;
 KW genetic disease; infectious disease; microorganism; food; forensic;
 KW paternity; primer; ss.

OS Synthetic.

PN US588779-A.

PD 30-MAR-1999.

PF 05-JUN-1995; 95US-0461654.

PR 10-JUL-1990; 90US-0550837.

PR 11-JUL-1989; 89US-0379501.

PR 05-JUN-1995; 95US-0461654.

PA (GENP-) GEN-PROBE INC.

DR Fultz TJ, Kacian DL;

WPI: 1999-253231/21.

Kit for autocatalytic amplification of RNA targets

Disclosure: Column 9; 51pp; English.

This invention describes a novel method for the autocatalytic amplification of an RNA target in a transcription-based amplification system without thermalcycling. The method generates oligonucleotides for diagnostic or environmental testing, for use e.g. as probes and in cloning. Typical applications are the detection of genetic or infectious diseases, the monitoring of responses to therapy, the quantitation or detection of microorganisms in foods, forensic studies and the establishment of paternity. Kits containing the products of the invention provide many copies of selected RNA targets under conditions of constant temperature, ionic strength and pH. Specific amplification of RNA targets increases sensitivity, convenience, accuracy and the reliability of assays.

Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;

Query Match 88.9%; Score 24; DB 20; Length 50;

Best Local Similarity 100.0%; Pred. No. 0.3;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 GACTTGAGCCTCAGGCTGAGT 27
 |||
 50 GACTTGAGCCTCAGGCTGAGT 27

Search completed: December 21, 2002, 11:54:42
 Job time : 94.6816 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:00:32 ; Search time 92.6816 Seconds
(without alignments)
656.052 Million cell updates/sec

Title:	US-09-121-239-23
Perfect score:	27
Sequence:	1 UCUGACUUUGAGCCUUCAGGUCUGAGU 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Searched:      2185239 seqs, 1125999159 residues
Total number of hits satisfying chosen parameters: 2390332
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Minimum DB seq length: 0
Maximum DB seq length: 100
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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Database :

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2: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT *
3: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT *
4: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT *
5: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT *
6: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT *
7: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT *
8: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT *
9: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT *
10: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT *
11: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT *
12: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT *
13: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT *
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15: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT *
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23: /SID5/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT *
24: /SID5/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	27	100.0	27	21	AAZ60859	Oligonucleotide us
c 2	27	100.0	27	21	AAZ60860	Oligonucleotide us
c 3	27	100.0	27	21	AAZ60861	Oligonucleotide us
4	27	100.0	27	21	AAZ60862	Oligonucleotide us
c 5	27	100.0	54	21	AAZ60841	Oligonucleotide us
c 6	27	100.0	54	21	AAZ60841	Oligonucleotide us
7	27	100.0	54	21	AAZ60842	Oligonucleotide us
8	27	100.0	54	21	AAZ60843	Oligonucleotide us
9	26	96.3	80	14	AAQ34631	Human PHL-positive

C	11	26	95.3	80	19	AAV0266
C	10	24	88.9	50	16	AAV08526
C	12	24	88.9	50	17	AAAT42417
C	13	24	88.9	50	17	AAAT15571
C	14	24	88.9	50	19	AAV66339
C	15	24	88.9	50	20	AAV23191
C	16	24	81.5	22	12	AAO14244
C	17	22	81.5	22	18	AAO62302
C	18	22	81.5	22	18	AAAT88787
C	19	22	81.5	22	24	AAV084198
C	20	20	74.1	50	19	AAV01841
C	21	19	70.4	24	19	AAV53784
C	22	19	70.4	70	19	AAV01832
C	23	18	66.7	63	19	AAV01831
C	24	17.4	64.4	23	16	AAO086124
C	25	17.4	64.4	49	24	AAH95372
C	26	17	63.0	56	14	AAH37652
C	27	17	63.0	56	14	AAO46949
C	28	17	63.0	68	19	AAV01830
C	29	16.4	60.7	28	20	AAH48408
C	30	16.4	60.7	65	24	AAH53875
C	31	16	59.3	67	19	AAO51057
C	32	15.8	58.5	20	14	AAO51029
C	33	15.8	58.5	60	24	AAH34614
C	34	15.8	58.5	60	24	AAH356106
C	35	15.8	58.5	65	24	AAH565106
C	36	15.6	57.8	90	24	AAH35611
C	37	15.6	57.0	80	20	AAH582463
C	38	15.6	57.0	38	24	AAH356139
C	39	15.2	56.3	29	17	AAAT38971
C	40	15.2	56.3	29	17	AAAT38971
C	41	15.2	56.3	51	22	AAH41436
C	42	15.2	56.3	60	24	AAH37050
C	43	15	55.6	16	18	AAV91968
C	44	15	55.6	20	19	AAV939479
C	45	15	55.6	21	21	AAV91680

ALIGNMENTS

Human bcr-abl onco
CML chromosomal tr
CML chromosomal tr
CML-2 chromosomal
CML-2 chromosomal
CML chromosomal tr
Primer CML1i. Syn
PCR primer for amp
Leukemic cell PCR
bcr/abl reverse PC
PCR primer ab50 u
Detection probe fo
Asymmetric hammer
Asymmetric hammer
bcr-abl mRNA junct
Human Ras GTP enzy
Human SNP flanking
Branched probe to
Asymmetric hammer
Primer for MLL1-MT
Mouse spliced tran
Asymmetric hammer
Human glucokinase
Human spliced tran
Human spliced tran
HIV DNA encoding G
Human spliced tran
Artificial NS4 mos
Human C10A1 gene e
Interleukin IL-3 r
Human interleukin-
Human DNA contain
Human spliced tran
RNA sequence disol
Chronic myelogenous
PCR primer for bcr

```

RESULT 1
AAZ60859/c
ID AAZ60859 standard; DNA; 27 BP.
XX
AC AAZ60859;
XX
DT 16-MAY-2000 (first entry)
XX
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX
DE Fusion transcript; translocation; bcr b3 region; abl gene;
XX amplification assay; detection assay; medical diagnosis;
XX clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX disease marker; cancer; leukemia; ss.
XX
OS Synthetic.
XX
PN WO200005418-A1.
XX
PD 03-FEB-2000.
XX
PF 23-JUL-1999; 99WD-0546832.
XX
PR 23-JUL-1998; 98UB-012139.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Harvey RC, Eastman PS;
XX
WI WPI; 2000-182730/16.
XX
PT Novel methods for preparing RNA from biological samples, used for the

```

PT detection and measurement of nucleic acids and fusion nucleic acids
XX
XX Claim 19; Page 43; 49pp; English.
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation
CC between the bcr b3 region and the abl gene. The specification describes
CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is
CC used for the simple and rapid preparation of RNA from a biological
CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC samples. The methods are useful in the human medical and veterinary
CC fields, for medical diagnoses and clinical monitoring of a patients
CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia.

SQ Sequence 27 BP; 9 A; 8 C; 6 G; 4 T; 0 other;

Query Match 100.0%; Score 27; DB 21; Length 27;

Best Local Similarity 66.7%; Pred. No. 0.013; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
QY 1 UCUGACUUGAGCCUCAGGUCUGAGU 27
DB 27 TCTGACTTTCAGCCACAGGCTCGAGT 1

RESULT 2

AAZ60860/C
ID AAZ60860 standard; RNA; 27 BP.

AC AAZ60860;

DT 16-MAY-2000 (first entry)

DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.

KW Fusion transcript; translocation; bcr b3 region; abl gene;

KW amplification assay; detection assay; medical diagnosis;

KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;

KW disease marker; cancer; leukemia; ss.

OS Synthetic.

PN WO200005418-A1.

PD 03-FEB-2000.

PF 23-JUL-1999; 99WO-US16832.

PR 23-JUL-1998; 98US-0121239.

PA (GENP-) GEN-PROBE INC.

PI Harvey RC, Eastman PS;

DR WPI; 2000-182730/16.

XX Novel methods for preparing RNA from biological samples, used for the
XX detection and measurement of nucleic acids and fusion nucleic acids
XX Claim 19; Page 43; 49pp; English.

CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation

CC between the bcr b3 region and the abl gene. The specification describes
CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is
CC used for the simple and rapid preparation of RNA from a biological
CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC samples. The methods are useful in the human medical and veterinary
CC fields, for medical diagnoses and clinical monitoring of a patients
CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia.

SQ Sequence 27 BP; 9 A; 8 C; 6 G; 4 U; 0 other;

Query Match 100.0%; Score 27; DB 21; Length 27;

Best Local Similarity 66.7%; Pred. No. 0.013; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
QY 1 UCUGACUUGAGCCUCAGGUCUGAGU 27
DB 27 TCTGACTTTCAGCCACAGGCTCGAGT 1

RESULT 3

AAZ60861
ID AAZ60861 standard; DNA; 27 BP.

AC AAZ60861;

DT 16-MAY-2000 (first entry)

DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.

KW Fusion transcript; translocation; bcr b3 region; abl gene;

KW amplification assay; detection assay; medical diagnosis;

KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;

KW disease marker; cancer; leukemia; ss.

OS Synthetic.

PN WO200005418-A1.

PD 03-FEB-2000.

PF 23-JUL-1999; 99WO-US16832.

PR 23-JUL-1998; 98US-0121239.

PA (GENP-) GEN-PROBE INC.

PI Harvey RC, Eastman PS;

DR WPI; 2000-182730/16.

XX Novel methods for preparing RNA from biological samples, used for the
XX detection and measurement of nucleic acids and fusion nucleic acids
XX Claim 19; Page 43; 49pp; English.

CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation
CC between the bcr b3 region and the abl gene. The specification describes
CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is
CC used for the simple and rapid preparation of RNA from a biological

CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC samples. The methods are useful in the human medical and veterinary
CC fields, for medical diagnoses and clinical monitoring of a patient's
CC response to therapy where a disease or medical condition is associated
CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia.

XX Sequence 27 BP; 4 A; 6 C; 8 G; 9 T; 0 other;

SO Query Match

Best Local Similarity 100.0%; Score 27; DB 21; Length 27;

Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

OY 1 UCUGACUUGAGCCUCAGGUCUGAGU 27

Db 1 TCTGACTTTGAGCCTCAGGCTCAGAGT 27

RESULT 4

AAZ60862 standard; RNA; 27 BP.

AAZ60862;

16-MAY-2000 (first entry)

Oligonucleotide used to detect bcr b3-abl fusion transcripts.

Fusion transcript; translocation; bcr b3 region; abl gene;

amplification assay; detection assay; medical diagnosis;

clinical monitoring; chimeric RNA; fusion RNA; condition marker;

disease marker; cancer; leukemia; ss.

Synthetic.

WO200005418-A1.

03-FEB-2000.

23-JUL-1999; 99WO-US16832.

23-JUL-1998; 98US-0121239.

(GENP-) GEN-PROBE INC.

Harvey RC, Eastman PS;

WPI; 2000-182730/16.

Claim 19; Page 44; 49pp; English.

Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
the invention to detect fusion transcripts produced from a translocation
between the bcr b3 region and the abl gene. The specification describes
a method for detecting a fusion nucleic acid (particularly chimeric RNA
species), in a biological sample. The method comprises contacting a
sample of fusion nucleic acid with primers, amplifying the hybridized
fusion nucleic acid, and detecting the target hybrid. The method is
used for the sample and rapid preparation of RNA from a biological
sample, particularly from the cytoplasm of eukaryotic cells, which is
suitable for use in an amplification and detection assay. The methods
are used for the analysis and detection of nucleic acids in biological
samples. The methods are useful in the human medical and veterinary
fields, for medical diagnoses and clinical monitoring of a patient's
response to therapy where a disease or medical condition is associated

CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia.

XX Sequence 27 BP; 4 A; 6 C; 8 G; 9 U; 0 other;

SO Query Match

Best Local Similarity 100.0%; Score 27; DB 21; Length 27;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 UCUGACUUGAGCCUCAGGUCUGAGU 27

Db 1 TCTGACTTTGAGCCTCAGGCTCAGAGT 27

RESULT 5

AAZ60840/C standard; DNA; 54 BP.

AAZ60840;

16-MAY-2000 (first entry)

Oligonucleotide used to detect bcr b3-abl fusion transcripts.

Fusion transcript; translocation; bcr b3 region; abl gene;

amplification assay; detection assay; medical diagnosis;

clinical monitoring; chimeric RNA; fusion RNA; condition marker;

disease marker; cancer; leukemia; ss.

Synthetic.

WO200005418-A1.

03-FEB-2000.

23-JUL-1999; 99WO-US16832.

23-JUL-1998; 98US-0121239.

(GENP-) GEN-PROBE INC.

Harvey RC, Eastman PS;

WPI; 2000-182730/16.

Claim 19; Page 39; 49pp; English.

Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
the invention to detect fusion transcripts produced from a translocation
between the bcr b3 region and the abl gene. The specification describes
a method for detecting a fusion nucleic acid (particularly chimeric RNA
species), in a biological sample. The method comprises contacting a
sample of fusion nucleic acid with primers, amplifying the hybridized
fusion nucleic acid, and detecting the target hybrid. The method is
used for the sample and rapid preparation of RNA from a biological
sample, particularly from the cytoplasm of eukaryotic cells, which is
suitable for use in an amplification and detection assay. The methods
are used for the analysis and detection of nucleic acids in biological
samples. The methods are useful in the human medical and veterinary
fields, for medical diagnoses and clinical monitoring of a patient's
response to therapy where a disease or medical condition is associated
with a particular type and/or level of mRNA present in the sample. The
methods are also useful for detecting or quantifying fusion or chimeric
RNA species, and for detecting a translocation as a marker for a given
condition or disease, e.g. translocations associate with cancers,
particularly forms of leukemia.

SQ Sequence 54 BP; 20 A; 12 C; 11 G; 11 T; 0 other;
Query Match 100.0%; Score 27; DB 21; Length 54;
Best Local Similarity 66.7%; Pred. No. 0.015;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
DB 54 TCTGACTTTGAGCCTCAGGCTCTGAGT 28

QY 1 UCUGACUUGAGCCUCAGGUCUGAGU 27
:|||||:|||||:|||||:|||||:
AAZ60841/c
ID AAZ60841 standard; RNA; 54 BP.
XX
AC AAZ60841;
XX
DT 16-MAY-2000 (first entry)
XX
XX Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX
XX Fusion transcript; translocation; bcr b3 region; abl gene;
XX amplification assay; detection assay; medical diagnosis;
XX clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX disease marker; cancer; leukemia; ss.
XX
XX Synthetic.
XX
XX WO200005418-A1.
XX
XX 03-FEB-2000.
XX
XX 23-JUL-1999; 99WO-US16832.
XX
XX 23-JUL-1998; 98US-0121239.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Harvey RC, Eastman PS;
XX
XX WPI: 2000-182730/16.
XX
XX Novel methods for preparing RNA from biological samples, used for the
XX detection and measurement of nucleic acids and fusion nucleic acids -
XX
XX Claim 19; Page 40; 49pp; English.

CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation
CC between the bcr b3 region and the abl gene. The specification describes
CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is
CC used for the simple and rapid preparation of RNA from a biological
CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC samples. The methods are useful in the human medical and veterinary
CC fields, for medical diagnoses and clinical monitoring of a patients
CC response to therapy where a disease or medical condition is associated
CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia.
XX
XX Sequence 54 BP; 20 A; 12 C; 11 G; 11 U; 0 other;
SQ
Query Match 100.0%; Score 27; DB 21; Length 54;
Best Local Similarity 66.7%; Pred. No. 0.015;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUGAGCCUCAGGUCUGAGU 27
:|||||:|||||:|||||:|||||:
DB 54 TCTGACTTTGAGCCTCAGGCTCTGAGT 28

RESULT 7
AAZ60842
ID AAZ60842 standard; DNA; 54 BP.
XX
XX AAZ60842;
XX
XX 16-MAY-2000 (first entry)
XX
XX Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX
XX Fusion transcript; translocation; bcr b3 region; abl gene;
XX amplification assay; detection assay; medical diagnosis;
XX clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX disease marker; cancer; leukemia; ss.
XX
XX Synthetic.
XX
XX WO200005418-A1.
XX
XX 03-FEB-2000.
XX
XX 23-JUL-1999; 99WO-US16832.
XX
XX 23-JUL-1998; 98US-0121239.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Harvey RC, Eastman PS;
XX
XX WPI: 2000-182730/16.
XX
XX Novel methods for preparing RNA from biological samples, used for the
XX detection and measurement of nucleic acids and fusion nucleic acids -
XX
XX Claim 19; Page 40; 49pp; English.

CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation
CC between the bcr b3 region and the abl gene. The specification describes
CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is
CC used for the simple and rapid preparation of RNA from a biological
CC sample, particularly from the cytoplasm of eukaryotic cells, which is
CC suitable for use in an amplification and detection assay. The methods
CC are used for the analysis and detection of nucleic acids in biological
CC samples. The methods are useful in the human medical and veterinary
CC fields, for medical diagnoses and clinical monitoring of a patients
CC response to therapy where a disease or medical condition is associated
CC with a particular type and/or level of mRNA present in the sample. The
CC methods are also useful for detecting or quantifying fusion or chimeric
CC RNA species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia.
XX
XX Sequence 54 BP; 11 A; 11 C; 12 G; 20 T; 0 other;
SQ
Query Match 100.0%; Score 27; DB 21; Length 54;
Best Local Similarity 66.7%; Pred. No. 0.015;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
DB 1 UCUGACUUGAGCCUCAGGUCUGAGU 27
:|||||:|||||:|||||:|||||:
DB 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27

RESULT 8

PF 15-SEP-1994; 94US-0306691.
 XX
 PR 15-SEP-1994; 94US-0306691.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Calabretta B, Skorski T;
 XX
 DR WPI; 1998-229882/20.
 XX
 PT Anticancer composition comprising two anti-sense oligo:nucleotide(s)
 PT - targeting cytoplasmic and nuclear oncogene(s)
 XX
 PS Claim 1; Column 109-110; 92pp; English.
 XX
 CC The present sequence represents an oncogene from the present invention.
 CC The present invention describes a composition which comprises two
 CC antisense oligonucleotides. The first oligonucleotide is specific for a
 CC cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1,
 CC c-fms, c-ros, c-kit, c-met, c-erb, c-src, c-abl, bcr-abl, c-fgr and
 CC c-yes. The second oligonucleotide is specific for a nuclear oncogene or
 CC proto-oncogene selected from myc, jun, c-ets, c-fos, c-myc, B-myc,
 CC c-rel, c-vav, c-ski, c-spl, cyclin D1, PML/RAR alpha, AML1/MF68,
 CC E2A/Pt1 and AUL-1/AF-4. The composition is used for treating cancer.
 CC The combination of antisense oligonucleotides has synergistically
 CC enhanced ability to inhibit growth of cancer cells.
 CC
 XX
 SQ Sequence 80 BP; 16 A; 22 C; 27 G; 15 T; 0 other;
 XX
 Query Match 96.3%; Score 26; DB 19; Length 80;
 Best Local Similarity 69.2%; Pred. No. 0.042; 0; Indels 0; Gaps 0;
 Matches 18; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
 OY 1 UCUGACUUUGAGCCUCAGGUCUGAG 26
 :|||||:|||||:|||||:|||||:
 Db 55 TCTGACTTTGAGCCTCAGGCTGTGAG 80
 {
 RESULT 11
 ID AA086626/c
 AA086626 standard; DNA; 50 BP.
 XX
 AC AA086626;
 XX
 DT 15-NOV-1995 (first entry)
 XX
 DE CML chromosomal translocation minus strand primer.
 XX
 CM Primer; autocatalytic; target; CML; translocation; ss.
 XX
 OS Synthetic.
 XX
 PN US5399491-A.
 XX
 PD 21-MAR-1995.
 XX
 PF 11-JUL-1989; 89US-0379501.
 XX
 PR 11-JUL-1989; 89US-0379501.
 PR 10-JUL-1990; 90US-0550837.
 PR 19-MAR-1992; 92US-0855732.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Fultz TJ, Kacian DL;
 XX
 DR WPI; 1995-130686/17.
 XX
 PT Amplification of nucleic acid targets - using a reverse
 PT transcriptase with RNase H activity and a RNA polymerase at
 PT constant temp.
 XX
 PS Disclosure; Column 9; 58pp; English.

XX
 CC AA086626-28 are primers and a probe for the CML chromosomal
 CC translocation. They are used to produce autocatalytic
 CC oligonucleotides which require no change in the experimental
 CC conditions i.e. constant temperature, pH and ionic strength.
 CC These sequences are useful in generating multiple copies of
 CC specific nucleic acid target sequences.
 CC
 XX
 SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;
 XX
 Query Match 88.9%; Score 24; DB 16; Length 50;
 Best Local Similarity 70.8%; Pred. No. 0.3;
 Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
 OY 4 GACUUGAGCCUCAGGUCUGAGU 27
 |||||:|||||:|||||:|||||:
 Db 50 GACTTTGAGCCTCAGGCTGTGAGT 27
 {
 RESULT 12
 ID AAT42417/c
 AAT42417 standard; DNA; 50 BP.
 XX
 AC AAT42417;
 XX
 DT 28-APR-1997 (first entry)
 XX
 DE CML chromosomal translocation primer #1.
 XX
 KW HIV; probe; primer; amplify; polymerase chain reaction; microorganism;
 KW BCL-2; PCR; hepatitis B virus; HBV; CML; ss.
 KW
 XX
 OS Synthetic.
 XX
 PN EP731175-A2.
 XX
 PD 11-SEP-1996.
 XX
 PF 10-JUL-1990; 90EP-0307503.
 XX
 PR 11-JUL-1989; 89US-0379501.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI McDonough S;
 XX
 DR WPI; 1996-403995/41.
 XX
 PT Detection of HIV nucleic acids in samples - using new specific
 PT oligo-nucleotide(s) for the amplification and detection of target
 PT sequences.
 XX
 PS Disclosure; Page 8; 66pp; English.
 XX
 CC AAT42417-T42419 represent primers and a probe for the CML chromosomal
 CC translocation t(9;22). These sequences can be used in modified versions
 CC of the kits of the invention. The kits of the invention, are for
 CC detecting the presence of HIV nucleic acid sequences in a sample. The
 CC kits comprise two amplification primers (such as AAT40182 and AAT40183),
 CC by using these sequences, the amplification of HIV nucleic acid sequences
 CC is improved. The kits can also be used for the detection of other
 CC microorganisms, by using different probe sequences. Other sequences
 CC that can be detected using this method include those from HBV (using the
 CC sequences shown in AAT42410-T42412), and BCL-2 (using AAT42413-T42415).
 CC The samples can be clinical, environmental or forensic samples, and the
 CC method produces large amounts of the target sequence for a variety of
 CC uses. The method can also be used to produce multiple copies of a
 CC target sequence for use in cloning, and sequencing, and to produce probes
 CC for the target sequence.
 CC
 XX
 SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;

```

Query Match      88.9%; Score 24; DB 17; Length 50;
Best Local Similarity 70.8%; Pred. No. 0.3;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACUUUGAGCCGUCGUCAGU 27
DB 50 GACUUGAGCCGUCGUCAGU 27

RESULT 13
AA15571/c
ID AA15571 standard; DNA; 50 BP.
AC AA15571;
AT 17-JUL-1996 (first entry)
DE CML-2 chromosomal translocation major breakpoint t(9;22) (-) primer.
XX
XX CML-2 chromosomal translocation major breakpoint; t(9;22); primer;
XX auto-catalytic; synthesis; RNA target sequence; assay; detection;
XX quantification; ss.
XX Synthetic.
XX OS
XX US5480784-A.
XX PN
XX 02-JAN-1996.
XX PD
XX 11-JUL-1989; 89US-0379501.
XX PE
XX 10-JUL-1990; 90US-0550837.
XX PR 11-JUL-1989; 89US-0379501.
XX PS (GENP-) GEN-PROBE INC.
XX PA
XX Fultz TJ, Kacian DL;
XX PI
XX WPI; 1996-068248/07.
XX DR
XX
XX PT Auto-catalytic synthesis of multiple copies of an RNA target
XX sequence - uses cooperative action of a DNA and RNA polymerase in
XX presence of RNase H, useful for detection of target sequence e.g. in
XX clinical or environmental sample
XX PT
XX PS Example; Columns 9-10; 51bp; English.
XX
XX CC The present sequence is a primer for the CML-2 chromosomal
XX translocation major breakpoint t(9;22), which was used to
XX demonstrate an improved method for synthesizing multiple copies of
XX a RNA target sequence. The method comprises combining the target
XX with a primer which hybridises to the 3'-terminal portion of the
XX target, a promoter primer which hybridises with a portion of the
XX DNA primer extension prod., reverse transcriptase, RNase H and
XX transcripase. It can be used as a component of an assay to detect
XX and/or quantitate specific target sequences in clinical,
XX environmental or forensic samples. It also has the advantages of
XX being autocatalytic, using the cooperative action of a DNA
XX polymerase, e.g. a reverse transcriptase and avoids repetitive
XX manipulations of reaction conditions, e.g. temp., ionic strength
XX and pH.
XX
XX SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;

Query Match      88.9%; Score 24; DB 17; Length 50;
Best Local Similarity 70.8%; Pred. No. 0.3;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACUUUGAGCCGUCGUCAGU 27
DB 50 GACUUGAGCCGUCGUCAGU 27

RESULT 14
AAV6349/c
ID AAV6349 standard; DNA; 50 BP.
AC AAV6349;
AT 06-JAN-1999 (first entry)
DE CML-2 chromosomal translocation t(9;22) primer.
XX
XX CML-2 chromosomal translocation t(9;22); block splice template;
XX autocatalytic RNA amplification; primer; ss.
XX
XX OS
XX Synthetic.
XX PN
XX US5824518-A.
XX PD
XX 20-OCT-1998.
XX PE
XX 06-JUN-1995; 95US-0469067.
XX PR 10-JUL-1990; 90US-0550837.
XX PR 11-JUL-1989; 89US-0379501.
XX PR 06-JUN-1995; 95US-0469067.
XX PS (GENP-) GEN-PROBE INC.
XX PA
XX Fultz TJ, Kacian DL;
XX PI
XX WPI; 1998-582557/49.
XX DR
XX
XX PT Block splice template useful for amplification of nucleic acids -
XX comprises two nucleic acid regions, the first region located 3' of
XX the second region and blocked at its 3' terminus to inhibit primer
XX extension by a DNA polymerase
XX PT
XX PS Example 15; Column 9; 51bp; English.
XX
XX CC AAV6349-50 represent CML-2 chromosomal translocation t(9;22) primers,
XX for the (+) and (-) strands respectively. The primers are used to
XX exemplify the invention, together with probe AAV6351. The specification
XX describes methods of synthesizing multiple copies of a target nucleic
XX acid sequence autocatalytically under conditions of substantially
XX constant temperature, ionic strength and pH are provided in which
XX multiple RNA copies of the target sequence autocatalytically
XX generate additional copies. The target sequence is a block splice
XX template which comprises two nucleic acid regions. The first region is
XX located 3' of the second region and is blocked at its 3' terminus to
XX inhibit primer extension by a DNA polymerase, and the second region
XX comprises a promoter sequence recognised by an RNA polymerase. The
XX methods are used to amplify nucleic acids, especially RNA, for
XX analysis, cloning or probe production.
XX
XX SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;

Query Match      88.9%; Score 24; DB 19; Length 50;
Best Local Similarity 70.8%; Pred. No. 0.3;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACUUUGAGCCGUCGUCAGU 27
DB 50 GACUUGAGCCGUCGUCAGU 27

RESULT 15
AA23191/c
ID AA23191 standard; DNA; 50 BP.
AC AA23191;
AT 11-JUN-1999 (first entry)
DE CML chromosomal translocation t(9;22) primer #1.

```

XX Autocatalytic amplification; transcription-based amplification; CMU;
 KW thermalcycling; diagnostic; environmental testing; probe; detection;
 KW genetic disease; infectious disease; microorganism; food; forensic;
 KW paternity; primer; ss.

OS Synthetic.

PN US5888779-A.

PD 30-MAR-1999.

PP 05-JUN-1995; 95US-0461654.

XX 10-JUL-1990; 90US-0550837.

PR 11-JUL-1989; 89US-0379501.

PR 05-JUN-1995; 95US-0461654.

XX (GENP-) GEN-PROBE INC.

PI Fultz TJ, Kacian DL;

DR WPI; 1999-253231/21.

XX Kit for autocatalytic amplification of RNA targets

PS Disclosure: Column 9; Sipp; English.

CC This invention describes a novel method for the autocatalytic
 CC amplification of an RNA target in a transcription-based amplification
 CC system without thermalcycling. The method generates oligonucleotides for
 CC diagnostic or environmental testing, for use e.g. as probes and in
 CC cloning. Typical applications are the detection of genetic or infectious
 CC diseases, the monitoring of responses to therapy, the quantitation or
 CC detection of microorganisms in foods, forensic studies and the
 CC establishment of paternity. Kits containing the products of the invention
 CC provide many copies of selected RNA targets under conditions of constant
 CC temperature, ionic strength and pH. Specific amplification of RNA targets
 CC increases sensitivity, convenience, accuracy and the reliability of
 CC assays.

XX Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 other;

Query Match 88.9%; Score 24; DB 20; Length 50;

Best Local Similarity 70.8%; Pred. No. 0.3;

Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

XX 4 GACUUUGAGCCUCAGGCGUCGAGU 27

DB 50 GACTTGGAGCCTCAGGCTCTGAGT 27

Search completed: December 21, 2002, 11:54:43
 Job time : 93.6816 secs

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:00:32 : Search time 82.3837 Seconds
(without alignments)
656.052 Million cell updates/sec

Title: US-09-121-239-16
Perfect score: 24
Sequence: 1 GTGGAACATGAAGCCCTWCAAGCG 24

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	24	100.0	24	AAZ60855
2	24	100.0	24	AAZ60856
3	24	100.0	24	AAZ60857
4	24	100.0	24	AAZ60858
5	17.2	71.7	60	ABN38552
6	17.2	71.7	65	ABN54940
7	15.8	65.8	56	AAO46947
8	15.8	65.8	60	ABN33790
9	15.6	65.0	35	AAA47720

C	10	15.6	65.0	35	22	AAZ16331	Human KOD delta (r
C	11	15.6	65.0	42	22	AAZ12048	Antisense oligonuc
C	12	15.6	65.0	95	22	ABAV3324	Human foetal liver
C	13	15.6	65.0	95	22	AAK21762	Human brain expres
C	14	15.6	65.0	95	22	AAK47927	Human bone marrow
C	15	15.6	65.0	95	22	AAI53756	Probe #22442 used
C	16	15.6	65.0	95	24	ABN21891	Human genome-deriv
C	17	15.4	64.2	23	16	AAZ56766	Human bcr/abl b2-a
C	18	15.4	64.2	23	16	AAZ56766	Human bcr/abl b2-a
C	19	15.4	64.2	40	15	AAO57147	Chromosomal trans
C	20	15.4	64.2	52	17	AAZ12637	T7 promoter-acute
C	21	15.4	64.2	60	17	AAZ29713	Chronic myeloid le
C	22	15.4	64.2	62	15	AAO66774	l6(1131 ribozyme s
C	23	15.2	63.3	61	22	AAK96535	Human neuroregulin
C	24	15.2	63.3	61	22	AAK98028	Human neuroregulin
C	25	15.2	62.5	33	17	AAZ10495	BCR-ABL oncogene f
C	26	15.2	62.5	33	17	AAZ10497	ABL oncogene-Intro
C	27	15.2	62.5	34	21	AAZ24225	M. thermophilus lac
C	28	15.2	62.5	34	21	AAZ24225	Ribozyme substrate
C	29	15.2	62.5	47	15	AAO66785	Human spliced tran
C	30	15.2	62.5	60	24	ABN3928	Mouse spliced tran
C	31	15.2	62.5	65	24	ABN35678	Human phi-positive
C	32	15.2	62.5	80	14	AAQ34631	Human bcr-abi onco
C	33	15.2	62.5	80	19	AAV20460	Sense PCR primer 7
C	34	14.8	61.7	31	20	AAV83517	Human b2a2 sense p
C	35	14.6	60.8	38	21	ABN38822	Forward PCR primer
C	36	14.4	60.0	23	14	AAQ34658	Human b2a2 sense p
C	37	14.4	60.0	23	22	AAZ27985	Human b2a2 junctio
C	38	14.4	60.0	26	14	AAO34653	Human b2a2 junctio
C	39	14.4	60.0	26	15	AAO64687	Human b2a2 junctio
C	40	14.4	60.0	26	15	AAO57148	Chromosomal trans
C	41	14.4	60.0	26	15	AAO56493	Probe for 3SR ampl
C	42	14.4	60.0	26	19	AAV20478	Human b2/a2 bcr-ab
C	43	14.4	60.0	33	24	AAV01856	Oligodeoxynucleot
C	44	14.4	60.0	33	24	AAV172671	Human retinoblasto
C	45	14.4	60.0	59	19	AAV61667	Fusarium sp. 188 r

ALIGNMENTS

RESULT 1
AAZ60855 standard; DNA: 24 BP.
AAZ60855:
16-MAY-2000 (first entry)
Oligonucleotide used to detect bcr b3-abi fusion transcripts.
Fusion transcript; translocation; bcr b3 region; abl gene;
amplification assay; detection assay; medical diagnosis;
clinical monitoring; chimeric RNA; fusion RNA; condition marker;
disease marker; cancer; leukemia; ss.
Synthetic
WO200005418-A1.
03-FEB-2000.
23-JUL-1999: 99WO-US16832.
23-JUL-1999: 99US-0121239.
(GENP-) GEN-PROBE INC.
Harvey RC, Eastman PS;
WPI: 2000-182730/16.
Novel methods for preparing RNA from biological samples, used for the

PT detection and measurement of nucleic acids and fusion nucleic acids
 XX
 PS Claim 19; Page 42; 49pp; English.
 CC
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
 CC the invention to detect fusion transcripts produced from a translocation
 CC between the bcr b3 region and the abl gene. The specification describes
 CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
 CC species), in a biological sample. The method comprises contacting a
 CC sample of fusion nucleic acid with primers, amplifying the hybridized
 CC fusion nucleic acid, and detecting the target hybrid. The method is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC samples. The methods are useful in the human medical and veterinary
 CC fields, for medical diagnoses and clinical monitoring of a patients
 CC response to therapy where a disease or medical condition is associated
 CC with a particular type and/or level of mRNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associate with cancers,
 CC particularly forms of leukemia.
 CC
 SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;
 Query Match 100.0%; Score 24; DB 21; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.088;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GTGGACATGAGCCCTTCAGCGG 24
 ||||||||||||||||||||
 Db 1 GTGGACATGAGCCCTTCAGCGG 24
 RESULT 2
 AAZ60856
 ID AAZ60856 standard; RNA; 24 BP.
 AC
 AC AAZ60856;
 DT 16-MAY-2000 (first entry)
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.
 DE
 XX Fusion transcript; translocation; bcr b3 region; abl gene;
 KW amplification assay; detection assay; medical diagnosis;
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
 KW disease marker; cancer; leukemia; ss.
 XX
 OS Synthetic.
 XX
 XX WO200005418-A1.
 PN
 XX
 PD 03-FEB-2000.
 PD
 XX
 PF 23-JUL-1999; 99WO-US16832.
 PF
 XX
 PR 23-JUL-1998; 98US-0121239.
 PR
 XX
 PA (GENP-) GEN-PROBE INC.
 PA
 XX Harvey RC, Eastman PS;
 PI
 XX
 DR WPI; 2000-182730/16.
 DR
 XX Novel methods for preparing RNA from biological samples, used for the
 PT detection and measurement of nucleic acids and fusion nucleic acids
 PT
 XX Claim 19; Page 42; 49pp; English.
 PS
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
 CC the invention to detect fusion transcripts produced from a translocation

CC between the bcr b3 region and the abl gene. The specification describes
 CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
 CC species), in a biological sample. The method comprises contacting a
 CC sample of fusion nucleic acid with primers, amplifying the hybridized
 CC fusion nucleic acid, and detecting the target hybrid. The method is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC samples. The methods are useful in the human medical and veterinary
 CC fields, for medical diagnoses and clinical monitoring of a patients
 CC response to therapy where a disease or medical condition is associated
 CC with a particular type and/or level of mRNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associate with cancers,
 CC particularly forms of leukemia.
 CC
 SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 U; 0 other;
 Query Match 100.0%; Score 24; DB 21; Length 24;
 Best Local Similarity 83.3%; Pred. No. 0.088;
 Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GTGGACATGAGCCCTTCAGCGG 24
 ||||||||||||||||||||
 Db 1 GTGGACATGAGCCCTTCAGCGG 24
 RESULT 3
 AAZ60857/c
 ID AAZ60857 standard; DNA; 24 BP.
 AC
 AC AAZ60857;
 DT 16-MAY-2000 (first entry)
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.
 DE
 XX Fusion transcript; translocation; bcr b3 region; abl gene;
 KW amplification assay; detection assay; medical diagnosis;
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
 KW disease marker; cancer; leukemia; ss.
 XX
 OS Synthetic.
 XX
 XX WO200005418-A1.
 PN
 XX
 PD 03-FEB-2000.
 PD
 XX
 PF 23-JUL-1999; 99WO-US16832.
 PF
 XX
 PR 23-JUL-1998; 98US-0121239.
 PR
 XX
 PA (GENP-) GEN-PROBE INC.
 PA
 XX Harvey RC, Eastman PS;
 PI
 XX
 DR WPI; 2000-182730/16.
 DR
 XX Novel methods for preparing RNA from biological samples, used for the
 PT detection and measurement of nucleic acids and fusion nucleic acids
 PT
 XX Claim 19; Page 43; 49pp; English.
 PS
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
 CC the invention to detect fusion transcripts produced from a translocation
 CC between the bcr b3 region and the abl gene. The specification describes
 CC a method for detecting a fusion nucleic acid (particularly chimeric mRNA
 CC species), in a biological sample. The method comprises contacting a
 CC sample of fusion nucleic acid with primers, amplifying the hybridized
 CC fusion nucleic acid, and detecting the target hybrid. The method is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC samples. The methods are useful in the human medical and veterinary
 CC fields, for medical diagnoses and clinical monitoring of a patients
 CC response to therapy where a disease or medical condition is associated
 CC with a particular type and/or level of mRNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associate with cancers,
 CC particularly forms of leukemia.

CC sample, particularly from the cytoplasm of eukaryotic cells, which is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC samples. The methods are useful in the human medical and veterinary
 CC fields, for medical diagnoses and clinical monitoring of a patient's
 CC response to therapy where a disease or medical condition is associated
 CC with a particular type and/or level of mRNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associate with cancers,
 CC particularly forms of leukemia.

SO Sequence 24 BP; 4 A; 8 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 24; DB 21; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.088;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGGACATGAGCCCTCAGCG 24
 ||||||||||||||||||||
 DB 24 GTGGACATGAGCCCTCAGCG 1

RESULT 4
 AA60858/C
 ID AA60858 standard; RNA; 24 BP.
 XX AA60858;
 AC
 XX
 DT 16-MAY-2000 (first entry)
 DE
 XX Oligonucleotide used to detect bcr b3-abl fusion transcripts.
 XX
 KW Fusion transcript; translocation; bcr b3 region; abl gene;
 KW amplification assay; detection assay; medical diagnosis;
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
 KW disease marker; cancer; leukemia; ss.
 XX
 OS Synthetic.
 XX
 PN WO200005418-A1.
 PD
 XX 03-FEB-2000.
 XX
 PF 23-JUL-1999; 99WO-US16832.
 XX
 PR 23-JUL-1998; 98US-0121239.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Harvey RC, Eastman PS;
 XX
 DR WPI; 2000-182730/16.
 XX
 PT Novel methods for preparing RNA from biological samples, used for the
 PT detection and measurement of nucleic acids and fusion nucleic acids -
 XX
 PS Claim 19; Page 43; 49pp; English.

CC Oligonucleotides AA60840-62 and AA60865-66 are used in the method of
 CC the invention to detect fusion transcripts produced from a translocation
 CC between the bcr b3 region and the abl gene. The specification describes
 CC a method for detecting a fusion nucleic acid (particularly chimeric RNA
 CC species), in a biological sample. The method comprises contacting a
 CC sample of fusion nucleic acid with primers, amplifying the hybridized
 CC fusion nucleic acid, and detecting the target hybrid. The method is
 CC used for the simple and rapid preparation of RNA from a biological
 CC sample, particularly from the cytoplasm of eukaryotic cells, which is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC fields, for medical diagnoses and clinical monitoring of a patient's
 CC response to therapy where a disease or medical condition is associated

CC with a particular type and/or level of mRNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associate with cancers,
 CC particularly forms of leukemia.

SO Sequence 24 BP; 4 A; 8 C; 6 G; 6 U; 0 other;

Query Match 100.0%; Score 24; DB 21; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.088;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGGACATGAGCCCTCAGCG 24
 ||||||||||||||||||||
 DB 24 GTGGACATGAGCCCTCAGCG 1

RESULT 5
 ABN38552
 ID ABN38552 standard; DNA; 60 BP.
 XX ABN38552;
 AC
 XX
 DT 15-JUL-2002 (first entry)
 DE
 XX Human spliced transcript detection oligonucleotide SEQ ID NO:11300.
 XX
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200210449-A2.
 PD
 XX 07-FEB-2002.
 XX
 PF 20-JUL-2001; 2001WO-IB01903.
 XX
 PR 28-JUL-2000; 2000US-221607P.
 XX
 PR 02-MAY-2001; 2001US-287724P.
 XX
 PA (COMP-) COMPUGEN INC.
 XX
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 XX
 DR WPI; 2002-257383/30.
 XX
 PT New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of
 PT a genome, useful for detecting tissue-, pathology-, and
 PT developmental-specific genes -
 XX
 PS Example 1; SEQ ID 11300; 47pp; English.

CC The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises
 CC several oligonucleotides, each capable of hybridizing selectively to a
 CC set of messenger RNAs transcribed from a given transcriptome unit of
 CC the genome, which encodes one or more messenger RNA splice variants.
 CC The oligonucleotide libraries are useful for detecting mRNAs from a
 CC biologically sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterizing the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a
 CC particular biological or pathological state, and so allowing the
 CC detection of tissue- and pathology-specific genes such as those genes
 CC only expressed in specific tissue under a specific pathological
 CC condition; to detect developmental specific genes; and to detect RNA
 CC transcripts and splice variants of a transcriptome of a patient suffering
 CC from a particular disorder. ABN27253 to ABN9589 represent

CC oligonucleotide sequences from rats, humans and mice, which are used in
 CC the exemplification of the present invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.

XX Sequence 60 BP; 16 A; 17 C; 17 G; 10 T; 0 other;

SO Query Match 71.7%; Score 17.2; DB 24; Length 60;

Best Local Similarity 86.4%; Pred. No. 1.5e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 GGACATGAGCCCTTCAGCG 24
 Db 23 GGACATGAGCTCATCAGCTG 44

RESULT 6
 ABN54940

ID ABN54940 standard; DNA: 65 BP.

AC ABN54940;

DE 15-JUL-2002 (first entry)

Mouse spliced transcript detection oligonucleotide SEQ ID NO:27688.

Human; mouse; rat; splice transcript; detection; RNA transcript;
 splice variant; transcriptome; oligonucleotide library; ss.

Mus musculus.

WO200210449-A2.

07-FEB-2002.

20-JUL-2001; 2001WO-1B01903.

28-JUL-2000; 2000US-221607P.

02-MAY-2001; 2001US-287724P.

(COMP-) COMPUGEN INC.

Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

WPI; 2002-257383/30.

New oligonucleotide libraries comprising oligonucleotides which
 selectively hybridize to mRNAs transcribed from a transcription unit of
 a genome, useful for detecting tissue-, pathology-, and
 developmental-specific genes

Example 1; SEQ ID 27688; 47pp; English.

The present invention describes oligonucleotide libraries for detecting
 messenger RNAs that populate a (sub-)transcriptome, where the
 (sub-)transcriptome comprises messenger RNAs transcribed from multiple
 transcription units that populate a genome. The library comprises
 several oligonucleotides, each capable of hybridizing selectively to a
 set of messenger RNAs transcribed from a given transcription unit of
 the genome, which encodes one or more messenger RNA splice variants.
 The oligonucleotide libraries are useful for detecting mRNAs from a
 biological sample, in expression profiling studies, in qualitatively or
 quantitatively characterizing the corresponding transcriptome, and in
 detecting RNA transcripts and splice variants of human or animal
 transcriptomes. The libraries may also be used as specialised mini
 libraries to detect transcripts of a sub-transcriptome under a
 particular biological or pathological state, and so allowing the
 detection of tissue- and pathology-specific genes such as those genes
 only expressed in specific tissue under a specific pathological
 condition; to detect developmental specific genes; and to detect RNA
 transcripts and splice variants of a transcriptome of a patient suffering
 from a particular disorder. ABN57253 to ABN59589 represent

CC oligonucleotide sequences from rats, humans and mice, which are used in
 CC the exemplification of the present invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.

XX Sequence 65 BP; 18 A; 16 C; 19 G; 12 T; 0 other;

SO Query Match 71.7%; Score 17.2; DB 24; Length 65;

Best Local Similarity 86.4%; Pred. No. 1.5e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GTGACATGAGCCCTTCAGC 22
 Db 7 GTGACATGAGCCCTTCAGC 28

RESULT 7
 AAQ46947/c

ID AAQ46947 standard; DNA: 56 BP.

AC AAQ46947;

DE 21-JAN-1994 (first entry)

Chronic myelogenous leukaemia probe strand 2.

Chronic myelogenous leukaemia; CMLA chimeric bcr/abl;
 genetic translocation; target sequence;

branched probe; chemiluminescent acridinium ester; ss.

Synthetic.

XX Key

EH misc_feature

FT 1..30

FT /tag= a

FT /note= "complementary to part of CMLA chimeric

FT bcr/abl target sequence"

FT misc_feature

FT 31..40

FT /tag= b

FT /note= "complementary to nucleotides 36-27 of

FT probe strand 1 (AAQ46946)"

FT misc_feature

FT 41..56

FT /tag= c

FT /note= "complementary to nucleotides 16,1 of

FT probe strand 3 (AAQ46948)"

FT misc_feature

FT 20-JAN-1993; 93EP-0300377.

22-JAN-1992; 92US-0827021.

(GERR-) GEN PROBE INC.

Arnold LJ, Bezerkov R, Hogan JT, Nelson NC;

WPI; 1993-236606/30.

Nucleic acid molecules which hybridise in presence of target
 nucleic acid - are used as probes in hybridisation assays or as
 therapeutic agents for diseases
 Example 5; Fig 10; 58pp; English.
 A probe for detection of a target sequence corresponding to the
 major genetic translocation associated with chronic myelogenous
 leukaemia consists of three separate strands (see AAQ46946-8).
 Strands 1 and 2 form a 3-way junction with the target and strand 3
 forms a 3-way junction with the other two. Hybridisation of strand
 3 is completely target-dependent even though it does not come into

CC contact with the target sequence
XX
SQ Sequence 56 BP; 13 A; 17 C; 13 G; 13 T; 0 other;

Query Match 65.8%; Score 15.8; DB 14; Length 56;
Best Local Similarity 89.5%; Pred No. 6,8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 ACATGAAGCCTTACGCG 24
||| ||||||||
DB 35 AGTTAAACCCTTCAGCG 17

RESULT 8
ID ABN33790 standard; DNA; 60 BP.
XX
XX ABN33790:
AC
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:6538.
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB01903.
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
PI Shoshun A, Wasserman A, Mintz E, Mintz L, Faigler S;
DR WPI; 2002-257383/30.
FI
FI New oligonucleotide libraries comprising oligonucleotides which
FT selectively hybridize to mRNAs transcribed from a transcription unit of
FT a genome, useful for detecting tissue-, pathology-, and
FT developmental-specific genes -
XX
XX
PS Example 1; SEQ ID 6538; 47pp; English.

The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies. In qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state and so allowing the detection of tissue- and pathology-specific genes such as those genes only expressed in specific tissues under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN3589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO

RESULT 10
AADI6331/c
ID AADI6331 standard; DNA: 35 BP.
XX
AC AADI6331;
XX
DT 19-NOV-2001 (first entry)
XX
DE Human KOD delta (removed) death domain mutant constructing primer #2.
XX
KW Human; protein activator; apoptosis; kinase of death; KOD; therapy;
KW cytosolic; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6267956-B1.
XX
PD 31-JUL-2001.
XX
PF 21-MAR-2000; 2000US-0531914.
XX
PR 10-JUN-1999; 99US-0329418.
XX
PA (ZENE) ZENECA LTD.
XX
PI Gomes BC, Kasof GM, Prosser JC;
XX
DR WPI; 2001-535022/59.
XX
PT New human protein activator protein, useful for treating dysfunctional
PT apoptosis conditions and in screening assays to identify agonists which
PT agonize or mimic biological and/or pharmacological activity -
XX
PS Example 13; Column 53; 31pp; English.
XX
CC The invention relates to human protein activator of apoptosis and
CC methods to identify compounds that modulate the biological and/or
CC pharmacological activity of the activator and hence regulate
CC apoptosis. The nucleic acid and amino acid sequences of the kinase
CC of death (KOD) are useful for identifying compounds that modulate
CC the biological and/or pharmacological activity of a native mediator
CC of apoptosis, for treating dysfunctional apoptosis conditions, in
CC screening assays to identify agonists which agonise or mimic
CC biological and/or pharmacological activity, induce production of or
CC prolong the biological half-life of the molecule in vivo or in vitro.
CC The present sequence is a PCR primer used to synthesise human KOD
CC delta (removed) death domain mutant.
XX
SQ Sequence 35 BP; 3 A; 12 C; 12 G; 8 T; 0 other:
XX
Query Match 65.0%; Score 15.6; DB 22; Length 35;
Best Local Similarity 81.8%; Pred. No. 7.9e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGAACATGAAGCCCTTCAGCGG 24
DB 35 GGAACACCAAGTCTTAAGCGG 14
IIIIII III IIII IIIII
IIIIII III IIII IIIII
IIIIII III IIII IIIII

RESULT 11
AASI2048
ID AASI2048 standard; DNA: 42 BP.
XX
AC AASI2048;
XX
DT 07-NOV-2001 (first entry)
XX
DE Antisense oligonucleotide used in study of PIP1L expression in rat brain.
XX
KW N-methyl-D-aspartate receptor; NMDA-R; protein tyrosine phosphatase; PTP;
KW vasotropic; cerebroprotective; vulnerary; neuroprotective; nootropic;
KW

KW anticonvulsant; neuroleptic; analgesic; PIP1L; ischaemic stroke; ss;
KW head trauma; brain injury; Huntington's disease; motor neuron disease;
KW spinocerebellar degeneration; epilepsy; neuropathic pain; chronic pain;
KW tolerance; schizophrenia; Alzheimer's disease; dementia; drug addiction;
KW psychosis; ethanol sensitivity; antisense; probe; rat; brain;
XX
XX in situ hybridisation.
XX
OS Rattus sp.
XX
PN WO200157240-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US03049.
XX
PR 01-FEB-2000; 2000US-0179453.
XX
PA (AGY-) AGY THERAPEUTICS INC.
XX
PI Melcher T, Kask K;
XX
DR WPI; 2001-522355/57.
XX
PT Identifying N-methyl-D-aspartate receptor signalling activity modulator,
PT involves detecting ability of agent to modulate activity of protein
PT tyrosine phosphatase on NMDA-R substrate or binding of PTP to NMDA-R -
XX
PS Example 4; Page 27; 34pp; English.
XX
CC The method of the invention comprises identifying a modulator of
CC N-methyl-D-aspartate receptor (NMDA-R) signalling activity by detecting
CC the ability of an agent to modulate the phosphatase activity of a protein
CC tyrosine phosphatase (PTP) e.g. PIP1L, on an NMDA-R substrate or to
CC modulate the binding of PTP to NMDA-R. This method is useful for treating
CC diseases which are mediated by abnormal NMDA-R signalling, by
CC administering a modulator of PIP1L activity, thus modulating the level
CC of tyrosine phosphorylation of NMDA-R. Treatable diseases include
CC ischaemic stroke; head trauma or brain injury; Huntington's disease,
CC spinocerebellar degeneration, motor neuron diseases, epilepsy,
CC neuropathic pain, chronic pain, tolerance, schizophrenia, Alzheimer's
CC disease, dementia, psychosis, drug addiction and ethanol sensitivity.
CC This sequence represents an antisense oligonucleotide used in situ
CC hybridisation studies carried out to examine PIP1L expression in rat
CC brain.
XX
SQ Sequence 42 BP; 9 A; 19 C; 6 G; 8 T; 0 other:
XX
Query Match 65.0%; Score 15.6; DB 22; Length 42;
Best Local Similarity 81.8%; Pred. No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGAACATGAAGCCCTTCAGCGG 24
DB 10 GCACACGAAAGCCCTTCAGCTG 31
IIIIII III IIII IIIII
IIIIII III IIII IIIII
IIIIII III IIII IIIII

RESULT 12
ABA73324
ID ABA73324 standard; DNA: 95 BP.
XX
AC ABA73324;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human foetal liver single exon nucleic acid probe #21629.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.

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XX 30-JAN-2001; 2001WO-US00669.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human fetal liver.
XX
XX Claim 4; SEQ ID NO 21629; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
XX measuring human gene expression in a sample derived from human foetal
XX liver. The single exon nucleic acid probes may be used for predicting,
XX measuring and displaying gene expression in samples derived from human
XX foetal liver. The present sequence is a single exon nucleic acid
XX probe of the invention.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at http://wipo.int/pub/published\_pct\_sequences.
XX
XX Sequence 95 BP; 27 A; 21 C; 31 G; 16 T; 0 other;
XX
XX Query Match 65.0%; Score 15.6; DB 22; Length 95;
XX Best Local Similarity 81.8%; Pred. No. 9.2e+02;
XX Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 GTGGACATGAGACCCCTTCAGC 22
XX 51 GGGAGAGATTAAGCCCTTCATC 72
XX
XX Db
XX
XX RESULT 13
XX AAK21762
XX AAK21762 standard; DNA; 95 BP.
XX
XX AAK21762;
XX
XX 05-NOV-2001 (first entry)
XX
XX Human brain expressed single exon probe SEQ ID NO: 21753.
XX
XX Human; brain expressed exon; gene expression analysis; probe;
XX microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX epilepsy; cancer; ss.
XX
XX Homo sapiens.
XX
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00667.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX

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PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
XX Example 4; SEQ ID NO: 21753; 650pp + Sequence listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention.
XX
XX Sequence 95 BP; 27 A; 21 C; 31 G; 16 T; 0 other;
XX
XX Query Match 65.0%; Score 15.6; DB 22; Length 95;
XX Best Local Similarity 81.8%; Pred. No. 9.2e+02;
XX Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 GTGGACATGAGACCCCTTCAGC 22
XX 51 GGGAGAGATTAAGCCCTTCATC 72
XX
XX Db
XX
XX RESULT 14
XX AAK47927
XX AAK47927 standard; DNA; 95 BP.
XX
XX AAK47927;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human bone marrow expressed single exon probe SEQ ID NO: 22484.
XX
XX Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
XX Homo sapiens.
XX
XX WO200157276-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00668.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human bone marrow.
XX
XX Example 4; SEQ ID NO: 22484; 658pp + Sequence listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX

```

Job time : 85.3837 secs

CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention.

SQ Sequence 95 BP; 27 A; 21 C; 31 G; 16 T; 0 other;

Query Match	65.0%;	Score 15.6;	DB 22;	Length 95;
Best Local Similarity	81.8%;	Pred. No. 9.2e+02;		
Matches 18; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

OY 1 GTGGAACATGAAGCCCTCAGC 22
| | | | | | | | | |
Db 51 GCGGAAGATAAAGCCCTTCATC 72

RESULT 15
AAI53756
ID AAI53756 standard; DNA; 95 BP.

AC AA153756;
xy

DT 17-OCT-2001 (first entry)

Probe #22442 used to measure gene expression in human placenta sample.

KW Probe; microarray; human; placenta; antenatal diagnosis;

KW genetic disorder; ss.

OS Homo sapiens

PN WO200157272-A2

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US006663.

PR 04-FEB-2000; 2000US-0180312.

30-JUN-2000; 2000US-0608408.

PR 21-SEP-2000; 2000US-0234687.

PR	27-SEP-2000; 2000GB-0220555
PR	04-OCT-2000; 2000GB-0024263

AA
PA
(MOLE-) MOLECULAR DYNAMICS I

AA Penn SG, Hanzel DK, Chen V
PI

XX
DR WPI: 2001-488897/53.

XX	Human genome-derived single
PT	

PT analyzing gene expression in nu
XX

PS Claim 25; SEQ ID NO 22442; 654bp; English.
XX

CC The present invention relates to single ex

CC producing a microarray for predicting, measuring and displaying
CC expression in samples derived from human placenta. The probes a

CC for antenatal diagnosis of human genetic disorders.
XY

sq Sequence 95 BP; 27 A; 21 C; 31 G; 16 T; 0 other;

Query Match	65.08;	Score 15.6;	DB 22;	Length 95;
Best local similarity	81.88;	Prod No	9 3e+03:	

Matches	18;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

QY 1 GTGGAACATGAAGCCCTTCAGC 22

Db 51 GGGGAGATAAGCCCTTCATC 72

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic acid - nucleic search, using sw model

Run on: December 21, 2002, 02:00:32 : Search time 61.7878 Seconds
(without alignments)
656.052 Million cell updates/sec

Title: US-09-121-239-26

Perfect score: 18

Sequence: 1 GAATTCATCGAGCAGC 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

1: N_GenSeq 101002.*
2: /SID2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
3: /SID2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
4: /SID2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
5: /SID2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
6: /SID2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
7: /SID2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
8: /SID2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
9: /SID2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
10: /SID2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
11: /SID2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
12: /SID2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
13: /SID2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
14: /SID2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
15: /SID2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
16: /SID2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
17: /SID2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
18: /SID2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
19: /SID2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
20: /SID2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
21: /SID2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001.DAT.*
23: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	AAZ60865	Oligonucleotide us
2	14.8	82.2	50	AAZ34141	Human PRO83 hbr1
3	14.8	82.2	50	AAZ78779	Human PRO83 hbr1
4	13.8	76.7	25	AAZ35206	Corn shrunken 1 in
5	13.8	76.7	37	AAZ93882	Fas intron 1 5' pc
6	13.8	76.7	73	AAZ16421	Ashbya gossypii pc
7	13.8	76.7	98	AAZ98049	RNA aptamer #26 fo
8	13.4	74.4	20	AAZ04133	PCR primer used to
9	13.4	74.4	20	AAZ03618	PCR primer used to

10	13.4	74.4	50	AAZ78629	Human silent SNP c
11	13.2	73.3	18	AAZ5810	Human/mouse tpat D
12	13.2	73.3	36	AAZ08598	Anti-EGFP hamster
13	13.2	73.3	36	AAZ78672	Anti-green fluores
14	13.2	73.3	65	AAZ93099	Cloning site from
15	13.2	73.3	65	AAZ93099	Mouse spliced tran
16	13.2	73.3	84	AAZ97066	184, reporter olig
17	12.8	71.1	23	AAZ98678	Adaptor ATG-sense
18	12.8	71.1	23	AAZ98678	Ras target protein
19	12.8	71.1	45	AAZ98083	Human SNP oligonuc
20	12.8	71.1	50	AAZ98083	Human spliced tran
21	12.8	71.1	50	AAZ98083	EST clone DF909.
22	12.8	71.1	60	AAZ98083	Human SNP oligonuc
23	12.8	71.1	65	AAZ98083	Human spliced tran
24	12.8	71.1	80	AAZ98083	Human spliced tran
25	12.8	71.1	90	AAZ98083	EST clone DF909.
26	12.8	71.1	95	AAZ98083	RNA aptamer #28 fo
27	12.8	71.1	95	AAZ98083	Human aptamer #27 fo
28	12.8	71.1	95	AAZ98083	Human nervous syst
29	12.8	71.1	95	AAZ98083	Human immune/haema
30	12.8	71.1	95	AAZ98083	Human immune/haema
31	12.8	71.1	95	AAZ98083	Human immune/haema
32	12.8	71.1	95	AAZ98083	Human immune/haema
33	12.8	71.1	100	AAZ98083	Human immune/haema
34	12.4	68.9	20	AAZ98083	Human caspase 6 an
35	12.4	68.9	20	AAZ98083	Human caspase 6 an
36	12.4	68.9	20	AAZ98083	Human caspase 6 an
37	12.4	68.9	20	AAZ98083	Human caspase 6 an
38	12.4	68.9	20	AAZ98083	Human caspase 6 an
39	12.4	68.9	20	AAZ98083	Human caspase 6 an
40	12.4	68.9	20	AAZ98083	Human caspase 6 an
41	12.2	67.8	23	AAZ98083	Human caspase 6 an
42	12.2	67.8	24	AAZ98083	Human caspase 6 an
43	12.2	67.8	24	AAZ98083	Human caspase 6 an
44	12.2	67.8	25	AAZ98083	Human caspase 6 an
45	12.2	67.8	27	AAZ98083	Human caspase 6 an

ALIGNMENTS

RESULT 1	AAZ60865	standard; RNA; 18 BP.
ID	AAZ60865	
AC	AAZ60865	
XX		
DT	16-MAY-2000	(first entry)
DE	Oligonucleotide used to detect bcr b3-abl fusion transcripts.	
XX		
KW	Fusion transcript; translocation; bcr b3 region; abl gene;	
KW	amplification assay; detection assay; medical diagnosis;	
KW	clinical monitoring; chimeric RNA; fusion RNA; condition marker;	
KW	disease marker; cancer; leukemia; ss.	
XX		
OS	Synthetic.	
XX		
FN	WO200005418-A1.	
XX		
PD	03-FEB-2000.	
XX		
PF	23-JUL-1999;	99WO-US16832.
XX		
PR	23-JUL-1998;	98US-0121239.
XX		
PA	(GENP-) GEN-PROBE INC.	
XX		
PI	Harvey RC, Eastman PS;	
XX		
DR	WPI: 2000-182730/16.	
XX		
PT	Novel methods for preparing RNA from biological samples, used for the	


```

XX (GETH ) GENENTECH INC.
PA Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX WPI; 1999-551358/46.
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
XX useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders -
XX
XX Example 45; page 220; 530pp; English.
XX
XX the present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as
XX sources of probes, primers, for chromosome mapping, and for generation
XX of antisense sequences. They can also be used to create transgenic
XX animals. The proteins can be used to treat a variety of diseases and
XX disorders, depending on their function. Diseases that may be treated
XX include blood coagulation disorders, cancers and cellular adhesion
XX disorders. They may also be used to raise antibodies. AAZ3891 to
XX AAZ34338, and AA41685 to AA41774 represent polynucleotide and
XX polypeptide sequence given in the exemplification of the present
XX invention.
XX
XX Sequence 50 BP; 13 A; 10 C; 13 G; 14 T; 0 other;
SQ
Query Match 82.2%; Score 14.8; DB 20; Length 50;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGAATCATCGAGCGATCG 18
Db 5 GGAATCATCGATCGAGG 22
|||||
RESULT 3
AAC78779 AAC78779 standard; DNA; 50 BP.
XX ID AAC78779;
XX AC AAC78779;
XX DT 08-FEB-2001 (first entry)
XX DE Human PRO983 hybridisation probe SEQ ID NO:294.
XX
XX Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
XX expressed sequence tag; detection; cancer; PCR primer; probe; ss.
XX
XX Homo sapiens.
XX
XX WO200053756-A2.
XX
XX 14-SEP-2000.
XX
XX 18-FEB-2000; 2000WO-US04341.
XX
XX 08-MAR-1999; 99WO-US05028.
XX 12-MAR-1999; 99US-0123957.
XX 29-MAR-1999; 99US-0126773.
XX 21-APR-1999; 99US-0130232.
XX 28-APR-1999; 99US-0131445.
XX 14-MAY-1999; 99US-0134287.
XX 23-JUN-1999; 99US-0141037.
XX 26-JUL-1999; 99US-0145698.
XX 29-OCT-1999; 99US-0162506.
XX 30-NOV-1999; 99WO-US28313.
XX 02-DEC-1999; 99WO-US28551.
XX 16-DEC-1999; 99WO-US30095.
XX 30-DEC-1999; 99WO-US31243.
XX 30-DEC-1999; 99WO-US31274.
XX 05-JAN-2000; 2000WO-US00219.

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PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Bolstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
XX Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
XX Kljavin IJ, Kuo SS, Nepler MA, Pan J, Paoni NF, Roy MA;
XX Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2000-611443/58.
XX
XX Novel PRO polypeptides and polynucleotides used in detection methods,
XX to target bioactive molecules to specific cells, and to modulate
XX cellular activities -
XX
XX Example 45; page 275; 636pp; English.
XX
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed
XX sequence tag) sequences which encode secreted or transmembrane PRO
XX polypeptides. The PRO polynucleotides and polypeptides have cytosolic
XX activity. The polynucleotides and polypeptides can be used for detecting
XX the presence of PRO polypeptides in samples, for linking bioactive
XX molecules to cells and for modulating biological activities of cells,
XX using the polypeptides for specific targeting. The polypeptide targeting
XX can be used to kill the target cells, e.g. for the treatment of cancers.
XX The polypeptide pairs provide specific targeting of bioactive molecules
XX to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
XX the isolation of the PRO polynucleotide sequences.
XX
XX Sequence 50 BP; 13 A; 10 C; 13 G; 14 T; 0 other;
SQ
Query Match 82.2%; Score 14.8; DB 21; Length 50;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGAATCATCGAGCGATCG 18
Db 5 GGAATCATCGATCGAGG 22
|||||
RESULT 4
AAZ35206/C
AAC35206 AAC35206 standard; DNA; 25 BP.
XX ID AAC35206;
XX AC AAC35206;
XX DT 13-MAR-2000 (first entry)
XX DE Corn shrunken 1 intron 1/exon 1 PCR primer.
XX
XX Corn shrunken 1 intron 1/exon 1 PCR primer.
XX
XX Corn; maize; transgenic plant; lipid; food; feedstuff;
XX vegetable oil; seed oil; fatty acid desaturase; oleosin; promoter;
XX shrunken; PCR; primer; ss.
XX
XX Synthetic.
XX Zea mays.
XX
XX WO9964579-A2.
XX
XX 16-DEC-1999.
XX
XX 09-JUN-1999; 99WO-US12884.
XX
XX 11-JUN-1998; 98US-0088987.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Shen JB;
XX WPI; 2000-097535/08.

```

PT New maize oleosin promoter, used for producing transgenic plants with
 altered fatty acid composition of the oil, used e.g. in animal feeds
 XX
 PS Example 6; Page 38; 108bp; English.
 CC This primer was used in the PCR amplification of the corn shrunk
 CC gene intron/exon1 region. The PCR product was used in an
 CC expression cassette utilized in oleosin 16 kDa promoter deletion
 CC studies. The invention relates to the preparation and use of
 CC nucleic acid fragments comprising a corn oleosin promoter (see
 CC AA35165-77), a stearyl-ACP desaturase (see AA235179-80) and/or a
 CC delta-12 desaturase (see AA235178) nucleic acid, which can be used to
 CC modify the lipid profile, e.g. the stearic acid or oleic acid
 CC content, of corn. Transgenic corn plants, their seeds, and oil
 CC produced from them are also claimed.
 XX
 SQ Sequence 25 BP; 3 A; 7 C; 8 G; 7 T; 0 other;
 Query Match 76.7%; Score 13.8; DB 21; Length 25;
 Best Local Similarity 88.2%; Pred. No. 5.3e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 GAATCATCGAGCATGG 18
 DB 25 GAACCATCGAGCATGG 9
 RESULT 5
 AA093882
 ID AA093882 standard; cDNA; 37 BP.
 XX
 AC AA093882;
 XX
 DT 06-NOV-1995 (first entry)
 XX
 DE Fas intron 1 5' PCR primer.
 XX
 KW Fas-delta-TM; transmembrane deletion; apoptosis; antibody;
 KW adoptive immunotherapy; transgenic animal; primer; PCR;
 KW polymerase chain reaction; ss.
 XX
 OS Synthetic.
 XX
 FN W09513701-A.
 XX
 PD 26-MAY-1995.
 XX
 PF 15-NOV-1994; 94WO-US13173.
 XX
 PR 15-NOV-1993; 93US-0152443.
 XX
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 XX
 PI Barr PJ, Kiefer MC, Shapiro JP;
 XX
 DR WPI; 1995-200120/26.
 XX
 PT New nucleic acid encoding Fas protein without its trans-membrane region
 PT - and related vectors, transformed cells, transgenic animals, protein and
 PT antibodies, useful for control of Fas mediated apoptosis
 XX
 PS Example 2; Page 14; 38bp; English.
 CC The intron-exon organization of the Fas transmembrane region was
 CC determined by PCR. Primers were designed to flank each of the
 CC putative introns, 1 and 2. The forward and reverse primers
 CC flanking intron 1 are given in AA093882-83, and those for intron 2
 CC in AA093884-85.
 XX
 SQ Sequence 37 BP; 12 A; 8 C; 8 G; 9 T; 0 other;
 Query Match 76.7%; Score 13.8; DB 16; Length 37;
 Best Local Similarity 88.2%; Pred. No. 5.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GAATCATCGAGCATG 17
 DB 14 GAATCATCAAGGAATG 30
 RESULT 6
 ABK16421
 ID ABK16421 standard; DNA; 73 BP.
 XX
 AC ABK16421;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Ashbya gossypii genomic DNA PCR primer #16.
 XX
 KW Fungal growth; fungicide; ss; PCR primer.
 XX
 OS Ashbya gossypii.
 OS Synthetic.
 XX
 PN US6307037-B1.
 XX
 PD 23-OCT-2001.
 XX
 PF 21-JUL-2000; 2000US-0625188.
 XX
 PR 21-JUL-2000; 2000US-0625188.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Gaffney TD, Flavler A, Cloyd Kirksey MW, Philippesen P, Dietrich F;
 PI Wendland J, Bernasconi P, White K, Filipowicz W;
 DR WPI; 2002-054476/07.
 XX
 PT New enzyme, useful as a fungicide to suppress the growth of pathogenic
 PT fungi, comprises IPC synthase, AURI gene (Mc017), derived from Ashbya
 PT gossypii.
 XX
 PS Example 1; Column 20; 48bp; English.
 XX
 CC The invention relates to Ashbya gossypii polynucleotides which encode
 CC polypeptides essential for normal fungal growth and development. The
 CC sequences are useful for identifying inhibitors which can be used as
 CC fungicides to suppress the growth of pathogenic fungi. The proteins are
 CC useful in discovering new fungicides, based on the essentiality of the
 CC gene for normal growth and development. Sequences ABK16406-ABK16429
 CC represent PCR primers specific for the Ashbya gossypii polynucleotides,
 CC used in the methods of the invention.
 XX
 SQ Sequence 73 BP; 23 A; 16 C; 17 G; 17 T; 0 other;
 Query Match 76.7%; Score 13.8; DB 24; Length 73;
 Best Local Similarity 88.2%; Pred. No. 5.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GAATCATCGAGCATG 17
 DB 44 GATCATCGAGCATG 60
 RESULT 7
 AA299049
 ID AA299049 standard; RNA; 98 BP.
 XX
 AC AA299049;
 XX
 DT 21-JUN-2000 (first entry)
 XX
 DE RNA aptamer #26 for binding Ras target protein.

KW Ras target protein; malignant tumour; signal transduction regulation;
 KW cell proliferation; cell differentiation; aptamer; inflammation; ss.
 OS Homo sapiens.
 XX WO200009684-A1.
 XX PD 24-FEB-2000.
 XX PF 13-AUG-1999; 99WO-JP04399.
 XX PR 14-AUG-1998; 98JP-0242596.
 XX PR 24-NOV-1998; 98JP-0333284.
 XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX PI Yokoyama S, Hirao I, Sakamoto K;
 DR WPI: 2000-224330/19.
 XX CC Nucleic acid e.g. RNA aptamer capable of binding specifically to Ras
 PT target protein like Raf-1, useful in drug compositions to treat and
 PR diagnose malignant tumours and inflammation
 XX PS Claim 6; Page 41; 59pp; Japanese.
 XX CC The invention relates to novel nucleic acids which bind specifically
 CC to the target protein of Ras, e.g. Raf-1. RNA aptamer (AA299024-299051)
 CC based on these sequences are useful in the treatment and diagnosis of
 CC malignant tumours and inflammation. The nucleic acids can be used to
 CC formulate medicinal compositions that are useful in the treatment of
 CC malignant tumours and inflammation and for disease diagnosis by binding
 CC specifically to Ras target protein and regulating transmission of signal
 CC causing proliferation or differentiation of cells.
 XX SQ Sequence 98 BP; 24 A; 24 C; 26 G; 24 U; 0 other;
 OY Query Match 76.7%; Score 13.8; DB 21; Length 98;
 Best Local Similarity 70.6%; Pred. No. 6.1e+02;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 DB 11 GAADUACAGCGAGCAGC 27
 OY 1 GGATCATCGAGGCATG 17
 11 GAADUACAGCGAGCAGC 27
 RESULT 8
 AA204133
 ID AA204133 standard; DNA: 20 BP.
 XX AC AA204133;
 XX DT 07-OCT-1999 (first entry)
 DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
 XX KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KW paratrachoma; inclusion conjunctivitis; genital disease; peritriptitis;
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 KW bartholinitis; pneumonia; venereal lymphogranulomatosis; ss.
 OS Synthetic.
 OS Chlamydia trachomatis.
 XX PN WO9928475-A2.
 XX PD 10-JUN-1999.
 XX PF 27-NOV-1998; 98WO-IB01939.
 XX PR 04-NOV-1998; 98US-0107077.
 XX PR 28-NOV-1997; 97FR-0015041.
 XX PR 17-DEC-1997; 97FR-0016034.

XX (GEST) GENSET.
 XX Griffais R;
 XX WPI: 1999-371125/31.
 XX PT Genome sequence of Chlamydia trachomatis
 XX PS Disclosure; Page 1663; 1755pp; English.
 XX CC PCR primers AA201426-206209 were used to amplify open reading frames
 CC (ORFs) of the genome of Chlamydia trachomatis (see AA201425). These ORFs
 CC encode polypeptides (see AA201425-206209) which can be used as vaccines
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences
 CC can also be used to control growth of the microorganism. Chlamydia
 CC trachomatis is responsible for a large number of diseases, e.g. eye
 CC diseases such as conventional trachoma, nonendemic trachoma,
 CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
 CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
 CC peritriptitis, bartholinitis; pneumonia; venereal lymphogranulomatosis.
 CC and venereal lymphogranulomatosis. The polypeptides of the
 CC invention may be of use in treating these diseases.
 XX SQ Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 other;
 OY Query Match 74.4%; Score 13.4; DB 20; Length 20;
 Best Local Similarity 93.3%; Pred. No. 8.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 5 GAATCATCGAGGCAT 19
 OY 2 GAATCATCGAGGCAT 16
 5 GAATCATCGAGGCAT 19
 RESULT 9
 AA203618/C
 ID AA203618 standard; DNA: 20 BP.
 XX AC AA203618;
 XX DT 07-OCT-1999 (first entry)
 DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
 XX KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KW paratrachoma; inclusion conjunctivitis; genital disease; peritriptitis;
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 KW bartholinitis; pneumonia; venereal lymphogranulomatosis; ss.
 OS Synthetic.
 OS Chlamydia trachomatis.
 XX PN WO9928475-A2.
 XX PD 10-JUN-1999.
 XX PF 27-NOV-1998; 98WO-IB01939.
 XX PR 04-NOV-1998; 98US-0107077.
 XX PR 28-NOV-1997; 97FR-0015041.
 XX PR 17-DEC-1997; 97FR-0016034.
 XX PA (GEST) GENSET.
 XX Griffais R;
 XX WPI: 1999-371125/31.
 XX PT Genome sequence of Chlamydia trachomatis
 XX PS Disclosure; Page 1621; 1755pp; English.

CC PCR primers AA201426-206209 were used to amplify open reading frames
 CC (ORFs) of the genome of Chlamydia trachomatis (see AA201425). These ORFs
 CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences
 CC can also be used to control growth of the microorganism. Chlamydia
 CC trachomatis is responsible for a large number of diseases, e.g. eye
 CC diseases such as conjunctival trachoma, nongonococcal urethritis,
 CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
 CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
 CC peritonitis, Bartholinitis; pneumonia; lymphogranulomatosis. The polypeptides of the
 CC invention may be of use in treating these diseases.

XX Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 other;

Query Match 74.4%; Score 13.4; DB 20; Length 20;
 Best Local Similarity 93.3%; Pred. No. 8.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAATCATCGAGGCAT 16
 DB 16 GAATCATCGAGGCAT 2

RESULT 10

ID AA178629 standard; DNA; 50 BP.

XX AA178629;

DE 09-NOV-2001 (first entry)

XX Human silent SNP containing nucleic acid SEQ:5570.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KM Protein therapy; vaccine; probe; diagnostic assay; detection;

KM quantitation; restorative therapy; polymorphic; ds.

OS Homo sapiens.

PN WO200140521-A2.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000WO-US2758.

XX 30-NOV-1999; 99US-0168138.

XX 29-NOV-2000; 2000US-0726173.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI: 2001-356160/37.

XX Polymorphic nucleic acid sequences, useful in genetic testing and

XX therapy -

XX Claim 1; Page 2214; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide

XX sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide

XX sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide

XX sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC in samples, and therefore which patients may be in need of restorative
 CC therapy. The polypeptides encoded by (1) may be used as antigens in the
 CC production of antibodies specific for polymorphic polypeptides. The
 CC antibodies may also be used to down regulate expression and activity.
 CC The antibodies may also be used as diagnostic agents for detecting the
 CC presence of polymorphic polypeptides in samples.

XX Sequence 50 BP; 13 A; 14 C; 13 G; 10 T; 0 other;

Query Match 74.4%; Score 13.4; DB 22; Length 50;
 Best Local Similarity 93.3%; Pred. No. 9.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ATCATCGAGGCATCG 18
 DB 17 ATCATCGAGGCATCG 31

RESULT 11

ID AAH25810/c standard; DNA; 18 BP.

XX AAH25810;

DE 20-AUG-2001 (first entry)

XX Human/mouse Iba1 DNA PCR primer #1.

KM Human; mouse; immunomodulatory; monocyte; macrophage; inhibitor;

XX PCR primer; ss.

XX Unidentified.

XX JP2001078775-A.

XX 27-MAR-2001.

XX 14-SEP-1999; 99JP-0260793.

XX 14-SEP-1999; 99JP-0260793.

XX (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.

XX (IYAK-) IYAKUIN FUKUSAYO HIGAI KYUSAI KENKYU SH.

XX (MOCH) MOCHIDA PHARM CO LTD.

XX WPI: 2001-313369/33.

XX A macrophage function modifier useful for preventing and treating

XX diseases caused by the increase or decrease in macrophage activity or

XX function -

XX Example 2; Page 8; 20pp; Japanese.

XX The present invention provides a number of murine and human Iba1

XX derivatives, which are capable of inhibiting the function of cells with

XX monocyte or macrophage activity. These can be used as immunomodulators

XX to prevent and treat diseases caused by a decrease or increase in the

XX activity or the function of macrophages or an activator or an inhibitor

XX of the function of cells of macrophage type. The present sequence is a

XX PCR primer used in the exemplification of the invention.

XX Sequence 18 BP; 4 A; 7 C; 2 G; 5 T; 0 other;

XX Query Match 73.3%; Score 13.2; DB 22; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAATCATCGAGGCATCG 18
 DB 18 GGAATCATCGAGGCATCG 1

RESULT 12

[illegible]

XX	Green fluorescent protein; GFP; anti-GFP; ribozyme; catalytic RNA;
KW	antigen; target; directionality; high-throughput screen; cleavage;
KW	gene function; virus replication; life cycle; antimicrobial; ds.
XX	
OS	Synthetic.
XX	
PN	MO9932618-A1.
XX	
PD	01-JUL-1999.
XX	
PT	18-DEC-1998; 98WO-US27942.
XX	
PR	19-DEC-1997; 97US-0995234.
XX	
PA	(STRA) STRATA BIOSCIENCES INC.
XX	
PI	Keck JG, Kuo SS, Molony JM;
XX	
DR	WPI; 1999-405170/34.
XX	
PT	Non-bacterial cloning in delivery and expression of nucleic acids
XX	
PS	Example 1; Fig 1C; 64p; English.
XX	
CC	This invention describes a novel double-stranded DNA which encodes a
CC	catalytic RNA targeted to an mRNA of a gene of interest and has a means
CC	for determining directionality of expression. The double-stranded DNA
CC	comprises a sense strand and an antisense strand. The sense strand codes
CC	for an antisense strand, which when expressed as RNA binds to an mRNA
CC	sequence transcribed from a target nucleic acid sequence so that
CC	expression of a product of the target nucleic acid is inhibited. A means
CC	for determining directionality of expression is included in the
CC	double-stranded DNA. The methods and compositions are useful in the
CC	high-throughput screens to assign gene functions of genes of interest.
CC	Cleavage of the mRNA results in an altered phenotype from which the
CC	function of a product encoded by the mRNA is determined. The function of
CC	genes can be identified that are involved in virus replication or life
CC	cycle. If the targeted nucleic acid is in a bacteria or microorganism,
CC	determining their function identifies new pathways and lead to the
CC	identification of targets for new antimicrobials. The ability to
CC	eliminate the amplification step of plasmid DNA in bacteria such as
CC	Escherichia coli is a major cost saving step as well as a time saving
CC	step over existing technologies. E. coli amplification can add several
CC	days onto the entire process. The new method lends itself to automation
CC	when implemented in a 96-well or similar multi-well format.
CC	High-throughput delivery and expression of the molecules from a gene
CC	vector family offers the advantage that multiple members of these
CC	molecules can be introduced into and expressed in host cell cultures to
CC	enable identification of genes by a manageable screening process.
CC	Directionality is achieved by incorporation of unique restriction enzyme
CC	sites at both ends of synthetic oligonucleotides used to prepare
CC	double-stranded DNA. This sequence represents an oligonucleotide which
CC	encodes an anti-green fluorescent protein (GFP) ribozyme.
XX	
SQ	Sequence 36 BP; 10 A; 8 C; 12 G; 6 T; 0 other;
XX	
QY	Query Match 73.3%; Score 13.2; DB 20; Length 36;
XX	Best Local Similarity 83.3%; Pred. No. 1.2e+03;
XX	Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db	18 GGCATCATCGAGCGCATGG 18
	1 GGCATCATCGAGCGCATGG 18
RESULT 14	
AA299099/C	
ID	AA299099 standard; DNA; 65 BP.
AC	
XX	AA299099;
XX	
XX	21-JUN-2000 (first entry)

```

XX Cloning site from plasmid pBAC-PAK-poly(His).
DE Mouse; angiotensin; AT2 receptor interactive protein; ATIP; ds;
XX two-hybrid screen; signal transduction.
XX Synthetic.
XX PR2782084-A1.
XX 11-FEB-2000.
XX 04-AUG-1998; 98FR-0009997.
XX 04-AUG-1998; 98FR-0009997.
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX Elbaz N, Nahmlas C, Strosberg AD;
XX WPI; 2000-248410/22.
XX P-PSDB; AAY83783.
XX Nucleic acids coding for angiotensin II receptor AT2 interacting
XX proteins useful in screening assays for receptor-protein interaction
XX Example 3; Fig 8; 63pp; French.
XX This sequence represents the cloning site from the plasmid
XX pBAC-PAK-poly(His) used for expression of the "short" clone of the mouse
XX angiotensin II (AT2) receptor interacting protein (ATIP; AAY83777).
XX Cells transformed with vectors containing the cDNA, or immobilized
XX proteins encoded by it, can be used to screen for substances that
XX modulate ATIP-AT2 interaction or substances that interact with ATIP,
XX especially using yeast two- or three-hybrid techniques. Such substances
XX may be useful for treating disorders associated with anomalous AT2
XX receptor signal transduction.
XX Sequence 65 BP; 12 A; 21 C; 18 G; 14 T; 0 other;
SQ
XX
XX Query Match 73.3%; Score 13.2; DB 21; Length 65;
XX Best Local Similarity 83.3%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGAATCATCGAGCATGG 18
DB 45 GGAACCCAGCAGCATGG 28

```

RESULT 15
ABN54496/C
ID ABN54496 standard; DNA; 65 BP.
XX
XX ABN54496;
XX
XX 15-JUL-2002 (first entry)
XX
XX Mouse spliced transcript detection oligonucleotide SEQ ID NO:27244.
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Mus musculus.
XX
XX WO200210449-A2.
XX
XX PD 07-FEB-2002.
XX
XX 20-JUL-2001; 2001WO-IB01903.
XX
XX 28-JUL-2000; 2000US-221607P.
XX
XX 02-MAY-2001; 2001US-287724P.
XX

```

PA (COMP-) COMPUGEN INC.
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of
XX a genome, useful for detecting tissue-, pathology-, and
XX developmental-specific genes.
XX Example 1; SEQ ID 27244; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridizing selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterizing the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialised mini
XX libraries to detect transcripts of a sub-transcriptome under a
XX particular biological or pathological state, and so allowing the
XX detection of tissue- and pathology-specific genes such as those genes
XX only expressed in specific tissue under a specific pathological
XX condition; to detect developmental specific genes; and to detect RNA
XX transcripts and splice variants of a transcriptome of a patient suffering
XX from a particular disorder. ABN27253 to ABN59589 represent
XX oligonucleotide sequences from rats, humans and mice, which are used in
XX the exemplification of the present invention.
XX N.B. The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.int/pub/published_pct_sequences.
XX
XX Sequence 65 BP; 20 A; 18 C; 12 G; 15 T; 0 other;
SQ
XX
XX Query Match 73.3%; Score 13.2; DB 24; Length 65;
XX Best Local Similarity 83.3%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGAATCATCGAGCATGG 18
DB 19 GGGATCATCGAGCATGG 2

```

Search completed: December 21, 2002, 11:54:46
Job time : 64.7878 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:00:32 ; Search time 89.249 Seconds
(without alignments)
656.052 Million cell updates/sec

Title:	US-09-121-239-27
Perfect score:	26
Sequence:	1 CACTCAGCCACTGGATTTCAGCAG 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

```
Searched:      2185239 segs, 1125999159 residues
Total number of hits satisfying chosen parameters: 2390332
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Minimum DB seq length: 0
Maximum DB seq length: 100

```

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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

```

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Database :
1 N.Geneseq_101.002.*
1 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA1980.DAT.*
2 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA1981.DAT.*
3 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA1982.DAT.*
4 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA1983.DAT.*
5 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA1984.DAT.*
6 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA1985.DAT.*
7 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA1986.DAT.*
8 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA1987.DAT.*
9 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA1988.DAT.*
10 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA1989.DAT.*
11 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA1990.DAT.*
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13 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA1992.DAT.*
14 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA1993.DAT.*
15 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA1994.DAT.*
16 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA1995.DAT.*
17 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA1996.DAT.*
18 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA1997.DAT.*
19 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA1998.DAT.*
20 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA1999.DAT.*
21 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA2000.DAT.*
22 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA2001A.DAT.*
23 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA2001B.DAT.*
24 /SIDS2/gcgdata/geneseq/geneseqn_emb1/NA2002.DAT.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	26	100.0	26	21	AA269866	Oligonucleotide us
2	26	100.0	52	19	AA269188	Antisense RNA sequ
3	26	100.0	53	19	AAV01789	Antisense RNA sequ
4	26	100.0	54	19	AAV01790	Antisense RNA sequ
5	26	100.0	55	19	AAV01791	Antisense RNA sequ
6	26	100.0	56	14	AA646950	Branched probe to
7	26	100.0	56	19	AAV01792	Antisense RNA sequ
8	26	100.0	57	19	AAV01793	Antisense RNA sequ
9	26	100.0	58	19	AAV01794	Antisense RNA sequ

C	10	25	100.0	59	19	AAV01795
C	11	25	96.2	40	21	AAAB6914
C	12	25	96.2	41	21	AAAB6915
C	13	25	96.2	59	10	AAAN7243
C	14	25	96.2	59	10	AAAN7243
C	15	25	96.2	59	15	AAOS5680
C	16	25	96.2	59	15	AAOS5681
C	17	25	96.2	59	20	AAZ09284
C	18	25	96.2	59	20	AAZ09285
C	19	25	96.2	59	21	AAZ60230
C	20	25	96.2	60	17	AAAT29714
C	21	25	96.2	66	16	AAQA6946
C	22	25	82.3	40	15	AAU39474
C	23	20	76.9	47	24	AAI72000
C	24	20	76.9	47	24	AAI72003
C	25	20	76.9	91	24	AAI71998
C	26	19.4	74.6	41	24	AAI71999
C	27	19	73.1	41	24	AAI72002
C	28	19	73.1	18	13	AAQ21921
C	29	18	69.2	18	19	AAV39476
C	30	18	69.2	50	22	AAAL3825
C	31	18	69.2	41	22	AAAH41253
C	32	17.2	66.2	31	22	AAI30925
C	33	16.8	64.6	30	22	AAAF50925
C	34	16	61.5	30	14	AAO37185
C	35	16	61.5	59	22	AAH89705
C	36	16	61.5	50	22	AAH89707
C	37	16	61.5	88	20	AAAX57895
C	38	16	61.5	88	20	AAAX57878
C	39	16	61.5	21	21	AAAF69302
C	40	15.8	60.8	21	22	AAAF69302
C	41	15.4	59.2	60	24	AAEN4A004
C	42	15.4	59.2	80	22	AALL24014
C	43	15.2	58.5	62	20	AAZ13290
C	44	15.2	57.7	22	21	AAA86916
C	45	15	57.7	22	21	AAA86916

ALIGNMENTS

RESULT 1	
AAZ60866	
ID AAZ60866	standard; RNA; 26 BP.
XX	
AC AAZ60866;	
XX	
DT 16-MAY-2000	(first entry)
XX	
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.	
XX	
DE Fusion transcript; translocation; bcr b3 region; abl gene;	
XX	
KW application assay; detection assay; medical diagnosis;	
RW clinical monitoring; chimeric RNA; fusion RNA; condition marker;	
XX	
OS disease marker; cancer; leukemia; ss.	
XX	
OS Synthetic.	
XX	
PN WO200005418-A1.	
PD	
XX 03-FEB-2000.	
XX	
PF 23-JUL-1999;	99WO-US16832.
XX	
PK 23-JUL-1998;	98US-0121239.
XX	
PA (GENP-) GEN-PROBE INC.	
XX	
PI Harvey RC,	Eastman PS;
XX	
DR WPI: 2000-182730/16.	
PT Novel methods for preparing RNA from biological samples, used for the	

PT detection and measurement of nucleic acids and fusion nucleic acids -
 XX
 XX Claim 19; Page 44; 49pp; English.
 PS
 XX Oligonucleotides AA260840-62 and AA260865-66 are used in the method of
 CC the invention to detect fusion transcripts produced from a translocation
 CC between the bcr b3 region and the abl gene. The specification describes
 CC a method for detecting a fusion nucleic acid (particularly chimeric RNA
 CC species), in a biological sample. The method comprises contacting a
 CC sample of fusion nucleic acid with primers, amplifying the hybridized
 CC fusion nucleic acid, and detecting the target hybrid. The method is
 CC used for the simple and rapid preparation of RNA from a biological
 CC sample, particularly from the cytoplasm of eukaryotic cells, which is
 CC suitable for use in an amplification and detection assay. The methods
 CC are used for the analysis and detection of nucleic acids in biological
 CC fields, for medical diagnoses and clinical monitoring of a patient's
 CC response to therapy where a disease or medical condition is associated
 CC with a particular type and/or level of mRNA present in the sample. The
 CC methods are also useful for detecting or quantifying fusion or chimeric
 CC RNA species, and for detecting a translocation as a marker for a given
 CC condition or disease, e.g. translocations associate with cancers,
 CC particularly forms of leukemia.
 XX
 S0 Sequence 26 BP; 8 A; 7 C; 6 G; 5 T; 0 other;

Query Match 100.0%; Score 26; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.009;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGATTTAAGCAGAG 26
 |||||
 Db 1 CACTCAGCCACTGATTTAAGCAGAG 26

RESULT 2

AAV01788/c
 ID AAV01788 standard; RNA; 52 BP.

XX AAV01788;

DT 04-JUN-1998 (first entry)

DE Antisense RNA sequence of the specification.

KW Antisense; inhibitor; gene expression; chromosomal translocation;

KW Translocation point; pharmaceutical composition;

KW chronic myelogenous leukemia; acute lymphoblastic leukemia;

XX acute myelogenous leukemia; Non-Hodgkin lymphoma; treatment; ss.

OS Synthetic.

PN WO9746672-A2.

PD 11-DEC-1997.

PF 05-JUN-1997; 97WO-EP02923.

PR 05-JUN-1996; 96EP-0109034.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Haas R, Kronenwett R, Sczakiel G;

DR WPI; 1998-042181/04.

PT Nucleic acid molecule containing chromosomal translocation point -

XX useful to treat chromosomal translocation disorders, e.g. chronic

XX myelogenous leukemia

PS Claim 6; Page 37; 49pp; English.

CC AAV01779-804 represent antisense RNA sequences. For long chain antisense

CC RNA, the association rate with their target RNA in vitro correlates
 CC with their effectiveness in vivo. Antisense molecules are potent
 CC inhibitors of gene expression and viral functions. The antisense
 CC molecules AAV01779-804 exemplify novel nucleic acid molecules of the
 CC invention. These nucleic acid molecules contain portions complementary
 CC to a first and second chromosomal DNA sequence. The nucleic acid
 CC molecule forms at least part of a chromosomal translocation resulting in
 CC a fusion gene containing the translocation point. The DNA sequence, as
 CC well as vectors and host cells containing it are useful in
 CC pharmaceutical compositions for treating disorders based on chromosomal
 CC translocations, preferably for chronic myelogenous leukemia. The
 CC pharmaceutical composition may also be used to treat acute lymphoblastic
 CC leukemias, acute myelogenous leukemias and Non-Hodgkin lymphomas.
 XX
 S0 Sequence 52 BP; 12 A; 10 C; 16 G; 14 U; 0 other;

Query Match 100.0%; Score 26; DB 19; Length 52;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGATTTAAGCAGAG 26
 |||||
 Db 43 CACTCAGCCACTGATTTAAGCAGAG 18

RESULT 3

AAV01789/c
 ID AAV01789 standard; RNA; 53 BP.

XX AAV01789;

DT 04-JUN-1998 (first entry)

DE Antisense RNA sequence of the specification.

KW Antisense; inhibitor; gene expression; chromosomal translocation;

KW Translocation point; pharmaceutical composition;

KW chronic myelogenous leukemia; acute lymphoblastic leukemia;

XX acute myelogenous leukemia; Non-Hodgkin lymphoma; treatment; ss.

OS Synthetic.

PN WO9746672-A2.

PD 11-DEC-1997.

PF 05-JUN-1997; 97WO-EP02923.

PR 05-JUN-1996; 96EP-0109034.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Haas R, Kronenwett R, Sczakiel G;

DR WPI; 1998-042181/04.

PT Nucleic acid molecule containing chromosomal translocation point -

XX useful to treat chromosomal translocation disorders, e.g. chronic

XX myelogenous leukemia

PS Claim 6; Page 37; 49pp; English.

CC AAV01779-804 represent antisense RNA sequences. For long chain antisense

CC RNA, the association rate with their target RNA in vitro correlates

CC with their effectiveness in vivo. Antisense molecules are potent

CC inhibitors of gene expression and viral functions. The antisense

CC molecules AAV01779-804 exemplify novel nucleic acid molecules of the

CC invention. These nucleic acid molecules contain portions complementary

CC to a first and second chromosomal DNA sequence. The nucleic acid

CC molecule forms at least part of a chromosomal translocation resulting in

CC a fusion gene containing the translocation point. The DNA sequence, as

CC well as vectors and host cells containing it are useful in

CC pharmaceutical compositions for treating disorders based on chromosomal

CC translocations, preferably for chronic myelogenous leukaemia. The
 CC pharmaceutical composition may also be used to treat acute lymphoblastic
 CC leukaemias, acute myelogenous leukaemias and Non-Hodgkin lymphomas.
 XX
 SO Sequence 53 BP; 13 A; 10 C; 16 G; 14 U; 0 other;
 Query Match 100.0%; Score 26; DB 19; Length 53;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CACTCAGCCACTGGATTAAAGCAGAG 26
 DB 43 CACTCAGCCACTGGATTAAAGCAGAG 18
 RESULT 4
 AAV01790/c
 ID AAV01790 standard; RNA; 54 BP.
 AC AAV01790;
 XX
 XX 04-JUN-1998 (first entry)
 DT
 DE Antisense RNA sequence of the specification.
 XX
 XX Antisense; inhibitor; gene expression; chromosomal translocation;
 XX translocation point; pharmaceutical composition;
 XX chronic myelogenous leukaemia; acute lymphoblastic leukaemia;
 XX acute myelogenous leukaemia; Non-Hodgkin lymphoma; treatment; ss.
 OS Synthetic.
 XX
 XX WO9746672-A2.
 PN
 XX 11-DEC-1997.
 PD
 XX 05-JUN-1997; 97WO-EP02923.
 PF
 XX 05-JUN-1996; 96EP-0109034.
 PR
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA
 XX Haas R, Kronenwett R, Szczakiel G;
 PI
 XX WPI; 1998-042181/04.
 DR
 XX Nucleic acid molecule containing chromosomal translocation point -
 PT useful to treat chromosomal translocation disorders, e.g. chronic
 PT myelogenous leukaemia
 PS
 XX Claim 6; Page 37; 49pp; English.
 XX
 XX AAV01779-804 represent antisense RNA sequences. For long chain antisense
 CC RNA, the association rate with their target RNA in vitro correlates
 CC with their effectiveness in vivo. Antisense molecules are potent
 CC inhibitors of gene expression and viral functions. The antisense
 CC molecules AAV01779-804 exemplify novel nucleic acid molecules of the
 CC invention. These nucleic acid molecules contain portions complementary
 CC to a first and second chromosomal DNA sequence. The nucleic acid
 CC molecule forms at least part of a chromosomal translocation resulting in
 CC a fusion gene containing the translocation point. The DNA sequence, as
 CC well as vectors and host cells containing it are useful in
 CC pharmaceutical compositions for treating disorders based on chromosomal
 CC translocations, preferably for chronic myelogenous leukaemia. The
 CC pharmaceutical composition may also be used to treat acute lymphoblastic
 CC leukaemias, acute myelogenous leukaemias and Non-Hodgkin lymphomas.
 CC
 SO Sequence 54 BP; 13 A; 10 C; 16 G; 15 U; 0 other;
 Query Match 100.0%; Score 26; DB 19; Length 54;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CACTCAGCCACTGGATTAAAGCAGAG 26
 DB 43 CACTCAGCCACTGGATTAAAGCAGAG 18
 RESULT 5
 AAV01791/c
 ID AAV01791 standard; RNA; 55 BP.
 AC AAV01791;
 XX
 XX 04-JUN-1998 (first entry)
 DT
 DE Antisense RNA sequence of the specification.
 XX
 XX Antisense; inhibitor; gene expression; chromosomal translocation;
 XX translocation point; pharmaceutical composition;
 XX chronic myelogenous leukaemia; acute lymphoblastic leukaemia;
 XX acute myelogenous leukaemia; Non-Hodgkin lymphoma; treatment; ss.
 OS Synthetic.
 XX
 XX WO9746672-A2.
 PN
 XX 11-DEC-1997.
 PD
 XX 05-JUN-1997; 97WO-EP02923.
 PF
 XX 05-JUN-1996; 96EP-0109034.
 PR
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA
 XX Haas R, Kronenwett R, Szczakiel G;
 PI
 XX WPI; 1998-042181/04.
 DR
 XX Nucleic acid molecule containing chromosomal translocation point -
 PT useful to treat chromosomal translocation disorders, e.g. chronic
 PT myelogenous leukaemia
 PS
 XX Claim 6; Page 37; 49pp; English.
 XX
 XX AAV01779-804 represent antisense RNA sequences. For long chain antisense
 CC RNA, the association rate with their target RNA in vitro correlates
 CC with their effectiveness in vivo. Antisense molecules are potent
 CC inhibitors of gene expression and viral functions. The antisense
 CC molecules AAV01779-804 exemplify novel nucleic acid molecules of the
 CC invention. These nucleic acid molecules contain portions complementary
 CC to a first and second chromosomal DNA sequence. The nucleic acid
 CC molecule forms at least part of a chromosomal translocation resulting in
 CC a fusion gene containing the translocation point. The DNA sequence, as
 CC well as vectors and host cells containing it are useful in
 CC pharmaceutical compositions for treating disorders based on chromosomal
 CC translocations, preferably for chronic myelogenous leukaemia. The
 CC pharmaceutical composition may also be used to treat acute lymphoblastic
 CC leukaemias, acute myelogenous leukaemias and Non-Hodgkin lymphomas.
 CC
 SO Sequence 55 BP; 13 A; 10 C; 16 G; 16 U; 0 other;
 Query Match 100.0%; Score 26; DB 19; Length 55;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CACTCAGCCACTGGATTAAAGCAGAG 26
 DB 43 CACTCAGCCACTGGATTAAAGCAGAG 18
 RESULT 6
 AAQ46950
 ID AAQ46950 standard; DNA; 56 BP.
 AC AAQ46950;

```

XX 21-JAN-1994 (first entry)
DE Branched probe to CMLA translocation region of chromosome 22.
XX
XX Chronic myelogenous leukaemia; CMLA chimeric bcr/abl;
XX acute lymphocytic leukaemia; ALL; genetic translocation;
XX chromosome 22; target sequence; universal detection oligomer;
XX branched probe; chemiluminescent acridinium ester; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_feature 1..40
XX /*tag= a
XX /*note= "complementary to region of chromosome 22
XX associated with CMLA translocation"
XX
XX misc_feature 41..56
XX /*tag= b
XX /*note= "complementary to nucleotides 16-1 of
XX universal detection probe AAQ46949"
XX
XX EP552931-A.
XX
XX 28-JUL-1993.
XX
XX 20-JAN-1993; 93EP-0300377.
XX
XX 22-JAN-1992; 92US-0827021.
XX
XX (GEP- ) GEN PROBE INC.
XX
XX Arnold LJ, Bezverkov R, Hogan JJ, Nelson NC;
XX WPI; 1993-236606/30.
XX
XX Nucleic acid molecules which hybridise in presence of target
XX protein acid - are used as probes in hybridisation assays or as
XX therapeutic agents for diseases
XX
XX Example 6; Fig 12A; 58pp; English.
XX
XX Chimeric targets were synthesised homologous to 3 different
XX genetic translocations between a constant abl region of chromosome
XX 9 and various regions of chromosome 22; two are the most common
XX translocations associated with chronic myelogenous leukaemia (CMLA
XX and CMLb) and the other is associated with acute lymphocytic
XX leukaemia (ALL). An AE-labelled universal detection oligomer (AAQ46949)
XX specific for the abl region was synthesised. Three different
XX strands were designed to contain a probe region specific for one of
XX the translocated chromosome 22 regions as well as an arm region
XX complementary to part of the universal probe (AAQ46950-2). The probe
XX mixes were found to detect only the correct chimeric targets and
XX did not cross-react significantly with the other targets.
XX
XX Sequence 56 BP; 16 A; 17 C; 9 G; 14 T; 0 other;
SQ
Query Match 100.0%; Score 26; DB 14; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CACTCAGCCACTGATTTAAGCAGAG 26
DB 10 CACTCAGCCACTGATTTAAGCAGAG 35

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XX Antisense RNA sequence of the specification.
DE
XX Antisense; inhibitor; gene expression; chromosomal translocation;
XX translocation point; pharmaceutical composition;
XX chronic myelogenous leukaemia; acute lymphoblastic leukaemia;
XX acute myelogenous leukaemia; Non-Hodgkin Lymphoma; treatment; ss.
XX
XX Synthetic.
XX
XX WO9746672-A2.
XX
XX 11-DEC-1997.
XX
XX 05-JUN-1997; 97WO-EP02923.
XX
XX 05-JUN-1996; 96EP-0109034.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSGEZENTRUM.
XX
XX Haas R, Kronenwett R, Sczakiel G;
XX WPI; 1998-042181/04.
XX
XX Nucleic acid molecule containing chromosomal translocation point -
XX useful to treat chromosomal translocation disorders, e.g. chronic
XX myelogenous leukaemia
XX
XX Claim 6; Page 37; 49pp; English.
XX
XX AA01779-804 represent antisense RNA sequences. For long chain antisense
XX RNA, the association rate with their target RNA in vitro correlates
XX with their effectiveness in vivo. Antisense molecules are potent
XX inhibitors of gene expression and viral functions. The antisense
XX molecules AA01779-804 exemplify novel nucleic acid molecules of the
XX invention. These nucleic acid molecules contain portions complementary
XX to a first and second chromosomal DNA sequence. The nucleic acid
XX molecule forms at least part of a chromosomal translocation resulting in
XX a fusion gene containing the translocation point. The DNA sequence, as
XX well as vectors and host cells containing it are useful in
XX pharmaceutical compositions for treating disorders based on chromosomal
XX translocations, preferably for chronic myelogenous leukaemia. The
XX pharmaceutical composition may also be used to treat acute lymphoblastic
XX leukaemias, acute myelogenous leukaemias and Non-Hodgkin lymphomas.
XX
XX Sequence 56 BP; 13 A; 11 C; 16 G; 16 U; 0 other;
SQ
Query Match 100.0%; Score 26; DB 19; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CACTCAGCCACTGATTTAAGCAGAG 26
DB 43 CACTCAGCCACTGATTTAAGCAGAG 18

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RESULT 7
AA01792/c
ID AA01792 standard; RNA; 56 BP.
XX
XX AA01792;
XX
XX 04-JUN-1998 (first entry)
DT

```

```

RESULT 8
AA01793/c
ID AA01793 standard; RNA; 57 BP.
XX
XX AA01793;
XX
XX 04-JUN-1998 (first entry)
DE
XX Antisense RNA sequence of the specification.
XX
XX Antisense; inhibitor; gene expression; chromosomal translocation;
XX translocation point; pharmaceutical composition;
XX chronic myelogenous leukaemia; acute lymphoblastic leukaemia;
XX acute myelogenous leukaemia; Non-Hodgkin Lymphoma; treatment; ss.
XX
XX Synthetic.
XX

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PN WO9746672-A2.
XX 11-DEC-1997.
PD
XX
XX 05-JUN-1997; 97WO-EP02923.
XX
XX 05-JUN-1996; 96EP-0109034.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
XX Haas R, Kronenwett R, Szczakiel G;
XX WPI: 1998-042181/04.
XX
XX Nucleic acid molecule containing chromosomal translocation point -
XX useful to treat chromosomal translocation disorders, e.g. chronic
XX myelogenous leukaemia
XX
XX
XX Claim 6; Page 37; 49pp; English.
XX
XX AAV01779-804 represent antisense RNA sequences. For long chain antisense
XX RNA, the association rate with their target RNA in vitro correlates
XX with their effectiveness in vivo. Antisense molecules are potent
XX inhibitors of gene expression and viral functions. The antisense
XX molecules AAV01779-804 exemplify novel nucleic acid molecules of the
XX invention. These nucleic acid molecules contain portions complementary
XX to a first and second chromosomal DNA sequence. The nucleic acid
XX molecule forms at least part of a chromosomal translocation resulting in
XX a fusion gene containing the translocation point. The DNA sequence, as
XX well as vectors and host cells containing it are useful in
XX pharmaceutical compositions for treating disorders based on chromosomal
XX translocations, preferably for chronic myelogenous leukaemia. The
XX pharmaceutical composition may also be used to treat acute lymphoblastic
XX leukaemias, acute myelogenous leukaemias and Non-Hodgkin lymphomas.
XX
XX
XX Sequence 57 BP; 14 A; 11 C; 16 G; 16 U; 0 other;
SQ
Query Match 100.0%; Score 26; DB 19; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Gaps 0;
Matches 26; Conservative 0; Indels 0;
OY 1 CACTCAGCAGCTGATTTAGCAGAG 26
DB 43 CACTCAGCAGCTGATTTAGCAGAG 18
RESULT 9
AAV01794/C
ID AAV01794 standard; RNA; 58 BP.
XX
XX AAV01794;
XX
XX 04-JUN-1998 (first entry)
XX
XX Antisense RNA sequence of the specification.
XX
XX Antisense; inhibitor; gene expression; chromosomal translocation;
XX translocation point; pharmaceutical composition;
XX chronic myelogenous leukaemia; acute lymphoblastic leukaemia;
XX acute myelogenous leukaemia; Non-Hodgkin lymphoma; treatment; ss.
XX
XX Synthetic:
XX MO9746672-A2.
XX 11-DEC-1997.
XX
XX 05-JUN-1997; 97WO-EP02923.
XX
XX 05-JUN-1996; 96EP-0109034.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX

PI Haas R, Kronenwett R, Szczakiel G;
XX WPI: 1998-042181/04.
XX
XX Nucleic acid molecule containing chromosomal translocation point -
XX useful to treat chromosomal translocation disorders, e.g. chronic
XX myelogenous leukaemia
XX
XX
XX Claim 6; Page 37; 49pp; English.
XX
XX AAV01779-804 represent antisense RNA sequences. For long chain antisense
XX RNA, the association rate with their target RNA in vitro correlates
XX with their effectiveness in vivo. Antisense molecules are potent
XX inhibitors of gene expression and viral functions. The antisense
XX molecules AAV01779-804 exemplify novel nucleic acid molecules of the
XX invention. These nucleic acid molecules contain portions complementary
XX to a first and second chromosomal DNA sequence. The nucleic acid
XX molecule forms at least part of a chromosomal translocation resulting in
XX a fusion gene containing the translocation point. The DNA sequence, as
XX well as vectors and host cells containing it are useful in
XX pharmaceutical compositions for treating disorders based on chromosomal
XX translocations, preferably for chronic myelogenous leukaemia. The
XX pharmaceutical composition may also be used to treat acute lymphoblastic
XX leukaemias, acute myelogenous leukaemias and Non-Hodgkin lymphomas.
XX
XX
XX Sequence 58 BP; 14 A; 11 C; 17 G; 16 U; 0 other;
SQ
Query Match 100.0%; Score 26; DB 19; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Gaps 0;
Matches 26; Conservative 0; Indels 0;
OY 1 CACTCAGCAGCTGATTTAGCAGAG 26
DB 43 CACTCAGCAGCTGATTTAGCAGAG 18
RESULT 10
AAV01795/C
ID AAV01795 standard; RNA; 59 BP.
XX
XX AAV01795;
XX
XX 04-JUN-1998 (first entry)
XX
XX Antisense RNA sequence of the specification.
XX
XX Antisense; inhibitor; gene expression; chromosomal translocation;
XX translocation point; pharmaceutical composition;
XX chronic myelogenous leukaemia; acute lymphoblastic leukaemia;
XX acute myelogenous leukaemia; Non-Hodgkin lymphoma; treatment; ss.
XX
XX Synthetic:
XX MO9746672-A2.
XX 11-DEC-1997.
XX
XX 05-JUN-1997; 97WO-EP02923.
XX
XX 05-JUN-1996; 96EP-0109034.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
XX Haas R, Kronenwett R, Szczakiel G;
XX WPI: 1998-042181/04.
XX
XX Nucleic acid molecule containing chromosomal translocation point -
XX useful to treat chromosomal translocation disorders, e.g. chronic
XX myelogenous leukaemia
XX
XX
XX Claim 6; Page 37; 49pp; English.
XX

CC AAV01779-804 represent antisense RNA sequences. For long chain antisense
CC RNA, the association rate with their target RNA in vitro correlates
CC with their effectiveness in vivo. Antisense molecules are potent
CC inhibitors of gene expression and viral functions. The antisense
CC molecules AAV01779-804 exemplify novel nucleic acid molecules of the
CC invention. These nucleic acid molecules contain portions complementary
CC to a first and second chromosomal DNA sequence. The nucleic acid
CC molecule forms at least part of a chromosomal translocation resulting in
CC a fusion gene containing the translocation point. The DNA sequence, as
CC well as vectors and host cells containing it are useful in
CC pharmaceutical compositions for treating disorders based on chromosomal
CC translocations, preferably for chronic myelogenous leukaemia. The
CC pharmaceutical composition may also be used to treat acute lymphoblastic
CC leukaemias, acute myelogenous leukaemias and Non-Hodgkin lymphomas.
XX
SQ Sequence 59 BP; 15 A; 11 C; 17 G; 16 U; 0 other;
Query Match 100.0%; Score 26; DB 19; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Gaps 0;
Matches 26; Conservative 0; Indels 0; Gaps 0;
OY 1 CACTCAGCCACTGATTTAAGCAGAG 26
Db 43 CACTCAGCCACTGATTTAAGCAGAG 18
|||||
RESULT 11
ID AAA86914/C
AAA86914 standard; DNA; 40 BP.
AC AAA86915;
DT 15-JAN-2001 (first entry)
DE Native bcr.
XX
DE Detection; nucleic acid hybrid; depolymerisation; analysis; SNP;
KW single nucleotide polymorphism; identification; viral load; probe;
KW genotyping; medical marker diagnostic; primer; target; mutation;
KW genetic disease; ss.
XX
OS Homo sapiens.
XX
PN WO200049180-A1.
PD 24-AUG-2000.
XX
PF 18-FEB-2000; 2000WO-US04242.
XX
PR 18-FEB-1999; 99US-0252436.
PR 21-JUL-1999; 99US-0358972.
PR 25-AUG-1999; 99US-0383316.
XX
PA (PROM-) PROMEGA CORP.
XX
PI Shultz JW, Lewis MK, Leippe D, Mandrekar M, Kephart D, Rhodes RB;
PI Andrews CA, Hartnett JR, Gu T, Olson RJ, Wood KV, Welch R;
XX
DR WPI; 2000-565377/52.
XX
PT Determining presence or absence of a predetermined endogenous nucleic
PT acid sequence by using an enzyme that depolymerizes the 3' end of an
PT oligonucleotide probe hybridized to a target sequence to release
PT identifier nucleotides -
XX
PS Example; Page 328; 389pp; English.
XX
CC The present invention describes a method (M1) for determining the
CC presence or absence of a predetermined endogenous nucleic acid target
CC sequence (ENAT). The method comprises hybridising a probe having an
CC identifier nucleotide (IN) with ENAT which is treated with an enzyme
CC that depolymerises the 3' end of hybridised NA to release the INs.
CC MI is used for determining the number of known sequence repeats present

CC in a nucleic acid target sequence in a nucleic acid sample. The method
CC is also useful for determining whether a nucleic acid target sequence in
CC a sample is an allele from a homozygous or heterozygous locus. The
CC method is also useful for detection of mutations, translocations and
CC SNPs in nucleic acids (including those associated with genetic disease),
CC determination of viral load, species identification, sample
CC contamination, and analysis of forensic samples. AAA86791 to AAA87079
CC and AAB12817 represent sequence which are used in the exemplification of
CC the present invention.
CC N.B. There is a discrepancy between the SEQ ID NO: and sequences given
CC in the examples, and the SEQ ID NO: and sequences given in the sequence
CC listing from the present invention.
XX
SQ Sequence 40 BP; 10 A; 9 C; 8 G; 13 T; 0 other;
Query Match 96.2%; Score 25; DB 21; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 ACTCAGCCACTGATTTAAGCAGAG 26
Db 40 ACTCAGCCACTGATTTAAGCAGAG 16
|||||
RESULT 12
ID AAA86915/C
AAA86915 standard; DNA; 41 BP.
AC AAA86915;
DT 15-JAN-2001 (first entry)
DE bcr/abl translocation.
XX
DE Detection; nucleic acid hybrid; depolymerisation; analysis; SNP;
KW single nucleotide polymorphism; identification; viral load; probe;
KW genotyping; medical marker diagnostic; primer; target; mutation;
KW genetic disease; ss.
XX
OS Homo sapiens.
XX
PN WO200049180-A1.
PD 24-AUG-2000.
XX
PF 18-FEB-2000; 2000WO-US04242.
XX
PR 18-FEB-1999; 99US-0252436.
PR 21-JUL-1999; 99US-0358972.
PR 25-AUG-1999; 99US-0383316.
XX
PA (PROM-) PROMEGA CORP.
XX
PI Shultz JW, Lewis MK, Leippe D, Mandrekar M, Kephart D, Rhodes RB;
PI Andrews CA, Hartnett JR, Gu T, Olson RJ, Wood KV, Welch R;
XX
DR WPI; 2000-565377/52.
XX
PT Determining presence or absence of a predetermined endogenous nucleic
PT acid sequence by using an enzyme that depolymerizes the 3' end of an
PT oligonucleotide probe hybridized to a target sequence to release
PT identifier nucleotides -
XX
PS Example; Page 329; 389pp; English.
XX
CC The present invention describes a method (M1) for determining the
CC presence or absence of a predetermined endogenous nucleic acid target
CC sequence (ENAT). The method comprises hybridising a probe having an
CC identifier nucleotide (IN) with ENAT which is treated with an enzyme
CC that depolymerises the 3' end of hybridised NA to release the INs.
CC MI is used for determining the number of known sequence repeats present
CC in a nucleic acid target sequence in a nucleic acid sample. The method
CC is also useful for determining whether a nucleic acid target sequence in

CC a sample is an allele from a homozygous or heterozygous locus. The
 CC method is also useful for detection of mutations, translocations and
 CC SNPs in nucleic acids (including those associated with genetic disease),
 CC determination of viral load, species identification, sample
 CC contamination, and analysis of forensic samples. AAB6791 to AAB87079
 CC and AAB12817 represent sequence which are used in the exemplification of
 CC the present invention.
 CC N.B. There is a discrepancy between the SEQ ID NO: and sequences given
 CC in the examples, and the SEQ ID NO: and sequences given in the sequence
 CC listing from the present invention.

XX Sequence 41 BP; 9 A; 8 C; 11 G; 13 T; 0 other;

SO Query Match 96.2%; Score 25; DB 21; Length 41;
 Best Local Similarity 100.0%; Pred. No. 0.029; 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ACTCAGCCACTGGATTAAAGCAGAG 26
 DB 41 ACTCAGCCACTGGATTAAAGCAGAG 17

RESULT 13
 AAN97243
 ID AAN97243-standard; DNA; 59 BP.
 AC AAN97243;
 XX 06-JUL-1993 (first entry)
 DT
 DE BCR/ABL target sequence.
 XX
 KW Deoxyoligonucleotide; probe; amine; label; acridinium ester; AE;
 KW hybridisation assay; protection; hydrolysis; stability;
 KW chimeric target sequence; chronic myelogenous leukemia; CML;
 KW translocation; abl; bcr; chromosome; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 31..59
 FT /*tag= a
 FT /label= abl_sequence

W08902476-A.
 PD 23-MAR-1989.
 XX
 PD 21-SEP-1988; 88WO-US03195.
 XX
 PR 21-SEP-1987; 87US-0099392.
 XX
 PA (GEP-) GEN PROBE INC.
 PA (MLTE-) ML TECHN VENTURES.
 XX
 PI Arnold LJ, Nelson NC, Arnold L;
 XX
 WI; 1989-100016/13.
 XX
 DR Homogeneous binding assay using degradable label esp. acridinium
 XX ester - with different stabilities in bound and unbound forms,
 XX esp. useful in hybridisation detection of specific polynucleotide
 XX
 PS Example 16; Page 43; 64pp; English.
 XX
 CC Example 16 illustrates the detection of a chimeric target sequence
 CC associated with chronic myelogenous leukemia (CML) using a probe
 CC internally labelled with acridinium ester (AE).
 CC The probe (AAN97243) is complementary to the chimeric mRNA transcript
 CC (common break) associated with CML. This chimeric mRNA is a product
 CC of the chimeric gene formed by the translocation of a region of the
 CC abl gene on chromosome 9 into a region of chromosome 22 contg. the
 CC bcr gene. The BCR/ABL and ABL target sequences are given in

CC AAN97243-44. The AE-labelled probe was able to discriminate between
 CC chimeric target and normal sequences (as well as unhybridised probe) using
 CC the homogeneous binding assay.

XX Sequence 59 BP; 16 A; 17 C; 13 G; 13 T; 0 other;

SO Query Match 96.2%; Score 25; DB 10; Length 59;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ACTCAGCCACTGGATTAAAGCAGAG 26
 DB 1 ACTCAGCCACTGGATTAAAGCAGAG 25

RESULT 14
 AAN97244
 ID AAN97244 standard; DNA; 59 BP.
 AC AAN97244;
 XX 06-JUL-1993 (first entry)
 DT
 DE ABL target sequence.
 XX
 KW Deoxyoligonucleotide; probe; amine; label; acridinium ester; AE;
 KW hybridisation assay; protection; hydrolysis; stability;
 KW chimeric target sequence; chronic myelogenous leukemia; CML;
 KW translocation; abl; bcr; chromosome; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..59
 FT /*tag= a
 FT /label= abl_sequence

W08902476-A.
 PD 23-MAR-1989.
 XX
 PD 21-SEP-1988; 88WO-US03195.
 XX
 PR 21-SEP-1987; 87US-0099392.
 XX
 PA (GEP-) GEN PROBE INC.
 PA (MLTE-) ML TECHN VENTURES.
 XX
 PI Arnold LJ, Nelson NC, Arnold L;
 XX
 WI; 1989-100016/13.
 XX
 DR Homogeneous binding assay using degradable label esp. acridinium
 XX ester - with different stabilities in bound and unbound forms,
 XX esp. useful in hybridisation detection of specific polynucleotide
 XX
 PS Example 16; Page 43; 64pp; English.
 XX
 CC Example 16 illustrates the detection of a chimeric target sequence
 CC associated with chronic myelogenous leukemia (CML) using a probe
 CC internally labelled with acridinium ester (AE).
 CC The probe (AAN97243) is complementary to the chimeric mRNA transcript
 CC (common break) associated with CML. This chimeric mRNA is a product
 CC of the chimeric gene formed by the translocation of a region of the
 CC abl gene on chromosome 9 into a region of chromosome 22 contg. the
 CC bcr gene. The BCR/ABL and ABL target sequences are given in
 CC AAN97243-44. The AE-labelled probe was able to discriminate between
 CC chimeric target and normal sequences (as well as unhybridised probe) using
 CC the homogeneous binding assay.

SO Query Match 96.2%; Score 25; DB 10; Length 59;

Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: December 21, 2002, 11:54:48
Job time : 91.249 secs

OY 2 ACTCAGCCACTGCGATTTAAGCAGAG 26
DB 1 ACTCAGCCACTGCGATTTAAGCAGAG 25

RESULT 15

AA055680
ID AA055680 standard; DNA; 59 BP.

AC AA055680;

DT 09-AUG-1994 (first entry)

DE N. gonorrhoeae 16S subunit BCR/ABL synthetic target sequence.

KW Probe; amine; linker arm; N-acridinium; ester; label; homogeneous;
hybridisation assay; detection; linear dilution series; Chlamydia;
KW rRNA; ss.

OS Synthetic.

PN US5283174-A.

PD 01-FEB-1994.

PF 21-SEP-1987; 87US-0099392.

PR 21-SEP-1987; 87US-0099392.

PR 12-DEC-1988; 88US-0294700.

PR 23-MAY-1990; 90US-0528920.

PR 08-NOV-1990; 90US-0613603.

PA (GENP-) GEN-PROBE INC.

PI Arnold LJ, Nelson NC;

DR WPI; 1994-048084/06.

PT Homogeneous nucleic acid hybridisation assay - using probe
labelled with acridinium ester for detection of linear dilution
series

PS Example 15; Column 25; 20pp; English.

CC The sequences given in AA055679-81 represent a probe, and a synthetic
and wild type target sequence which was used in the method of the
invention. The probes corresponds to the 16S subunit of Neisseria
gonorrhoeae and contains an amine linker arm which may bear an N-
acridinium ester label. Probes such as this may be used in an
homogeneous hybridisation assay for determining the presence or
amount of a target nucleic acid in a sample. This method comprises
contacting the sample with an N-acridinium bearing probe, such that
the acridinium ester label may be degraded by a chemical, eg. acid,
base or oxidising agent, while duplex-linked N-acridinium ester remains
undegraded. The hybridisation mixture is treated with the chemical and
the amount of undegraded N-acridinium ester is measured without
physically separating any unhybridised probe. The method is capable of
detecting linear dilution series, eg. Chlamydia rRNA with a detection
limit of 0.1-1 ng.

CC Sequence 59 BP; 16 A; 17 C; 13 G; 13 T; 0 other;

Query Match 96.2%; Score 25; DB 15; Length 59;

Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ACTCAGCCACTGCGATTTAAGCAGAG 26
DB 1 ACTCAGCCACTGCGATTTAAGCAGAG 25

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:28:32 Search time 46.5061 Seconds
(without alignments)
356.094 Million cell updates/sec

Title: US-09-121-239-1

Perfect score: 54 TAAATTATATACGACTGCTCACTA.....CCCTGAGGCTCAAGTCAGA 54

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

Issued Patents_NA.*
1: /cgn2_6/prodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/prodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/prodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/prodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/prodata/1/ina/PCITUS.COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	59.3	52	4	US-09-493-491-39 Sequence 39, Appl
2	32	59.3	54	4	US-09-493-491-29 Sequence 29, Appl
3	31	57.4	49	1	US-07-931-473B-50 Sequence 50, Appl
4	31	57.4	49	1	US-07-714-111C-50 Sequence 50, Appl
5	31	57.4	49	1	US-08-413-110-50 Sequence 50, Appl
6	31	57.4	49	1	US-08-409-442A-50 Sequence 50, Appl
7	31	57.4	49	2	US-08-469-609A-50 Sequence 50, Appl
8	31	57.4	49	3	US-09-143-190-50 Sequence 50, Appl
9	31	57.4	49	4	US-09-502-344-50 Sequence 50, Appl
10	31	57.4	73	1	US-08-409-442A-350 Sequence 350, App
11	31	57.4	73	2	US-08-469-609A-350 Sequence 350, App
12	31	57.4	73	3	US-09-143-190-350 Sequence 350, App
13	31	57.4	73	4	US-09-502-344-350 Sequence 350, App
14	30.8	57.0	49	1	US-08-384-541-5 Sequence 5, Appl
15	30.8	57.0	49	1	US-08-384-541-6 Sequence 6, Appl
16	30.8	57.0	49	1	US-08-384-541-7 Sequence 7, Appl
17	30.8	57.0	49	1	US-08-384-541-8 Sequence 8, Appl
18	30.8	56.3	52	4	US-09-493-491-40 Sequence 40, Appl
19	30.2	55.9	49	4	US-09-493-491-35 Sequence 35, Appl
20	30.2	55.9	62	1	US-08-345-861-1 Sequence 1, Appl
21	30	55.6	49	4	US-09-493-491-34 Sequence 34, Appl
22	30	55.6	50	4	US-09-493-491-28 Sequence 28, Appl
23	29.8	55.2	71	4	US-09-493-491-49 Sequence 49, Appl
24	29.8	54.8	60	1	US-09-495-152A-2 Sequence 2, Appl
25	29.4	54.4	36	3	US-08-099-867-7 Sequence 7, Appl
26	29.4	54.4	36	3	US-08-095-636-7 Sequence 7, Appl
27	29.4	54.4	49	4	US-09-710-200-1 Sequence 1, Appl

C 28	29.4	54.4	62	4	US-09-308-759A-29	Sequence 29, Appl
C 29	29.4	54.4	67	4	US-09-308-759A-49	Sequence 49, Appl
C 30	29.4	54.4	91	4	US-09-308-759A-40	Sequence 40, Appl
C 31	29.4	54.4	96	4	US-09-308-759A-36	Sequence 36, Appl
C 32	29.4	54.4	37	1	US-08-099-867-5	Sequence 5, Appl
C 33	29.4	53.7	47	1	US-08-162-836-10	Sequence 10, Appl
C 34	29.4	53.7	47	1	US-08-345-861-6	Sequence 6, Appl
C 35	29.4	53.7	47	2	US-08-479-105A-6	Sequence 6, Appl
C 36	29.4	53.7	47	4	US-09-502-966-3	Sequence 3, Appl
C 37	29.4	53.7	50	3	US-08-972-799A-25	Sequence 25, Appl
C 38	29.4	53.7	50	3	US-09-506-282-25	Sequence 25, Appl
C 39	29.4	53.7	52	5	PCT-US95-03339-25	Sequence 25, Appl
C 40	29.4	53.7	52	4	US-09-493-491-33	Sequence 33, Appl
C 41	29.4	53.7	54	4	US-09-493-491-27	Sequence 27, Appl
C 42	29.4	53.7	55	4	US-09-493-491-47	Sequence 47, Appl
C 43	29.4	53.0	79	1	US-08-099-867-3	Sequence 3, Appl
C 44	28.6	53.0	51	2	US-08-663-688A-2	Sequence 2, Appl
C 45	28.6	53.0	97	2	US-08-663-688A-5	Sequence 5, Appl

ALIGNMENTS

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RESULT 1
US-09-493-491-39
; Sequence 39, Application US/09493491
; Patent No. 6391556
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-02.UT
; CURRENT FILING DATE: 2000-01-28
; EARLIER APPLICATION NUMBER: 60/117,640 US
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
US-09-493-491-39
Query Match          59.3%; Score 32; DB 4; Length 52;
Best Local Similarity 79.2%; Pred. No. 0.0011;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
OY 1 TAAATTATATACGACTGCTCACTATAGGAGACGACCCCTGAGGCTCAAA 48
Db 1 TAAATTATATACGACTGCTCACTATAGGAGACCTGTCTTCAGATGAAA 48
RESULT 2
US-09-493-491-29
; Sequence 29, Application US/09493491
; Patent No. 6391556
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-02.UT
; CURRENT FILING DATE: 2000-01-28
; EARLIER APPLICATION NUMBER: 60/117,640 US
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 29
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-493-491-29

Query Match
Best Local Similarity 100.0%; Score 32; DB 4; Length 54;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTATAGACTACTATAGGAGACTCA 32
Db 1 TAAATTATAGACTACTATAGGAGACTCA 32

RESULT 3
US-07-931-473B-50
; Sequence 50, Application US/07931473B
; Patent No. 5270163
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; TITLE OF INVENTION: Nucleic Acid Ligands
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beaton & Swanson, P.C.
; STREET: 4582 South Ulster Street Parkway, #403
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80237
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/931,473B
; FILING DATE: 19920817
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 850-9900
; TELEFAX: (303) 850-9401
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 nucleotides
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-931-473B-50

Query Match
Best Local Similarity 57.4%; Score 31; DB 1; Length 49;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 6 TATAGACTCACTATAGGAGACTCAAGCCTGAGGCTCAAGTCA 52
Db 1 TATAGACTCACTATAGGAGACTCAAGCCTTATATCTGACAAATCA 47

RESULT 4
US-07-714-131C-50
; Sequence 50, Application US/07714131C
; Patent No. 5473096
; GENERAL INFORMATION:
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; APPLICANT: Larry Gold
; TITLE OF INVENTION: Nucleic Acid Ligands
; NUMBER OF SEQUENCES: 344
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beaton & Swanson, P.C.
; STREET: 4582 South Ulster Street Parkway, #403
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80237
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/714,131C
; FILING DATE: June 10, 1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 850-9900
; TELEFAX: (303) 850-9401
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-714-131C-50

Query Match
Best Local Similarity 57.4%; Score 31; DB 1; Length 49;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 6 TATAGACTCACTATAGGAGACTCAAGCCTGAGGCTCAAGTCA 52
Db 1 TATAGACTCACTATAGGAGACTCAAGCCTTATATCTGACAAATCA 47

RESULT 5
US-08-412-110-50
; Sequence 50, Application US/08412110
; Patent No. 5670637
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; TITLE OF INVENTION: Nucleic Acid Ligands
; NUMBER OF SEQUENCES: 344
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/412,110
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: June 10, 1991
; PRIOR APPLICATION DATA:
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Mon Dec 23 08:47:52 2002

us-09-121-239-1.rn1

Page 3

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APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-412-110-50

Query Match      57.4%; Score 31; DB 1; Length 49;
Best Local Similarity 78.7%; Pred. No. 0.0026;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 6 TAATACGACTCACTATAGGAGACGACCTGAGGCTCAAGTCA 52
Db 1 TAATACGACTCACTATAGGAGACGACCTTTTATCTGACAATCA 47

RESULT 6
US-08-409-442A-50
Sequence 50, Application US/08409442A
Patent No. 5696249
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,442A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-409-442A-50

Query Match      57.4%; Score 31; DB 1; Length 49;
Best Local Similarity 78.7%; Pred. No. 0.0026;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 6 TAATACGACTCACTATAGGAGACGACCTGAGGCTCAAGTCA 52
Db 1 TAATACGACTCACTATAGGAGACGACCTTTTATCTGACAATCA 47

RESULT 7
US-08-469-609A-50
Sequence 50, Application US/08469609A
Patent No. 5843653
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,609A
FILING DATE: June 6, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/412,110
FILING DATE: March 27, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/409,442
FILING DATE: March 24, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-469-609A-50

Query Match      57.4%; Score 31; DB 2; Length 49;
Best Local Similarity 78.7%; Pred. No. 0.0026;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 6 TAATACGACTCACTATAGGAGACGACCTGAGGCTCAAGTCA 52
Db 1 TAATACGACTCACTATAGGAGACGACCTTTTATCTGACAATCA 47

RESULT 8
US-09-143-190-50
Sequence 50, Application US/09143190
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Patent No. 6110900
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/143,190
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/469,609
FILING DATE: June 6, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/412,110
FILING DATE: March 27, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/409,442
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-143-190-50
Query Match 57.4%; Score 31; DB 3; Length 49;
Best Local Similarity 78.7%; Pred. No. 0.0026;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 6 TATATGAGCTACTATAGGAGCATCAGACCTTGAAGCTCAAGTCA 52
Db 1 TATATGAGCTACTATAGGAGCATCAGACCTTGAATCTGACATCA 47

RESULT 9
US-09-502-344-50
Sequence 50, Application US/09502344
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/502,344
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/143,190
FILING DATE: August 27, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/469,609
FILING DATE: June 6, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/412,110
FILING DATE: March 27, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/409,442
FILING DATE: March 24, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-502-344-50
Query Match 57.4%; Score 31; DB 4; Length 49;
Best Local Similarity 78.7%; Pred. No. 0.0026;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 6 TATATGAGCTACTATAGGAGCATCAGACCTTGAAGCTCAAGTCA 52
Db 1 TATATGAGCTACTATAGGAGCATCAGACCTTGAATCTGACATCA 47

RESULT 10
US-08-409-442A-350
Sequence 350, Application US/08409442A
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado

```

? COUNTRY: USA
? ZIP: 80111
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
? COMPUTER: IBM compatible
? OPERATING SYSTEM: MS-DOS
? SOFTWARE: Wordperfect 5.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/409,442A
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/714,131
? FILING DATE: June 10, 1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/536,428
? FILING DATE: June 11, 1990
? ATTORNEY/AGENT INFORMATION:
? NAME: Barry J. Swanson
? REGISTRATION NUMBER: 33,215
? REFERENCE/DOCKET NUMBER: NEX01/C3
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (303) 793-3333
? TELEFAX: (303) 793-3433
? INFORMATION FOR SEQ ID NO: 350:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 73 nucleotides
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
?
US-08-409-442A-350
?
Query Match 57.4%; Score 31; DB 1; Length 73;
Best Local Similarity 78.7%; Pred. No. 0.0028;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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OY 6 TAATAGCACTACTATAGGAGACTGAGACCTGAGGCTCAAAAGTCA 52
DB 1 TAATAGCACTACTATAGGAGACTGAGACCTGAGGCTCAAAAGTCA 47
?
RESULT 11
US-08-469-609A-350
? Sequence 350, Application US/08469609A
? Patent No. 5843653
? GENERAL INFORMATION:
? APPLICANT: Larry Tuerk
? TITLE OF INVENTION: Nucleic Acid Ligands
? NUMBER OF SEQUENCES: 374
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Swanson & Bratschun, L.L.C.
? STREET: 8400 E. Prentice Avenue, Suite 200
? CITY: Englewood
? STATE: Colorado
? COUNTRY: USA
? ZIP: 80111
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
? COMPUTER: IBM compatible
? OPERATING SYSTEM: MS-DOS
? SOFTWARE: Wordperfect 5.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/469,609A
? FILING DATE: June 6, 1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/428,964
? FILING DATE: April 25, 1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/412,110
? FILING DATE: March 27, 1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/409,442
? FILING DATE: March 24, 1995

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? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/714,131
? FILING DATE: June 10, 1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/536,428
? FILING DATE: June 11, 1990
? ATTORNEY/AGENT INFORMATION:
? NAME: Barry J. Swanson
? REGISTRATION NUMBER: 33,215
? REFERENCE/DOCKET NUMBER: NEX01/C5
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (303) 793-3333
? TELEFAX: (303) 793-3433
? INFORMATION FOR SEQ ID NO: 350:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 73 nucleotides
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
?
US-08-469-609A-350
?
Query Match 57.4%; Score 31; DB 2; Length 73;
Best Local Similarity 78.7%; Pred. No. 0.0028;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
?
OY 6 TAATAGCACTACTATAGGAGACTGAGACCTGAGGCTCAAAAGTCA 52
DB 1 TAATAGCACTACTATAGGAGACTGAGACCTGAGGCTCAAAAGTCA 47
?
RESULT 12
US-09-143-190-350
? Sequence 350, Application US/09143190
? Patent No. 6110900
? GENERAL INFORMATION:
? APPLICANT: Larry Tuerk
? TITLE OF INVENTION: Nucleic Acid Ligands
? NUMBER OF SEQUENCES: 374
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Swanson & Bratschun, L.L.C.
? STREET: 8400 E. Prentice Avenue, Suite 200
? CITY: Englewood
? STATE: Colorado
? COUNTRY: USA
? ZIP: 80111
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
? COMPUTER: IBM compatible
? OPERATING SYSTEM: MS-DOS
? SOFTWARE: Wordperfect 8.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/143,190
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/469,609
? FILING DATE: June 6, 1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/428,964
? FILING DATE: April 25, 1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/412,110
? FILING DATE: March 27, 1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/409,442
? FILING DATE: March 24, 1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/714,131
? FILING DATE: June 10, 1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/536,428
? FILING DATE: June 11, 1990
? ATTORNEY/AGENT INFORMATION:

```

NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 350:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-143-190-350

Query Match 57.4%; Score 31; DB 3; Length 73;
Best Local Similarity 76.7%; Pred. No. 0.0028;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 6 TAATACGACTCATTATAGGAGACTCAGACCTTGAGGCTCAAGTCA 52
DB 1 TAATACGACTCATTATAGGAGACTCAGACCTTTATCTGCAATCA 47

RESULT 13
US-09-502-344-350
Sequence 350, Application US/09502344
Patent No. 6331398
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Iuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/502,344
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/143,190
FILING DATE: August 27, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/469,609
FILING DATE: June 6, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/412,110
FILING DATE: March 27, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/409,442
FILING DATE: March 24, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C7
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 350:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-502-344-350

Query Match 57.4%; Score 31; DB 4; Length 73;
Best Local Similarity 78.7%; Pred. No. 0.0028;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 6 TAATACGACTCATTATAGGAGACTCAGACCTTGAGGCTCAAGTCA 52
DB 1 TAATACGACTCATTATAGGAGACTCAGACCTTTATCTGCAATCA 47

RESULT 14
US-08-384-541-5
Sequence 5, Application US/08384541
Patent No. 5622827
GENERAL INFORMATION:
APPLICANT: McAllister, Diane L. and
APPLICANT: Clark, Kathy A.
TITLE OF INVENTION: AMPLIFICATION PRIMERS AND
TITLE OF INVENTION: NUCLEIC ACID PROBES
TITLE OF INVENTION: TARGETED TO COCCIDIOIDES
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,541
FILING DATE: February 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 210/060
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-384-541-5

Query Match 57.0%; Score 30.8; DB 1; Length 49;
Best Local Similarity 94.1%; Pred. No. 0.0031;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 AAATTATACGACTCAGTATAGGAGAGACTCAGAC 35
 1 AAATTATACGACTCAGTATAGGAGAGACTCAGAC 34

RESULT 15

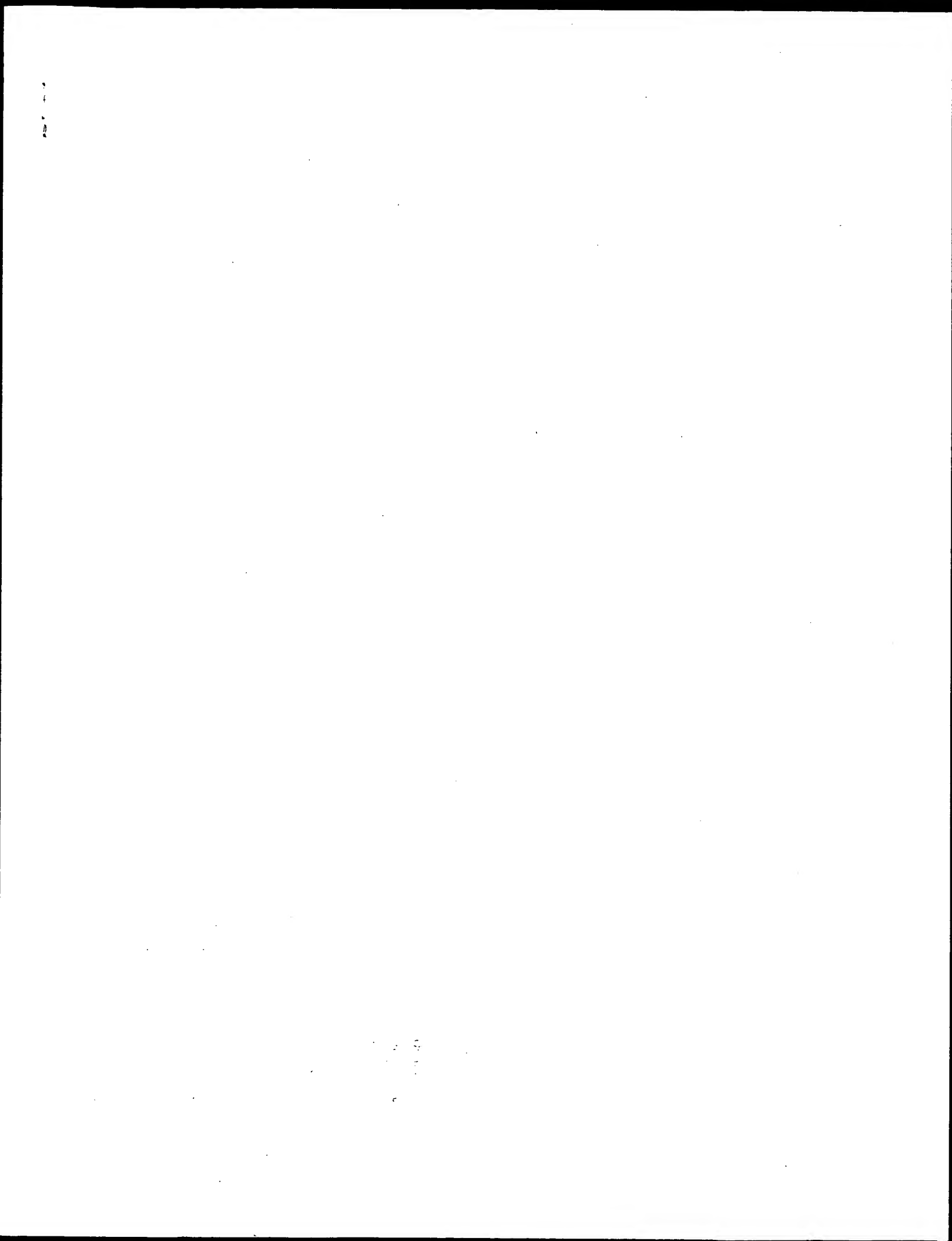
US-08-384-541-6/c
 : Sequence 6, Application US/08384541
 : Patent No. 5622827
 : GENERAL INFORMATION:
 : APPLICANT: McAllister, Diane L. and
 : TITLE OF INVENTION: AMPLIFICATION PRIMERS AND
 : TITLE OF INVENTION: NUCLEIC ACID PROBES
 : TITLE OF INVENTION: TARGETED TO COCCIDIOIDES
 : TITLE OF INVENTION: IMMUTIS NUCLEIC ACID
 : NUMBER OF SEQUENCES: 41
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Lyon & Lyon
 : STREET: 633 West Fifth Street
 : CITY: Los Angeles
 : STATE: California
 : COUNTRY: U.S.A.
 : ZIP: 90071
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 : MEDIUM TYPE: storage
 : COMPUTER: IBM compatible
 : OPERATING SYSTEM: IBM P.C. DOS 5.0
 : SOFTWARE: Word Perfect 5.1
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/384,541
 : FILING DATE: February 7, 1995
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER:
 : FILING DATE:
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Hebert, Sheldon O.
 : REGISTRATION NUMBER: 38,179
 : REFERENCE/DOCKET NUMBER: 210/060
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (213) 489-1600
 : TELEFAX: (213) 955-0440
 : TELEX: 67-3510
 : INFORMATION FOR SEQ ID NO: 6:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 49 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : US-08-384-541-6

Query Match 57.0%; Score 30.8; DB 1; Length 49;
 Best Local Similarity 94.1%; Pred. No. 0.00311;
 Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 AAATTATACGACTCAGTATAGGAGAGACTCAGAC 35
 1 AAATTATACGACTCAGTATAGGAGAGACTCAGAC 34

OY 2 AAATTATACGACTCAGTATAGGAGAGACTCAGAC 35
 1 AAATTATACGACTCAGTATAGGAGAGACTCAGAC 34

Search completed: December 21, 2002, 11:58:18
 Job time : 47.5061 secs



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:28:32 : Search time 20.6694 Seconds
(Without alignments)
356.094 Million cell updates/sec

Title: US-09-121-239-5

Perfect score: 24 GACCACTCGTGTGTAACCTCA 24

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents, NA.*

- 1: /cgn2_6/pdata/1/ina/5A.COMB.seq.*
- 2: /cgn2_6/pdata/1/ina/5B.COMB.seq.*
- 3: /cgn2_6/pdata/1/ina/6A.COMB.seq.*
- 4: /cgn2_6/pdata/1/ina/6B.COMB.seq.*
- 5: /cgn2_6/pdata/1/ina/ECTUS.COMB.seq.*
- 6: /cgn2_6/pdata/1/ina/Backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	21	87.5	40 3	US-08-448-446B-16 Sequence 16, Appl
2	20	83.3	20 1	US-08-363-233B-5 Sequence 5, Appl
3	14	58.3	33 2	US-08-343-923-12 Sequence 12, Appl
4	14	58.3	60 4	US-09-257-581-3 Sequence 3, Appl
5	13.6	56.7	46 4	US-09-199-737-19 Sequence 19, Appl
6	13.6	56.7	46 4	US-09-058-333A-19 Sequence 19, Appl
7	13.4	55.8	32 1	US-08-868-506-10 Sequence 10, Appl
8	13.4	55.8	32 3	US-09-128-967-10 Sequence 10, Appl
9	13.4	55.8	95 4	US-09-221-298-35 Sequence 35, Appl
10	13	54.2	27 4	US-08-584-040-35 Sequence 35, Appl
11	13	54.2	27 4	US-08-584-040-35 Sequence 35, Appl
12	13	54.2	56 1	US-08-468-674B-31 Sequence 31, Appl
13	13	54.2	56 1	US-08-468-674B-31 Sequence 31, Appl
14	13	54.2	78 4	US-08-981-988A-21 Sequence 21, Appl
15	13	54.2	98 1	US-08-472-255A-38 Sequence 38, Appl
16	13	54.2	98 1	US-08-472-255A-38 Sequence 38, Appl
17	13	54.2	98 3	US-08-479-724A-38 Sequence 38, Appl
18	13	54.2	98 3	US-08-479-724A-38 Sequence 38, Appl
19	13	54.2	98 3	US-08-952-793-38 Sequence 38, Appl
20	13	54.2	98 5	US-08-952-793-38 Sequence 38, Appl
21	12.8	53.3	20 4	US-09-161-994A-51 Sequence 21, Appl
22	12.8	53.3	24 3	US-08-641-291A-54 Sequence 54, Appl
23	12.8	53.3	27 1	US-08-623-428D-13 Sequence 13, Appl
24	12.8	53.3	37 1	US-08-061-889-3 Sequence 3, Appl
25	12.8	53.3	37 1	US-08-462-611-3 Sequence 3, Appl
26	12.8	53.3	37 5	US-08-623-428D-7 Sequence 7, Appl
27	12.8	53.3	45 4	US-09-266-462-10 Sequence 10, Appl

28	12.8	53.3	45 4	US-09-266-462-12 Sequence 12, Appl
29	12.8	53.3	86 1	US-07-964-624D-57 Sequence 57, Appl
30	12.8	53.3	86 1	US-08-442-062-57 Sequence 57, Appl
31	12.8	53.3	86 1	US-08-748-697A-57 Sequence 57, Appl
32	12.8	53.3	86 4	US-09-165-616-57 Sequence 57, Appl
33	12.4	51.7	29 1	US-07-638-512-12 Sequence 12, Appl
34	12.4	51.7	32 1	US-08-644-664B-39 Sequence 39, Appl
35	12.4	51.7	47 2	US-08-761-272A-39 Sequence 39, Appl
36	12.4	51.7	47 4	US-08-641-638-1120 Sequence 1120, Appl
37	12.4	51.7	78 3	US-08-945-734-48 Sequence 48, Appl
38	12.4	51.7	78 3	US-09-258-797-43 Sequence 43, Appl
39	12.4	51.7	78 5	US-09-258-797-43 Sequence 43, Appl
40	12.2	50.8	23 5	PCT-US96-00451-43 Sequence 5, Appl
41	12.2	50.8	23 5	PCT-US96-00451-43 Sequence 5, Appl
42	12.2	50.8	27 1	US-08-435-350-53 Sequence 53, Appl
43	12.2	50.8	29 3	US-08-484-661A-46 Sequence 46, Appl
44	12.2	50.8	29 3	US-08-656-664-46 Sequence 46, Appl
45	12.2	50.8	29 3	PCT-US96-09641-46 Sequence 46, Appl
			33 3	US-08-484-661A-45 Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-08-448-446B-16
Sequence 16, Application US/08448446B
Patent No. 6080851
GENERAL INFORMATION:
APPLICANT: Pachuk et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment of Leukemias
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kurtz Mackiewicz & No. 6080851iris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,446B
CLASSIFICATION: 435
FILING DATE: July 10, 1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/989,852
FILING DATE: December 4, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Doreen Yalko Trujillo
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: APOL-0020
TELECOMMUNICATION INFORMATION: C
TELEPHONE: (215) 568-3439
FAX: (215) 568-3100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 40
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE:
US-08-448-446B-16
Query Match 87.5%; Score 21; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 CAACCTCGTGTGTAACCTCA 24

Db 20 CAACCTGCTGTGAACCTCA 40

RESULT 2

US-08-363-233B-5
Sequence 5, Application US/08363233B
Patent No. 5714383

GENERAL INFORMATION:

APPLICANT: Thompson, James D.
TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC
TITLE OF INVENTION: MYELOGENOUS LEUKEMIA
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,233B
FILING DATE: December 23, 1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:

2

APPLICATION NUMBER: 07/882,822
FILING DATE: May 14, 1992
APPLICATION NUMBER: 08/193,922
FILING DATE: February 7, 1994
ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/165

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-363-233B-5

Query Match 83.3%; Score 20; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 0.15;

Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAACCTGCTGTGAACCTCC 23

Db 1 CAACCTGCTGTGAACCTCC 20

RESULT 3

US-08-343-923-12

Sequence 12, Application US/08343923
Patent No. 5856153

GENERAL INFORMATION:

APPLICANT: Tiraby, Gerard et al.

TITLE OF INVENTION: NEW SUICIDE GENES AND NEW ASSOCIATIONS

TITLE OF INVENTION: OF PYRIMIDINE NUCLEOBASE AND NUCLEOSIDE ANALOGS . . .

NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:

ADDRESSEE: LARSON AND TAYLOR
STREET: 727 SOUTH 23RD STREET
CITY: ARLINGTON
STATE: VA
COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/343,923

FILING DATE: 17-NOV-1994

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: SCHULMAN, B. AARON

REGISTRATION NUMBER: 31,877

REFERENCE/DOCKET NUMBER: XX

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-920-7200

TELEFAX: 703-892-8428

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-343-923-12

Query Match 58.3%; Score 14; DB 2; Length 33;
Best Local Similarity 77.3%; Pred. No. 1.9e+02;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ACCAATGCTGTGTGAACCTCC 23

Db 9 ACCAATGCTGTGTGAACCTCC 30

RESULT 4

US-09-257-581-3/C

Sequence 3, Application US/09257581
Patent No. 6207419

GENERAL INFORMATION:

APPLICANT: Church, Frank C.

APPLICANT: Bauman, Susannah J.

TITLE OF INVENTION: THROMBIN INHIBITORY AGENTS AND METHODS OF USING SAME

FILE REFERENCE: 3470-232

CURRENT APPLICATION NUMBER: US/09/257,581

CURRENT FILING DATE: 1999-02-25

EARLIER APPLICATION NUMBER: 60/076,210

EARLIER FILING DATE: 1998-02-27

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3

LENGTH: 60

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: primer

US-09-257-581-3

Query Match 58.3%; Score 14; DB 4; Length 60;
Best Local Similarity 77.3%; Pred. No. 2.1e+02;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CCAACTGCTGTGAACCTCA 24

Db 59 CCAACTGCTGTGAACCTCA 38

RESULT 5

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US-09-199-737-19/C
; Sequence 19, Application US/09199737A
; Patent No. 6287788
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Borowsky, Beth
; APPLICANT: Smith, Kelli E.
; APPLICANT: Branchek, Theresa A.
; APPLICANT: Jones, Kenneth A.
; TITLE OF INVENTION: DNA Encoding Galanin GALR3 Receptors And Uses Thereof
; FILE REFERENCE: 52241-D-PCT-US
; CURRENT APPLICATION NUMBER: US/09/199,737A
; CURRENT FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patent In Ver. 2.0 - beta
; SEQ ID NO: 19
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide
US-09-199-737-19
Query Match          56.7%; Score 13.6; DB 4; Length 46;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 CCAACTCGTGTGTGAAGCTC 22
Db 39 CCAACTCGTGTGTGAAGCTC 20

RESULT 6
US-09-058-333A-19/C
; Sequence 19, Application US/09058333A
; Patent No. 6368812
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Borowsky, Beth
; APPLICANT: Smith, Kelli E.
; TITLE OF INVENTION: DNA ENCODING GALANIN GALR3 RECEPTORS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/058,333A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 278 0400
; TELEFAX: 212 391 0525
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-058-333A-19
Query Match          56.7%; Score 13.6; DB 4; Length 46;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 CCAACTCGTGTGTGAAGCTC 22
Db 39 CCAACTCGTGTGTGAAGCTC 20

RESULT 7
US-08-869-506-10
; Sequence 10, Application US/08869506
; Patent No. 5827710
; GENERAL INFORMATION:
; APPLICANT: Uchida, Kohji
; APPLICANT: Matsukawa, Hirokazu
; APPLICANT: Matuo, Yushi
; APPLICANT: Fujita, Tutosi
; TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 No. 5827710th Giebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,506
; FILING DATE: 05-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 73797/1996
; FILING DATE: 29-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 159-43
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4100
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer"
US-08-869-506-10
Query Match          55.8%; Score 13.4; DB 1; Length 32;
Best Local Similarity 73.9%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 GACCAACTCGTGTGTGAAGCTC 23
Db 8 GCCCAACTCGTGTGTGAAGCTC 30

RESULT 8
US-09-128-967-10
; Sequence 10, Application US/09128967
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```

: Patent No.6057141
: GENERAL INFORMATION:
: APPLICANT: Uchida, Kohji
: APPLICANT: Matsukawa, Hirokazu
: APPLICANT: Matsu, Yushi
: APPLICANT: Fujita, Tutosi
: TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN
: TITLE OF INVENTION: LACTATE DEHYDROGENASE
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NIXON & VANDERHAYE P.C.
: STREET: 1100 No. 6057141th Giebe Rd. 8th floor
: CITY: Arlington
: STATE: VA
: COUNTRY: USA
: ZIP: 22201-4741
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/128,967
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/869,506
: FILING DATE: 05-JUN-1997
: APPLICATION NUMBER: JP 73797/1996
: FILING DATE: 29-MAR-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Crawford, Arthur R.
: REGISTRATION NUMBER: 25,327
: REFERENCE/DOCKET NUMBER: 159-43
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-816-4000
: TELEFAX: 703-816-4100
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 32 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: other nucleic acid
: DESCRIPTION: /desc = "primer"
: US-09-128-967-10
:
: Query Match 55.8%; Score 13.4; DB 3; Length 32;
: Best Local Similarity 73.9%; Pred. No. 3,7e+02;
: Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0
:
: QY 1 GACCACTGCTGTGTGAACCTCC 23
: | | | | | | | | | | | | | | |
: Db 8 GCCCAACTGCTGTGTGAACCTCC 30
:
: RESULT 9
: US-09-221-298-53/C
: Sequence 53, Application US/09221298
: Patent No. 6284241
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS
: TITLE OF INVENTION: OF COLON CANCER
: FILE REFERENCE: 210121.471
: CURRENT APPLICATION NUMBER: US/09/721,298
: NUMBER OF SEQ ID NOS: 112
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 53
: LENGTH: 95
: TYPE: DNA
: ORGANISM: Human

```

```

1  FEATURE:
2  NAME/KEY: modified_base
3  LOCATION: (37)
4  OTHER INFORMATION: Where n is a, c, g or t
5  FEATURE:
6  NAME/KEY: modified_base
7  LOCATION: (60)
8  OTHER INFORMATION: Where n is a, c, g or t
9  FEATURE:
10 NAME/KEY: modified_base
11 LOCATION: (73)
12 OTHER INFORMATION: Where n is a, c, g or t
13 FEATURE:
14 NAME/KEY: modified_base
15 LOCATION: (76)
16 OTHER INFORMATION: Where n is a, c, g or t
17 FEATURE:
18 NAME/KEY: modified_base
19 LOCATION: (92)
20 OTHER INFORMATION: Where n is a, c, g or t
21
22 US-09-221-298-53

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Query Match	55.8%;	Score 13.4;	DB 4;	Length 95;
Best Local Similarity	73.9%;	Pred. No. 4.6e+02;		
Matches 17; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0;

QY	2	ACCAACTCGTGTGTGA	AACTCCA	24
Db	28	AACAACAAGTGTCA	GAAACTGCA	6

RESULT 10
US-08-584-040-3546
Sequence 3546 Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TREATMENT OF DISEASES OR
CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440
TELEX: 67-3510
OTHER INFORMATION: The letter "N" represents the stem II region
of an HH ribozyme.
US-08-584-040-3546

Query Match
Best Local Similarity 54.2%; Score 13; DB 4; Length 27;
Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 3 CCACTCGTGTGTGAACCTCA 24
DB 5 CCACTCGTGTGTGAACCTCA 26

RESULT 11
US-08-584-040-4969
Sequence 4969, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Payco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
OF VASCULAR ENDOTHELIAL
GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4969:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:

OTHER INFORMATION: The letter "N" represents the stem II region
of an HH ribozyme.
US-08-584-040-4969

Query Match
Best Local Similarity 54.2%; Score 13; DB 4; Length 27;
Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 3 CCACTCGTGTGTGAACCTCA 24
DB 5 CCACTCGTGTGTGAACCTCA 26

RESULT 12
US-08-468-674B-31/C
Sequence 31, Application US/08468674B
Patent No. 5639642
GENERAL INFORMATION:
APPLICANT: Kjeldsen, Thomas B
APPLICANT: Vad, Knud
TITLE OF INVENTION: SYNTHETIC LEADERS PEPTIDE SEQUENCES
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56396420 No. 5639642disk of No. 5639642th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,674B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,852
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4085,220-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-468-674B-31

Query Match
Best Local Similarity 54.2%; Score 13; DB 1; Length 56;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

RESULT 13
US-08-780-571-31/C
Sequence 31, Application US/08780571
Patent No. 5795746
GENERAL INFORMATION:
APPLICANT: Kjeldsen, Thomas B
APPLICANT: Vad, Knud

;; TITLE OF INVENTION: SYNTHETIC LEADERS PEPTIDE SEQUENCES
;; NUMBER OF SEQUENCES: 89
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: NO. 57957460 No. 5795746disk of No. 5795746th America, Inc.
;; STREET: 405 Lexington Avenue, 64th Floor
;; CITY: New York
;; STATE: New York
;; COUNTRY: United States of America
;; ZIP: 10174-6401
;;
;; COMPUTER READABLE FORM:
;;
;; MEDIUM TYPE: Tape
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/780,571
;; FILING DATE: 08-JAN-1997
;; CLASSIFICATION: 435
;;
;; PRIORITY INFORMATION:
;; APPLICATION NUMBER: US 08/468,674
;; FILING DATE: 06-JUN-1995
;; APPLICATION NUMBER: US 08/282,852
;; FILING DATE: 29-JUL-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lambiris, Elias J.
;; REGISTRATION NUMBER: 33,728
;; REFERENCE/DOCKET NUMBER: 4085,220-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-867-0123
;; TELEFAX: 212-878-9655
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 56 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: CDNA
;; US-08-780-571-31
;;
Query Match 54.2%; Score 13; DB 1; Length 56;
Best Local Similarity 76.2%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 ACCAAGCTGTGTGTAATC 22
DB 43 ACCAAGCTGTGTGTTCTC 23
;;
RESULT 14
US-08-981-988A-21
;; Sequence 21, Application US/08981988A
;; Patent No. 6337194
;; GENERAL INFORMATION:
;; APPLICANT: Vittal Mallaya Scientific Research Foundation
;; APPLICANT: The University of Leicester
;; TITLE OF INVENTION: Insulin
;; NUMBER OF SEQUENCES: 43
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: VITTAL MALLAYA SCIENTIFIC RESEARCH FOUNDATION
;; STREET: K. R. ROAD
;; CITY: BANGALORE
;; COUNTRY: INDIA
;; ZIP: 560 004
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/981,988A
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIORITY INFORMATION: DATA;

;; APPLICATION NUMBER: GB 9513967.1
;; FILING DATE: 08-JUL-1995
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 78 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-981-988A-21
;;
Query Match 54.2%; Score 13; DB 4; Length 78;
Best Local Similarity 76.2%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 ACCAAGCTGTGTGTAATC 22
DB 12 ACCAAGCTGTGTGTTCTC 32
;;
RESULT 15
US-08-472-255A-38/C
;; Sequence 38, Application US/08472255A
;; Patent No. 5766853
;; GENERAL INFORMATION:
;; APPLICANT: PARMA, DAVID
;; APPLICANT: GOLD, LARRY
;; TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
;; TITLE OF INVENTION: TO SELECTINS (AS AMENDED)
;; NUMBER OF SEQUENCES: 173
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Swanson & Bratschun, L.L.C.
;; STREET: 8400 E. Prentice Avenue, Suite 200
;; CITY: Englewood
;; STATE: Colorado
;; COUNTRY: USA
;; ZIP: 80111
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: MS-DOS
;; SOFTWARE: Wordperfect 6.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/472,255A
;; FILING DATE: 07-JUNE-1995
;; CLASSIFICATION: 536
;; PRIORITY INFORMATION:
;; APPLICATION NUMBER: 07/714,131
;; FILING DATE: 10-JUNE-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/536,428
;; FILING DATE: 11-JUNE-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/964,624
;; FILING DATE: 21-OCTOBER-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Barry J. Swanson
;; REGISTRATION NUMBER: 33,215
;; REFERENCE/DOCKET NUMBER: NEX40-3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (303) 793-3333
;; TELEFAX: (303) 793-3433
;; INFORMATION FOR SEQ ID NO: 38:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 98 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: RNA
;; FEATURE:
;; OTHER INFORMATION: All C's are 2'-NH2 cytosine
;; FEATURE:
;; OTHER INFORMATION: All U's are 2'-NH2 uracil
;; US-08-472-255A-38

Mon Dec 23 08:48:05 2002

us-09-121-239-5.rni

Page 7

Query Match 54.2%; Score 13; DB 1; Length 98;
Best Local Similarity 76.2%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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||||| |
Db 30 ACCAAGCTGTGTGATGATTC 10
Search completed: December 21, 2002, 11:58:20
Job time : 22.6694 secs

Mon Dec 23 08:48:08 2002

us-09-121-239-9.rml

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
December 21, 2002, 02:28:32 ; Search time 21.5306 Seconds
(without alignments)
356.094 Million cell updates/sec

Run on: December 21, 2002, 02:28:32 ; Search time 21.5306 Seconds
(without alignments)
356.094 Million cell updates/sec

Title: US-09-121-239-9
Perfect score: 25
Sequence: 1 GACTGTCCACAGCATTCGCGTACC 25

Scoring table: IDENTITY NUC
Gapop 10.0, Gapect 1.0

Searched: 441362 seqs, 15338381 residues
Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents.NA.*
1: /cgn2_6/prodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/prodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/prodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/prodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/prodata/1/ina/PCRTS.COMB.seq.*
6: /cgn2_6/prodata/1/ina/Backfiles1.seq.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	25	100.0	56	1	US-07-940-652-17
2	25	100.0	56	1	US-08-255-553-17
3	24	96.0	26	1	US-08-323-2338-6
4	18	72.0	22	1	US-08-152-621-11
5	18	72.0	22	1	PCT-US32-05035-11
6	18	72.0	62	3	US-08-448-446B-1
7	18	72.0	81	3	US-08-448-446B-2
8	16	64.0	28	4	US-09-341-955-2
9	14.2	56.8	86	2	US-08-477-527A-130
10	14.2	56.8	86	2	US-08-477-527A-139
11	14.2	56.8	86	2	US-08-477-527A-148
12	14.2	56.8	86	3	US-08-481-710-139
13	14.2	56.8	86	3	US-08-481-710-148
14	14.2	56.8	86	3	US-08-481-710-149
15	14.2	56.8	86	5	PCT-US96-09537-130
16	14.2	56.8	86	5	PCT-US96-09537-139
17	14.2	56.8	86	5	PCT-US96-09537-148
18	14.2	56.8	86	5	PCT-US96-09537-149
19	14.2	56.8	86	5	PCT-US96-09537-150
20	13.8	55.2	33	1	US-08-462-733-7
21	13.8	55.2	33	1	US-08-462-733-8
22	13.8	55.2	33	1	US-08-455-742-5
23	13.8	55.2	33	1	US-08-455-742-6
24	13.8	55.2	33	1	US-08-176-402-8
25	13.8	55.2	33	1	US-08-176-402-9
26	13.8	55.2	33	1	US-08-454-464-5
27	13.8	55.2	33	1	US-08-454-464-6

28	13.8	55.2	33	1	US-08-453-222-6
29	13.8	55.2	33	1	US-08-452-802-5
30	13.8	55.2	33	1	US-08-452-802-6
31	13.8	55.2	33	1	US-08-464-148-13
32	13.8	55.2	33	1	US-08-464-148-14
33	13.8	55.2	33	1	US-08-385-500-13
34	13.8	55.2	33	1	US-08-385-500-14
35	13.8	55.2	33	1	US-08-846-784-13
36	13.8	55.2	33	1	US-08-846-784-14
37	13.8	55.2	33	1	US-08-678-194-4
38	13.8	55.2	34	2	US-08-890-011-4
39	13.8	55.2	34	4	US-09-262-724-4
40	13.4	53.6	45	4	US-08-681-935-13
41	13.4	53.6	45	4	US-08-939-323-13
42	13.4	53.6	45	4	US-08-319-492B-716
43	13.4	53.6	54	1	US-08-484-686B-12
44	13.4	53.6	54	1	US-08-463-160B-12
45	13.4	53.6	74	4	US-08-939-323-19

ALIGNMENTS

RESULT 1
US-07-940-652-17
Sequence 17, Application US/07940652
Patent No. 5424413
GENERAL INFORMATION:
APPLICANT: James J. Hogan et al.
TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS Version 3.30
SOFTWARE WORDPERFECT (Version 5.1)
CURRENT APPLICATION NUMBER: US/07940, 652
FILING DATE: 19920904
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/827, 021
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: WARDURF, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOC. NUMBER: 199/201
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELE: 673511
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 56
TYPE: NUCLEIC ACID
STRANDEDNESS: Single
TOPOLOGY: Linear
US-07-940-652-17

Query Match 100.0%; Score 25; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ox 1 GACTGTCCACAGCATTCGCGTACC 25
DB 3 GACTGTCCACAGCATTCGCGTACC 27

RESULT 2

US-08-255-553-17
Sequence 17, Application US/08255553
Patent No. 5451503

GENERAL INFORMATION:

APPLICANT: James J. Hogan et al.
TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS Version 3.30
SOFTWARE: WordPerfect (Version 5.1)CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/255,553
FILING DATE: 07-JUN-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/940,652
FILING DATE: 04-SEP-1992APPLICATION NUMBER: US/07/827,021
FILING DATE: 22-JAN-1992ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 199/201TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 56
TYPE: nucleic acidSTRANDEDNESS: single
TOPOLOGY: linear

Query Match

Best Local Similarity 100.0%; Score 25; DB 1; Length 56;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;DB 1 GACTGTCCACAGCATTCGCGTGACC 25
3 GACTGTCCACAGCATTCGCGTGACC 27

RESULT 3

US-08-363-233B-6
Sequence 6, Application US/08363233B
Patent No. 5714383

GENERAL INFORMATION:

APPLICANT: Thompson, James D.
TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:APPLICATION NUMBER: US/08/363,233B
FILING DATE: December 23, 1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application
APPLICATION NUMBER: described below:
FILING DATE: May 14, 1992APPLICATION NUMBER: 08/193,922
FILING DATE: February 7, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/165TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs
TYPE: nucleic acidSTRANDEDNESS: single
TOPOLOGY: linear

US-08-363-233B-6

Query Match

Best Local Similarity 96.0%; Score 24; DB 1; Length 26;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;DB 1 GACTGTCCACAGCATTCGCGTGAC 24
3 GACTGTCCACAGCATTCGCGTGAC 26

RESULT 4

US-08-152-621-11
Sequence 11, Application US/08152621
Patent No. 5652222

GENERAL INFORMATION:

APPLICANT: Calabretta, Bruno
TITLE OF INVENTION: Selective inhibition of
TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:ADDRESSEE: SEIDEL, GONDA, LAVORGNA
ADDRESSEE: & MONACO, P.C.
STREET: 1800 Two Penn Center
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 Inch, 720 Kb
COMPUTER: IBM PS/2OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,621
FILING DATE: No. 5652222ember 15, 1993CLASSIFICATION: 514
PRIOR APPLICATION DATA:APPLICATION NUMBER: 07/718,302
FILING DATE: June 18, 1991

ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: NO. 56522228
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 Nucleotides
TYPE: nucleic acid
STRADEDNESS: double stranded
TOPOLOGY: linear
US-08-152-621-11

Query Match 72.0%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CACAGCATTCGGCTGACC 25
|||||

RESULT 5
PCT-US92-05035-11
Sequence 11, Application PC/TUS9205035
GENERAL INFORMATION:
APPLICANT: Galabreta, Bruno
TITLE OF INVENTION: Selective inhibition of
TITLE OF INVENTION: Leukemic cell proliferation by bor-abi
TITLE OF INVENTION: Antisense oligonucleotides
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Temple University - Of The Common-
ADDRESSEE: wealth system of Higher Education
STREET: 406 University Services Building
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19122
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05035
FILING DATE: 19920615
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/718,302
FILING DATE: June 18, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/869,911
FILING DATE: April 14, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-120 (CTP) 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: NO. 56522228
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 Nucleotides
TYPE: NUCLEIC ACID
STRADEDNESS: double stranded
TOPOLOGY: linear
PCT-US92-05035-11

Query Match 72.0%; Score 18; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CACAGCATTCGGCTGACC 25
|||||

RESULT 6
US-08-448-446B-1
Sequence 1, Application US/08448446B
Patent No. 6080851
GENERAL INFORMATION:
APPLICANT: Pachuk et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: of Leukemias
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn
ADDRESSEE: Kurtz Mackiewicz & No. 6080851
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,446B
FILING DATE: July 10, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/989,852
FILING DATE: December 4, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Doreen Yalko Trujillo
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: APOL-0020
TELECOMMUNICATION INFORMATION: C
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 62
TYPE: Nucleic Acid
STRADEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: No
US-08-448-446B-1

Query Match 72.0%; Score 18; DB 3; Length 62;
Best Local Similarity 83.3%; Pred. No. 4.8;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1 CACAGCAUCCGCGUAGACC 18
|||||

RESULT 7
US-08-448-446B-2/C
Sequence 2, Application US/08448446B
Patent No. 6080851
GENERAL INFORMATION:
APPLICANT: Pachuk et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: of Leukemias
NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn
ADDRESSEE: Kurtz Mackiewicz & No. 608085111s
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,446B
FILING DATE: July 10, 1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/989,852

FILING DATE: December 4, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Doreen Yanko Trujillo

REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: APOL-0020
TELECOMMUNICATION INFORMATION: C

TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 81

TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

ANTI-SENSE:
US-08-448-446B-2

Query Match
Best Local Similarity 72.0%; Score 18; DB 3; Length 81;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACGACATTCGCGTGACC 25
DB 81 CACGACATTCGCGTGACC 64

RESULT 8
US-09-341-955-2/c
Sequence 2, Application US/09341955
Patent No. 6251690

GENERAL INFORMATION:
APPLICANT: Kulmala, Sakari

APPLICANT: Ala-Kleme, Timo
APPLICANT: Eskola, Jarkko

TITLE OF INVENTION: ELECTRICAL EXCITATION OF LABEL SUBSTANCES AT COATED
FILE REFERENCE: TUR-080

CURRENT APPLICATION NUMBER: US/09/341,955
CURRENT FILING DATE: 1999-07-21

EARLIER APPLICATION NUMBER: PCT/FI98/00114
EARLIER FILING DATE: 1999-02-10

NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2

LENGTH: 28
TYPE: DNA
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
US-09-341-955-2
OTHER INFORMATION: Oligonucleotide containing an amino group

Query Match
64.0%; Score 16; DB 4; Length 28;

Best Local Similarity 100.0%; Pred. No. 39;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CACGATTCGCGTGACC 25
DB 28 CACGATTCGCGTGACC 13

RESULT 9

US-08-477-527A-130/c
Sequence 130, Application US/08477527A
Patent No. 5972599

GENERAL INFORMATION:
APPLICANT: DIANE TASSET

APPLICANT: NIKOS PAGRATIS
APPLICANT: SIMEDHA JAYASENA

APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: OF CYTOKINES

NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.

STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado

COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage

COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS

SOFTWARE: WORDPERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,527A

FILING DATE: 7-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131

FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473

FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624

FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991

FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McLearn

REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX41-1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-NH2

US-08-477-527A-130
OTHER INFORMATION: modified

Query Match
Best Local Similarity 56.8%; Score 14.2; DB 2; Length 86;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Page 5

OY 4 TGTCCAGCATTCGCGTG 22
|||||
db 52 TGCCTCCGATTCGCGTG 34

RESULT 10

US-08-477-527A-139/C
Sequence 139, Application US/08477527A
Patent No. 5972599

GENERAL INFORMATION:

APPLICANT: DIANE TASSET
APPLICANT: NIKOS PAGRATIS
APPLICANT: SUMEDHA JAYASENA
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: OF CYTOKINES
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 6.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,527A

FILING DATE: 7-JUNE-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131

FILING DATE: 10-JUNE-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473

FILING DATE: 17-AUGUST-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624

FILING DATE: 21-OCTOBER-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991

FILING DATE: 8-SEPTEMBER-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClearn

REGISTRATION NUMBER: 33,960

REFERENCE/DOCKET NUMBER: NEX41-1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433

TELEFAX: (303) 793-3433

INFORMATION FOR SRO ID NO: 139:

SEQUENCE CHARACTERISTICS:
LENGTH: 86 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: RNA

FEATURE:

OTHER INFORMATION: All pyrimidines are 2'-NH2

OTHER INFORMATION: modified

US-08-477-527A-139

Query Match 56.88; Score 14.2; DB 2; Length 86;
Best Local Similarity 84.28; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 TGTCCAGCATTCGCGTG 22
|||||
db 52 TGCCTCCGATTCGCGTG 34

RESULT 11

US-08-477-527A-148/C
Sequence 148, Application US/08477527A
Patent No. 5972599

GENERAL INFORMATION:

APPLICANT: DIANE TASSET
APPLICANT: NIKOS PAGRATIS
APPLICANT: SUMEDHA JAYASENA
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: OF CYTOKINES
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 6.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,527A

FILING DATE: 7-JUNE-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131

FILING DATE: 10-JUNE-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473

FILING DATE: 17-AUGUST-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624

FILING DATE: 21-OCTOBER-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991

FILING DATE: 8-SEPTEMBER-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClearn

REGISTRATION NUMBER: 33,960

REFERENCE/DOCKET NUMBER: NEX41-1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433

TELEFAX: (303) 793-3433

INFORMATION FOR SRO ID NO: 148:

SEQUENCE CHARACTERISTICS:
LENGTH: 86 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: RNA

FEATURE:

OTHER INFORMATION: All pyrimidines are 2'-NH2

OTHER INFORMATION: modified

US-08-477-527A-148

Query Match 56.88; Score 14.2; DB 2; Length 86;
Best Local Similarity 84.28; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 TGTCCAGCATTCGCGTG 22
|||||
db 52 TGCCTCCGATTCGCGTG 34

RESULT 12

US-08-481-710-130/c
; Sequence 130, Application US/08481710
; Patent No. 6028186
; GENERAL INFORMATION:
; APPLICANT: DIANE TASSET
; APPLICANT: NIKOS PAGRATIS
; APPLICANT: SUMEDHA JAYASENA
; APPLICANT: LARRY GOLD
; TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
; TITLE OF INVENTION: OF CYTOKINES
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,710
; FILING DATE: 7-JUNE-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 8-SEPTEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Diane H. McLearn
; REGISTRATION NUMBER: 33,960
; REFERENCE/DOCKET NUMBER: NEX41-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 130:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; FEATURE:
; OTHER INFORMATION: All pyrimidines are 2'-NH2
; US-08-481-710-130

Query Match 56.8%; Score 14.2; DB 3; Length 86;
Best Local Similarity 84.2%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TGTCCACGACATTCGCTG 22
||| | |||||
DB 52 TGCCTCCGACATTCGCTG 34

RESULT 13
US-08-481-710-139/c
; Sequence 139, Application US/08481710

Patent No. 6028186
; GENERAL INFORMATION:
; APPLICANT: DIANE TASSET
; APPLICANT: NIKOS PAGRATIS
; APPLICANT: SUMEDHA JAYASENA
; APPLICANT: LARRY GOLD
; TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
; TITLE OF INVENTION: OF CYTOKINES
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,710
; FILING DATE: 7-JUNE-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 8-SEPTEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Diane H. McLearn
; REGISTRATION NUMBER: 33,960
; REFERENCE/DOCKET NUMBER: NEX41-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; FEATURE:
; OTHER INFORMATION: All pyrimidines are 2'-NH2
; US-08-481-710-139

Query Match 56.8%; Score 14.2; DB 3; Length 86;
Best Local Similarity 84.2%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TGTCCACGACATTCGCTG 22
||| | |||||
DB 52 TGCCTCCGACATTCGCTG 34

RESULT 14
US-08-481-710-148/c
; Sequence 148, Application US/08481710
; Patent No. 6028186
; GENERAL INFORMATION:

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Page 7

APPLICANT: DIANE TASSET
APPLICANT: NIKOS PAGRATIS
APPLICANT: SUMEDHA JAYASENA
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS OF CYTOKINES
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,710
FILING DATE: 7-JUNE-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: DIANE TASSET
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX41-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3333
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-NH2
US-08-481-710-148
Query Match 56.8%; Score 14.2; DB 3; Length 86;
Best Local Similarity 84.2%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 4 TGTCCACAGCATTCGCGTG 22
Db 52 TGCCCTCCGCAATTCGCGTG 34
RESULT 15
PCT-US96-09537-130/c
Sequence 130, Application PC/TUS9609537
GENERAL INFORMATION:
APPLICANT: NEXSTAR PHARMACEUTICALS, INC.
APPLICANT: DIANE TASSET
APPLICANT: NIKOS PAGRATIS

APPLICANT: SUMEDHA JAYASENA
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS OF CYTOKINES
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09537
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/481,710
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: BARRY J. SWANSON
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX41/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3333
INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-NH2
PCT-US96-09537-130
Query Match 56.8%; Score 14.2; DB 5; Length 86;
Best Local Similarity 84.2%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 4 TGTCCACAGCATTCGCGTG 22
Db 52 TGCCCTCCGCAATTCGCGTG 34
Search completed: December 21, 2002, 11:58:22
Job time: 23.5306 secs

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:28:32 : Search time 17,2245 Seconds
(without alignments)
356,094 Million cell updates/sec

Title: US-09-121-239-13
Perfect score: 20
Sequence: 1 CAAGGAGCAGGAGGAGG 20

Indexing table: IDENTITY_NUC
Gapex 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCRUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	17.4	87.0	78	US-08-523-125-6	Sequence 6, Appl
2	17.4	87.0	78	US-08-660-561A-6	Sequence 6, Appl
3	17.4	87.0	96	US-08-523-125-9	Sequence 9, Appl
4	17.4	87.0	96	US-08-660-561A-8	Sequence 9, Appl
5	17.4	87.0	96	US-08-366-627A-8	Sequence 8, Appl
6	17.4	87.0	96	US-08-323-125-5	Sequence 5, Appl
7	14.8	74.0	66	US-08-660-561A-5	Sequence 5, Appl
8	14.8	74.0	66	US-08-523-125-7	Sequence 7, Appl
9	14.8	74.0	69	US-08-660-561A-7	Sequence 7, Appl
10	14.8	74.0	84	US-08-523-125-8	Sequence 8, Appl
11	14.8	74.0	84	US-08-660-561A-8	Sequence 8, Appl
12	14.8	74.0	84	US-08-366-627A-7	Sequence 7, Appl
13	14.8	74.0	87	US-08-523-125-10	Sequence 10, Appl
14	14.8	74.0	87	US-08-660-561A-10	Sequence 10, Appl
15	14.8	74.0	87	US-09-366-627A-9	Sequence 9, Appl
16	14.2	71.0	21	US-08-065-844A-14	Sequence 14, Appl
17	14.2	71.0	45	US-08-171-383A-5	Sequence 5, Appl
18	13.8	69.0	51	US-08-461-041-5	Sequence 5, Appl
19	13.8	69.0	59	US-08-313-127A-2	Sequence 2, Appl
20	13.8	69.0	66	US-08-313-127A-4	Sequence 4, Appl
21	13.8	69.0	68	US-08-313-127A-6	Sequence 6, Appl
22	13.8	69.0	68	US-08-313-127A-8	Sequence 8, Appl
23	13.8	69.0	68	US-08-313-127A-3	Sequence 3, Appl
24	13.8	69.0	75	US-08-313-127A-5	Sequence 5, Appl
25	13.8	69.0	75	US-08-313-127A-7	Sequence 7, Appl
26	13.8	69.0	75	US-08-313-127A-9	Sequence 9, Appl
27	13.8	69.0	75	US-08-313-127A-1	Sequence 1, Appl

28	13.6	68.0	30	US-09-674-460-2	Sequence 2, Appl
29	13.6	68.0	82	US-08-051-962-7	Sequence 7, Appl
30	13.6	68.0	89	US-08-461-658B-42	Sequence 42, Appl
31	13.6	68.0	89	US-08-477-504A-42	Sequence 42, Appl
32	13.6	68.0	89	US-08-486-756A-42	Sequence 42, Appl
33	13.6	68.0	89	US-08-485-862B-42	Sequence 42, Appl
34	13.6	68.0	89	US-08-787-739-42	Sequence 42, Appl
35	13.6	68.0	89	US-08-487-077A-42	Sequence 42, Appl
36	13.6	68.0	89	US-08-485-863A-42	Sequence 42, Appl
37	13.6	68.0	89	US-08-485-049D-42	Sequence 42, Appl
38	13.6	68.0	89	US-09-178-115-42	Sequence 42, Appl
39	13.6	68.0	89	US-09-177-776-42	Sequence 42, Appl
40	13.4	67.0	20	US-09-658-687A-82	Sequence 82, Appl
41	13.2	66.0	71	US-09-363-939A-30	Sequence 30, Appl
42	13.2	66.0	71	US-09-363-939A-43	Sequence 43, Appl
43	13.2	66.0	85	US-09-051-962-9	Sequence 9, Appl
44	12.6	64.0	20	US-08-788-750-4	Sequence 4, Appl
45	12.8	64.0	20	US-08-765-340-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-08-523-125-6
Sequence 6, Application US/08523125
Patent No. 5830866
GENERAL INFORMATION:
APPLICANT: Redel, Eva
TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 5830866ris
Street: One Liberty Place - 1700 Market Street
City: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,125
FILING DATE: Herewith
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/304,383
FILING DATE: 12-SEP-94
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kathryn Leary, Ph.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: UPN-2535
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
STANDARDS: single
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-523-125-6
Query Match 87.0% Score 17.4; DB 2: Length 78;
Best Local Similarity 94.7% Pred. No. 13;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CAAAGAGCAGGAGAGAG 19
|||||
DB 19 CAAAGAGCTGGGAGAGAG 37

RESULT 2

US-08-660-561A-6
; Sequence 6, Application US/08660561A
; Patent No. 6039956
; GENERAL INFORMATION:

APPLICANT: Redel, Eva
APPLICANT: Aird, Fraser
TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
TITLE OF INVENTION: and Methods of Using Same
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pantich Schwarze Jacobs & Nadel
STREET: One Commerce Square, 2005 Market Street, 22nd Flr.
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,561A
FILING DATE: 17-JUN-96
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/304,383
FILING DATE: 12-SEP-94
CLASSIFICATION: 514
APPLICATION NUMBER: 08/523,125
FILING DATE: 08-SEP-95

ATTORNEY/AGENT INFORMATION:

NAME: Kathryn Doyle Leary, Ph.D., J.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 0054-102 (G-1191)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-08-660-561A-6

Query Match 87.0%; Score 17.4; DB 3; Length 78;
Best Local Similarity 94.7%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CAAAGAGCAGGAGAGAG 19
|||||
DB 19 CAAAGAGCTGGGAGAGAG 37

RESULT 3

US-08-523-125-9
; Sequence 9, Application US/08523125
; Patent No. 5830866
; GENERAL INFORMATION:

APPLICANT: Redel, Eva
APPLICANT: Aird, Fraser
TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
TITLE OF INVENTION: and Methods of Using Same

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5830866r1s
STREET: One Liberty Place - 1700 Market Street
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,125
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/304,383
FILING DATE: 12-SEP-94
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Kathryn Leary, Ph.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: UPN-2535
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-08-523-125-9

Query Match 87.0%; Score 17.4; DB 2; Length 96;
Best Local Similarity 94.7%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CAAAGAGCAGGAGAGAG 19
|||||
DB 37 CAAAGAGCTGGGAGAGAG 55

RESULT 4

US-08-660-561A-9
; Sequence 9, Application US/08660561A
; Patent No. 6039956
; GENERAL INFORMATION:

APPLICANT: Redel, Eva
APPLICANT: Aird, Fraser
TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
TITLE OF INVENTION: and Methods of Using Same
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pantich Schwarze Jacobs & Nadel
STREET: One Commerce Square, 2005 Market Street, 22nd Flr.
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,561A
FILING DATE: 17-JUN-96
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/304,383
FILING DATE: 12-SEP-94
CLASSIFICATION: 514
APPLICATION NUMBER: 08/523,125
FILING DATE: 08-SEP-95
ATTORNEY/AGENT INFORMATION:
NAME: Kathryn Doyle Leary, Ph.D., J.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 0054-102 (G-1191)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-660-561A-9

Query Match
Best Local Similarity 87.0%; Score 17.4; DB 3; Length 96;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CAAGAGCAGCAGGAAG 19
DB 37 CAAGAGCAGCAGGAAG 55

RESULT 5
US-09-366-627A-8
Sequence 8, Application US/0936627A
Patent No. 6348571
GENERAL INFORMATION:
APPLICANT: REDEL, Eva
ATTORNEY/AGENT INFORMATION:
NAME: Alrid, Fraser
REGISTRATION NUMBER: 0054-103
REFERENCE/DOCKET NUMBER: 0054-103
CURRENT APPLICATION NUMBER: US/09/366,627A
FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 09/366,627
PRIOR FILING DATE: 1996-06-07
PRIOR APPLICATION NUMBER: 08/523,125
PRIOR FILING DATE: 1995-09-08
PRIOR APPLICATION NUMBER: 08/304,383
PRIOR FILING DATE: 1994-09-12
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 96
TYPE: DNA
ORGANISM: Homo sapiens
US-09-366-627A-8

Query Match
Best Local Similarity 87.0%; Score 17.4; DB 4; Length 96;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CAAGAGCAGCAGGAAG 19
DB 37 CAAGAGCAGCAGGAAG 55

RESULT 6
US-08-523-125-5
Sequence 5, Application US/08523125
Patent No. 5830866
GENERAL INFORMATION:
APPLICANT: Redel, Eva
ATTORNEY/AGENT INFORMATION:
NAME: Alrid, Fraser

TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
TITLE OF INVENTION: and Methods of Using Same
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5830866 is
STREET: One Liberty Place - 1700 Market Street
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,125
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/304,383
FILING DATE: 12-SEP-94
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kathryn Leary, Ph.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: UPN-2535
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-523-125-5

Query Match
Best Local Similarity 74.0%; Score 14.8; DB 2; Length 66;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAGAGCAGCAGGAAG 18
DB 19 CAAGAGCAGCAGGAAG 36

RESULT 7
US-08-660-561A-5
Sequence 5, Application US/08660561A
Patent No. 6039956
GENERAL INFORMATION:
APPLICANT: Redel, Eva
ATTORNEY/AGENT INFORMATION:
NAME: Alrid, Fraser
REGISTRATION NUMBER: Corticotropin Release Inhibiting Factor
TITLE OF INVENTION: and Methods of Using Same
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia Schwarz Jacobs & Nadel
STREET: One Commerce Square, 2005 Market Street, 22nd Flr.
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,561A

FILING DATE: 17-JUN-96
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/304,383
FILING DATE: 12-SEP-94
CLASSIFICATION: 514
APPLICATION NUMBER: 08/523,125
FILING DATE: 08-SEP-95
ATTORNEY/AGENT INFORMATION:
NAME: Kathryn Doyle Leary, Ph.D., J.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 0054-102 (G-1191)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-660-561A-5

Query Match 74.0%; Score 14.8; DB 3; Length 66;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGAGCAGGAGAGAA 18
||||| ||| ||| ||| |||
Db 19 CAAGAGCTGGAGAGAA 36

RESULT 8
US-08-523-125-7
Sequence 7, Application US/08523125
Patent No. 5830866
GENERAL INFORMATION:
APPLICANT: Redel, Eva
TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
TITLE OF INVENTION: and Methods of Using Same
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5830866r1s
STREET: One Liberty Place - 1700 Market Street
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,125
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/304,383
FILING DATE: 12-SEP-94
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kathryn Leary, Ph.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: UPN-2535
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-523-125-7

Query Match 74.0%; Score 14.8; DB 2; Length 69;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGAGCAGGAGAGAA 18
||||| ||| ||| ||| |||
Db 19 CAAGAGCTGGAGAGAA 36

RESULT 9
US-08-660-561A-7
Sequence 7, Application US/08660561A
Patent No. 6036956
GENERAL INFORMATION:
APPLICANT: Redel, Eva

TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
TITLE OF INVENTION: and Methods of Using Same
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pantlich Schwarze Jacobs & Nadel
STREET: One Commerce Square, 2005 Market Street, 22nd Flr.
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,561A
FILING DATE: 17-JUN-96
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/304,383
FILING DATE: 12-SEP-94
CLASSIFICATION: 514
APPLICATION NUMBER: 08/523,125
FILING DATE: 08-SEP-95
ATTORNEY/AGENT INFORMATION:
NAME: Kathryn Doyle Leary, Ph.D., J.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 0054-102 (G-1191)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-660-561A-7

US-08-660-561A-7

Query Match 74.0%; Score 14.8; DB 3; Length 69;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGAGCAGGAGAGAA 18
||||| ||| ||| ||| |||
Db 19 CAAGAGCTGGAGAGAA 36

RESULT 10
US-08-523-125-8
; Sequence 8, Application US/08523125
; Patent No. 5830866
; GENERAL INFORMATION:
; APPLICANT: Redel, Eva
; TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
; TITLE OF INVENTION: and Methods of Using Same
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5830866r1s
; STREET: One Liberty Place - 1700 Market Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,125
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/304,383
; FILING DATE: 12-SEP-94
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kathryn Leary, Ph.D.
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: UPN-2535
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-523-125-8

Query Match 74.0%; Score 14.8; DB 2; Length 84;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

QY 1 CAAAGGAGCGAGGAGAA 18
DB 37 CAAAGGAGCGTGGAGAA 54

RESULT 11
US-08-660-561A-8
; Sequence 8, Application US/08660561A
; Patent No. 6039956
; GENERAL INFORMATION:
; APPLICANT: Redel, Eva
; TITLE OF INVENTION: Corticotropin Release Inhibiting Factor
; TITLE OF INVENTION: and Methods of Using Same
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pantich Schwarz Jacobs & Nadel
; STREET: One Commerce Square, 2005 Market Street, 22nd Flr.
; CITY: Philadelphia
; STATE: PA

COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,561A
FILING DATE: 17-JUN-96
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/304,383
FILING DATE: 12-SEP-94
CLASSIFICATION: 514
APPLICATION NUMBER: 08/523,125
FILING DATE: 08-SEP-95
ATTORNEY/AGENT INFORMATION:
NAME: Kathryn Doyle Leary, Ph.D., J.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 0054-102 (G-1191)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-660-561A-8

Query Match 74.0%; Score 14.8; DB 3; Length 84;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

QY 1 CAAAGGAGCGAGGAGAA 18
DB 37 CAAAGGAGCGTGGAGAA 54

RESULT 12
US-09-366-627A-7
; Sequence 7, Application US/09366627A
; Patent No. 6348571
; GENERAL INFORMATION:
; APPLICANT: Redel, Eva
; TITLE OF INVENTION: CORTICOTROPIN RELEASE INHIBITING FACTOR AND METHODS OF USING S
; FILE REFERENCE: 0054-103
; CURRENT APPLICATION NUMBER: US/09/366,627A
; PRIORITY FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 09/366,627
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: 08/523,125
; PRIOR FILING DATE: 1995-09-08
; PRIOR APPLICATION NUMBER: 08/304,383
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 7
; LENGTH: 84
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-366-627A-7

Query Match 74.0%; Score 14.8; DB 4; Length 84;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

QY 1 CAAAGGAGCGAGGAGAA 18

Mon Dec 23 08:47:54 2002

us-09-121-239-13.rni

Page 6

DB 37 CAAAGAACCTGGGAGAA 54

RESULT 13

US-08-523-125-10
Sequence 10, Application US/08523125

Patent No. 5830866

GENERAL INFORMATION:

APPLICANT: Redel, Eva

APPLICANT: Aird, Fraser

TITLE OF INVENTION: Corticotropin Release Inhibiting Factor

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 5830866r1s

STREET: One Liberty Place - 1700 Market Street

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/523,125

FILING DATE: Herewith

CLASSIFICATION: 530

PRIOR APPLICATION NUMBER: 08/304,383

FILING DATE: 12-SEP-94

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Kathryn Leary, Ph.D.

REGISTRATION NUMBER: 36,317

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 87 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOHETICAL: NO

ANTI-SENSE: NO

US-08-523-125-10

Query Match

Best Local Similarity 88.9%; Pred. No. 2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAAGACGACGAGAA 18

DB 37 CAAAGAACCTGGGAGAA 54

RESULT 14

US-08-660-561A-10

Sequence 10, Application US/08660561A

Patent No. 6039956

GENERAL INFORMATION:

APPLICANT: Redel, Eva

APPLICANT: Aird, Fraser

TITLE OF INVENTION: Corticotropin Release Inhibiting Factor

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

STREET: One Commerce Square, 2005 Market Street, 22nd Flr.

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/660,561A

FILING DATE: 17-JUN-96

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/304,383

FILING DATE: 12-SEP-94

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Kathryn Doyle Leary, Ph.D., J.D.

REGISTRATION NUMBER: 36,317

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-567-2020

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 87 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOHETICAL: NO

ANTI-SENSE: NO

US-08-660-561A-10

Query Match

Best Local Similarity 88.9%; Pred. No. 2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAAGACGACGAGAA 18

DB 37 CAAAGAACCTGGGAGAA 54

RESULT 15

US-09-366-627A-9

Sequence 9, Application US/09366627A

Patent No. 6348571

GENERAL INFORMATION:

APPLICANT: Redel, Eva

APPLICANT: Aird, Fraser

TITLE OF INVENTION: CORTICOTROPIN RELEASE INHIBITING FACTOR AND METHODS OF USING S

FILE REFERENCE: 0054-103

CURRENT APPLICATION NUMBER: US/09/366,627A

PRIOR FILING DATE: 2001-06-20

PRIOR APPLICATION NUMBER: 09/366,627

PRIOR FILING DATE: 1996-06-07

PRIOR APPLICATION NUMBER: 08/523,125

PRIOR FILING DATE: 1995-09-08

PRIOR APPLICATION NUMBER: 08/304,383

PRIOR FILING DATE: 1994-09-12

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.0

SEQ ID NO: 9

LENGTH: 87

TYPE: DNA

ORGANISM: MUS SP.

US-09-366-627A-9

Query Match

Best Local Similarity 88.9%; Pred. No. 2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

us-09-121-239-13.rni

Page 7 .

Search completed: December 21, 2002, 11:58:22
Job time : 17.2245 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:28:32 : Search time 20.6694 Seconds
(without alignments)
356.094 Million cell updates/sec

Title: US-09-121-239-16

Sequence: 1 GTGACATGAGCCCTTCAGCGG 24

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Issued_Patents.NA.*
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2: /cgn2_6/pdata/1/ina/5B.COMB.seq.*
3: /cgn2_6/pdata/1/ina/6A.COMB.seq.*
4: /cgn2_6/pdata/1/ina/6B.COMB.seq.*
5: /cgn2_6/pdata/1/ina/PC109.COMB.seq.*
6: /cgn2_6/pdata/1/ina/Backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	15.8	65.8	56 1	US-07-940-652-14 Sequence 14, Appl
2	15.8	65.8	56 1	US-08-255-553-14 Sequence 14, Appl
3	15.6	65.0	29 4	US-09-125-891-7 Sequence 7, Appl
4	15.6	65.0	35 3	US-09-329-418-27 Sequence 27, Appl
5	15.6	65.0	35 4	US-09-531-914-27 Sequence 27, Appl
6	15.4	64.2	23 1	US-08-363-233B-22 Sequence 21, Appl
7	15.4	64.2	23 1	US-08-448-446B-1 Sequence 22, Appl
8	15.4	64.2	62 3	US-08-448-446B-1 Sequence 1, Appl
9	15.4	64.2	62 3	US-08-793-408-9 Sequence 1, Appl
10	15.4	64.2	62 3	US-08-793-408-9 Sequence 11, Appl
11	15.4	64.2	62 3	US-09-139-762A-11 Sequence 9, Appl
12	15.4	64.2	33 3	US-09-139-762A-11 Sequence 11, Appl
13	15.4	64.2	33 3	US-09-139-762A-11 Sequence 11, Appl
14	15.4	64.2	33 3	US-09-139-762A-11 Sequence 11, Appl
15	15.4	64.2	33 3	US-09-139-762A-11 Sequence 11, Appl
16	15.4	64.2	33 3	US-09-139-762A-11 Sequence 11, Appl
17	15.4	64.2	33 3	US-09-139-762A-11 Sequence 11, Appl
18	15.4	64.2	33 3	US-09-139-762A-11 Sequence 11, Appl
19	15.4	64.2	33 3	US-09-139-762A-11 Sequence 11, Appl
20	15.4	64.2	33 3	US-09-139-762A-11 Sequence 11, Appl
21	15.4	64.2	33 3	US-09-139-762A-11 Sequence 11, Appl
22	15.4	64.2	33 3	US-09-139-762A-11 Sequence 11, Appl
23	15.4	64.2	33 3	US-09-139-762A-11 Sequence 11, Appl
24	15.4	64.2	33 3	US-09-139-762A-11 Sequence 11, Appl
25	15.4	64.2	33 3	US-09-139-762A-11 Sequence 11, Appl
26	15.4	64.2	33 3	US-09-139-762A-11 Sequence 11, Appl
27	15.4	64.2	33 3	US-09-139-762A-11 Sequence 11, Appl

C	28	14.2	59.2	23	4	US-09-634-262-26	Sequence 26, Appl
	29	14.2	58.3	23	1	US-08-363-233B-24	Sequence 24, Appl
	30	14.2	58.3	23	1	US-08-363-233B-25	Sequence 25, Appl
	31	14.2	58.3	26	4	US-08-152-621-33	Sequence 33, Appl
	32	14.2	58.3	26	4	US-09-341-955-1	Sequence 1, Appl
	33	14.2	58.3	26	5	PCT-US92-05035-13	Sequence 33, Appl
	34	14.2	58.3	26	5	PCT-US93-07541-25	Sequence 25, Appl
	35	14.2	58.3	32	3	US-08-946-914-57	Sequence 57, Appl
	36	14.2	58.3	32	4	US-09-626-450-57	Sequence 57, Appl
	37	14.2	58.3	42	2	US-08-768-177-3	Sequence 3, Appl
	38	14.2	58.3	42	2	US-08-991-675A-3	Sequence 3, Appl
	39	14.2	58.3	56	1	US-07-940-652-19	Sequence 19, Appl
	40	14.2	58.3	56	1	US-08-255-553-19	Sequence 19, Appl
	41	13.6	56.7	32	1	US-08-706-037-12	Sequence 12, Appl
	42	13.6	56.7	32	2	US-09-005-397-12	Sequence 12, Appl
	43	13.6	56.7	60	4	US-09-128-354-20	Sequence 20, Appl
	44	13.4	55.8	23	1	US-08-399-675-15	Sequence 15, Appl
	45	13.4	55.8	23	3	US-08-281-203-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-07-940-652-14/c
Sequence 14, Application US/07940652
Patent No. 5424413
GENERAL INFORMATION:
APPLICANT: James J. Hogan et al.
TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS Version 3.30
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/940,652
FILING DATE: 19920904
CLASSIFICATION: 435
PRIOR APPLICATION DATA: US/07/827,021
APPLICATION NUMBER: 22-JAN-1992
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Walburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 199/201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 14:
LENGTH: 56
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-940-652-14
Query Match 65.8% Score 15.8; DB 1; Length 56;
Best Local Similarity 89.5%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 ACATGAAGCCCTTCAGCGG 24
DB 35 ACATGAAGCCCTTCAGCGG 17

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RESULT 2
US-08-255-553-14/c
; Sequence 14, Application US/08255553
; Patent No. 5451503
; GENERAL INFORMATION:
; APPLICANT: James J. Hogan et al.
; TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS Version 3.30
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/255,553
; FILING DATE: 07-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/940,652
; FILING DATE: 04-SEP-1992
; APPLICATION NUMBER: US/07/827,021
; FILING DATE: 22-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 199/201
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-255-553-14
;
Query Match          65.8%; Score 15.8; DB 1; Length 56;
Best Local Similarity 89.5%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
QY      6  ACATGAGCCCTTCAGCGG 24
DB      35  ACGTAAAGCCCTTCAGCGG 17
;
RESULT 3
US-09-125-891-7
; Sequence 7, Application US/09125891
; Patent No. 6462185
; GENERAL INFORMATION:
; APPLICANT: TAKAKURA, Yoshimitsu
; APPLICANT: INOUE, Tsuyoshi
; APPLICANT: SAITO, Hideaki
; APPLICANT: ITO, Toru
; TITLE OF INVENTION: Flower Organ-Specific Gene and Its Promoter Sequence
; FILE REFERENCE: 0230-0125P
; CURRENT APPLICATION NUMBER: US/09/125,891
; CURRENT FILING DATE: 1998-08-27
; EARLIER APPLICATION NUMBER: PCT/JP97/04892
; EARLIER FILING DATE: 1997-12-26
; EARLIER APPLICATION NUMBER: 349505/1996 JAPAN
; EARLIER FILING DATE: 1996-12-27
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; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid psp24
; US-09-125-891-7
;
Query Match          65.0%; Score 15.6; DB 4; Length 29;
Best Local Similarity 81.8%; Pred. No. 93;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
;
QY      2  TGAACATGAGCCCTTCAGCG 23
DB      5  TAGACATGAGATCCCTTCAGCG 26
;
RESULT 4
US-09-329-418-27/c
; Sequence 27, Application US/09329418
; Patent No. 6096539
; GENERAL INFORMATION:
; APPLICANT: ZENECA Limited
; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
; FILE REFERENCE: PHM.70536
; CURRENT APPLICATION NUMBER: US/09/329,418
; CURRENT FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
; US-09-329-418-27
;
Query Match          65.0%; Score 15.6; DB 3; Length 35;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
;
QY      3  GGAACATGAGCCCTTCAGCGG 24
DB      35  GGAACACCAAGTCCTTAAGCGG 14
;
RESULT 5
US-09-531-914-27/c
; Sequence 27, Application US/09531914
; Patent No. 6267956
; GENERAL INFORMATION:
; APPLICANT: ZENECA Limited
; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
; FILE REFERENCE: PHM.70536
; CURRENT APPLICATION NUMBER: US/09/531,914
; CURRENT FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/329,418
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
; US-09-531-914-27
;
Query Match          65.0%; Score 15.6; DB 4; Length 35;
Best Local Similarity 81.8%; Pred. No. 96;
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Matches 18; Conservative 0; Mismatches 4; Indels 0; Caps 0;

QY 3 GGAACATGAGCCCTTCACGG 24
||||| ||| ||| ||| ||| |||

DB 35 GGAACACAGATCCTTAGCGG 14

RESULT 6

US-08-363-233B-21

Sequence 21, Application US/08363233B

Patent No 5714383

GENERAL INFORMATION:

APPLICANT: Thompson, James D.

TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FASTSEQ FOR WINDOWS 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/363,233B

FILING DATE: December 23, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA: Including application

PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER: 07/882,822

FILING DATE: May 14, 1992

APPLICATION NUMBER: 08/193,922

FILING DATE: February 7, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/165

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-363-233B-21

Query Match 64.2%; Score 15.4; DB 1; Length 23;

Best Local Similarity 82.4%; Pred. No. 1.1e+02;

Matches 14; Conservative 2; Mismatches 1; Indels 0; Caps 0;

QY 8 ATGAAGCCCTTCACGG 24
||||| ||| ||| ||| ||| |||

DB 2 AAGAGCCCTTCACGG 18

RESULT 7

US-08-363-233B-22

Sequence 22, Application US/08363233B

Patent No. 5714383

GENERAL INFORMATION:

APPLICANT: Thompson, James D.

TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC

TITLE OF INVENTION: MYELOGENOUS LEUKEMIA

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FASTSEQ FOR WINDOWS 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/363,233B

FILING DATE: December 23, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA: Including application

PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER: 07/882,822

FILING DATE: May 14, 1992

APPLICATION NUMBER: 08/193,922

FILING DATE: February 7, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/165

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-363-233B-22

Query Match 64.2%; Score 15.4; DB 1; Length 23;

Best Local Similarity 82.4%; Pred. No. 1.1e+02;

Matches 14; Conservative 2; Mismatches 1; Indels 0; Caps 0;

QY 8 ATGAAGCCCTTCACGG 24
||||| ||| ||| ||| ||| |||

DB 1 AAGAGCCCTTCACGG 17

RESULT 8

US-08-448-446B-1

Sequence 1, Application US/08448446B

Patent No. 6080851

GENERAL INFORMATION:

APPLICANT: Pachuk et al.

TITLE OF INVENTION: Compounds and Methods for the Treatment

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn

STREET: Kutz Mackiewicz & No. 6080851

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

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1 SOFTWARE: WORDPERFECT 5.1
2 CURRENT APPLICATION DATA:
3 APPLICATION NUMBER: US/08/448,446B
4 FILING DATE: July 10, 1995
5 CLASSIFICATION: 435
6
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: 07/989,852
9 FILING DATE: December 4, 1992
10 ATTORNEY/AGENT INFORMATION:
11 NAME: Doreean Yaecko Trujillo
12 REGISTRATION NUMBER: 35,719
13 REFERENCE/DOCKET NUMBER: APOL-0020
14 TELECOMMUNICATION INFORMATION: C
15 TELEPHONE: (215) 568-3100
16 TELEFAX: (215) 568-4439
17 INFORMATION FOR SEO ID NO: 1:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 62
20 TYPE: Nucleic Acid
21 STRANDEDNESS: Single
22 TOPOLOGY: Linear
23 ANTI-SENSE: NO
24
25 US-08-448-446B-1

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Query Match      64.2%;   Score 15.4; DB 3; Length 62;
Best Local Similarity 82.4%;   Pred. No. 1.3e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0.

QY      8 ATGAGCCCTTCAGCGG 24
        | | | | | | | | | |
Db      29 AAGAGCCCTTCAGCGG 45

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RESULT 9
 US-08-793-408-9
 : Sequence 9, Application US/08793408
 : Patent No. 6007988
 : GENERAL INFORMATION:
 : APPLICANT: Choo, Yen
 : APPLICANT: Kluo, Aaron
 : APPLICANT: Sanchez Garcia, Isidro
 : TITLE OF INVENTION: Improvements In or Relating to
 : NUMBER OF INVENTION: Binding Proteins For Recognition of DNA
 : NUMBER OF SEQUENCES: 18
 : CORRESPONDENCE ADDRESSES:
 : ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
 : STREET: 1100 New York Avenue, N.W.
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20005-3918
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Word Perfect
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/793,408
 : FILING DATE:
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: PCT/GB95/01949
 : FILING DATE: 17-AUG-1995
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: GB 9514698.1
 : FILING DATE: 18-JUL-1995
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: GB 9422534.9
 : FILING DATE: 08-NOV-1994
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: GB 9416680.4
 : FILING DATE: 20-AUG-1994
 : INFORMATION FOR SEQ ID NO: 9:

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; SEQUENCE CHARACTERISTICS
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-793-408-9

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Query Match	62.5%;	Score 15;	DB 3;	Length 33;
Best Local Similarity	100.0%;	Pred. No. 1.8e+02;		
Matches 15;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	10	GAAGCCCTTCAGCGG	24
Db	16	GAAGCCCTTCAGCGG	30

RESULT 10
US-08-793-408-11
Sequence 11, Application US/08793408
Patent No. 6007988
GENERAL INFORMATION:
APPLICANT: Choo, Yen
APPLICANT: Klug, Aaron
APPLICANT: Sanchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington

```

? ZIP: 20005-3918
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Word Perfect
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/793,408
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: PCT/GB95/01949
? FILING DATE: 17-AUG-1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: GB 9514698.1
? FILING DATE: 18-JUL-1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: GB 9432534.9
? FILING DATE: 08-NOV-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: GB 9416880.4
? FILING DATE: 20-AUG-1994
? INFORMATION FOR SEQ ID NO: 11:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 33 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
PS-08-793-408-11

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Query Match      62.5%; Score 15; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	10	GAAGCCCTCAGCGG	24
Db	16	GAA GCCCTCAGCGG	30

RESULT 11

US-09-139-762A-9
 ; Sequence 9, Application US/09139762A
 ; Patent No. 6013453
 ; GENERAL INFORMATION:
 ; APPLICANT: Choo, Yen
 ; APPLICANT: Klug, Aaron
 ; APPLICANT: Sanchez Garcia, Isidro
 ; TITLE OF INVENTION: Improvements in or Relating to
 ; TITLE OF INVENTION: Binding Proteins for Recognition of DNA
 ; NUMBER OF SEQUENCES: 125
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
 ; STREET: 1100 New York Avenue, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3918
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/139,762A
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/793,408
 ; FILING DATE: 02-JUN-1997
 ; APPLICATION NUMBER: PCT/GB95/01949
 ; FILING DATE: 17-AUG-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9514698.1
 ; FILING DATE: 18-JUL-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9422534.9
 ; FILING DATE: 08-NOV-1994
 ; APPLICATION NUMBER: GB 9416880.4
 ; FILING DATE: 20-AUG-1994
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 33 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-139-762A-9
 ; Query Match 62.5%; Score 15; DB 3; Length 33;
 ; Best Local Similarity 100.0%; Pred. No. 1.Be+02;
 ; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ; QY 10 GAAGCCTTCAGCGG 24
 ; DB 16 GAAGCCTTCAGCGG 30
 ; RESULT 12
 ; US-09-139-762A-11
 ; Sequence 11, Application US/09139762A
 ; Patent No. 6013453
 ; GENERAL INFORMATION:
 ; APPLICANT: Choo, Yen
 ; APPLICANT: Klug, Aaron
 ; APPLICANT: Sanchez Garcia, Isidro
 ; TITLE OF INVENTION: Improvements in or Relating to
 ; TITLE OF INVENTION: Binding Proteins for Recognition of DNA
 ; NUMBER OF SEQUENCES: 125
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
 ; STREET: 1100 New York Avenue, N.W.
 ; CITY: Washington
 ; STATE: D.C.

COUNTRY: USA
 ZIP: 20005-3918
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/139,762A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/793,408
 FILING DATE: 02-JUN-1997
 APPLICATION NUMBER: PCT/GB95/01949
 FILING DATE: 17-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9514698.1
 FILING DATE: 18-JUL-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9422534.9
 FILING DATE: 08-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9416880.4
 FILING DATE: 20-AUG-1994
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 ; US-09-139-762A-11
 ; Query Match 62.5%; Score 15; DB 3; Length 33;
 ; Best Local Similarity 100.0%; Pred. No. 1.Be+02;
 ; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ; QY 10 GAAGCCTTCAGCGG 24
 ; DB 16 GAAGCCTTCAGCGG 30
 ; RESULT 13
 ; US-08-706-037-14
 ; Sequence 14, Application US/08706037
 ; Patent No. 5770419
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Feng
 ; APPLICANT: Berka, Randy M.
 ; APPLICANT: Wahleithner, Jill A.
 ; TITLE OF INVENTION: BLUE COPPER OXIDASE MUTANTS WITH
 ; TITLE OF INVENTION: ENHANCED ACTIVITY
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 57704190 No. 5770419disk of No. 5770419th America, Inc.
 ; STREET: 405 Lexington Avenue, 64th floor
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States of America
 ; ZIP: 10174-6401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/706,037
 ; FILING DATE: 30-AUG-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/002,800
 ; FILING DATE: 1-SEP-1996
 ; ATTORNEY/AGENT INFORMATION:

NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4526,200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-706-037-14

Query Match 62.5%; Score 15; DB 1; Length 34;
Best Local Similarity 78.3%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 TGAACATGAGCCCTTCAGCG 24
DB 10 TGATGATGAGCTTCATCAG 32

RESULT 14
US-09-005-397-14
Sequence 14, Application US/09005397
Patent No. 5972670
GENERAL INFORMATION:
APPLICANT: Xu, Feng
APPLICANT: Berka, Randy M.
APPLICANT: Wahleithner, Jill A.
TITLE OF INVENTION: BLUE COPPER OXIDASE MUTANTS WITH
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59726700 No. 5972670disk of No. 5972670th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,397
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/706,037
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: US 60/002,800
FILING DATE: 1-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4526,200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-005-397-14

Query Match 62.5%; Score 15; DB 2; Length 34;

Best Local Similarity 78.3%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 TGAACATGAGCCCTTCAGCG 24
DB 10 TGATGATGAGCTTCATCAG 32

RESULT 15
US-08-448-446B-12
Sequence 12, Application US/08448446B
Patent No. 6080851
GENERAL INFORMATION:
APPLICANT: Pachuk et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment
of Leukemias
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn
ADDRESSEE: Kurtz Mackiewicz & No. 6080851r1s
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,446B
FILING DATE: July 10, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/989,852
FILING DATE: December 4, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Doreen Yalko Trujillo
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: APOL-0020
TELECOMMUNICATION INFORMATION: C
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 47
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE:
US-08-448-446B-12

Query Match 62.5%; Score 15; DB 3; Length 47;
Best Local Similarity 86.7%; Pred. No. 1.9e+02;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 10 GAAGCCCTTCAGCG 24
DB 16 GAAGCCCTTCAGCG 30

Search completed: December 21, 2002, 11:58:23
Job time: 21.6694 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:28:32 ; Search time 23.2531 Seconds
(56.094 Million cell updates/sec)

Title: US-09-121-239-22

Sequence: 1 TGTGACTTGTGAGCTCAGGCTGTGAGT 27

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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2	26	96.3	80 1	US-08-306-618-38
3	26	96.3	80 5	PCT-US92-05035-7
4	22	81.5	22 1	US-08-013-419-1
5	22	81.5	22 1	US-08-122-795B-10
6	22	81.5	22 1	US-08-522-818-1
7	22	81.5	22 2	US-09-028-184-1
8	22	81.5	22 5	PCT-US94-00680-1
9	22	81.5	22 5	PCT-US94-09963A-10
10	17	63.0	56 1	US-07-940-652-19
11	17	63.0	56 1	US-08-255-553-19
12	15.8	57.8	67 1	US-07-872-678A-13
13	15.6	57.8	67 1	US-08-170-095B-35
14	15.6	57.8	80 3	US-08-921-887-48
15	15.6	57.8	20 1	US-07-784-131-7
16	15.6	57.8	20 1	US-07-784-131-7
17	15.6	57.8	21 3	US-08-998-099-278
18	15.6	57.8	40 1	US-08-761-131-1
19	15.6	57.8	40 1	US-08-761-131-1
20	14.6	54.1	27 4	US-08-584-040-1123
21	14.4	53.3	27 4	US-08-985-162-994
22	14.4	53.3	27 4	US-08-584-040-1204
23	14.4	53.3	37 1	US-08-428-733A-7
24	14.4	53.3	37 1	US-08-428-733A-38
25	14.4	53.3	37 1	US-08-428-733A-39
26	14.4	53.3	43 3	US-08-732-708C-6
27	14.2	52.6	33 1	US-08-463-224-61

28	14.2	52.6	33 2	US-08-463-377-61	Sequence 61, Appl
29	14.2	52.6	36 2	US-08-292-620A-1109	Sequence 1109, Ap
30	14.2	52.6	36 3	US-09-071-845-1109	Sequence 4, Appl
31	14.2	52.6	41 1	US-08-654-773-4	Sequence 4, Appl
32	14.2	52.6	41 2	US-08-909-768-4	Sequence 17, Appl
33	14.2	52.6	42 1	US-07-834-539A-17	Sequence 25, Appl
34	14.2	52.6	42 1	US-08-645-641-25	Sequence 25, Appl
35	14.2	52.6	42 1	US-08-053-131-25	Sequence 25, Appl
36	14.2	52.6	42 1	US-07-853-408B-25	Sequence 17, Appl
37	14.2	52.6	42 1	US-08-096-762-25	Sequence 17, Appl
38	14.2	52.6	42 2	US-08-800-353-17	Sequence 13, Appl
39	14.2	52.6	42 2	US-08-308-865-25	Sequence 11, Appl
40	14.2	52.6	42 4	US-08-758-417A-17	Sequence 11, Appl
41	14.2	52.6	42 5	PCT-US92-06183-17	Sequence 25, Appl
42	14.2	52.6	42 5	PCT-US92-10983-25	Sequence 122, App
43	14.2	52.6	69 1	US-08-434-001-122	Sequence 122, App
44	14.2	52.6	69 1	US-08-433-585-122	
45	14.2	52.6			

ALIGNMENTS

RESULT 1
US-08-152-621-7
Sequence 7, Application US/08452621
Patent No. 5652222
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Gewirtz, Alan M.
TITLE OF INVENTION: Selective Inhibition of
TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl
TITLE OF INVENTION: Antisense Oligonucleotides
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: SETDEL, CONDA, LAVORIGNA
STREET: 1800 Two Penn Center
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,621
FILING DATE: No. 5652222ember 15, 1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/718,302
FILING DATE: June 18, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Monico, Daniel A.
REGISTRATION NUMBER: 6056-120 (CT.) 1
REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1
TELEPHONE: (215) 568-8983
TELEFAX: (215) 568-5549
TELEX: No. 5652222e
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-08-152-621-7
Query Match 96.3%; Score 26; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGCTCTGAG 26
|||||
DB 55 TCTGACTTTGAGCCTCAGGCTCTGAG 80

RESULT 2

US-08-306-691B-38
Sequence 38, Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: No. 5734039e
INFORMATION FOR SEQ. ID NO.: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-306-691B-38

Query Match 96.3%; Score 26; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGCTCTGAG 26
|||||
DB 55 TCTGACTTTGAGCCTCAGGCTCTGAG 80

RESULT 3

PCT-US92-05035-7
Sequence 7, Application PC/TUS9205035
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Gewiltz, Alan M.
TITLE OF INVENTION: Selective inhibition of
TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl
TITLE OF INVENTION: Antisense Oligonucleotides
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Temple University - Of The Common-
ADDRESSER: Wealth System of Higher Education

STREET: 406 University Services Building
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19122

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05035
FILING DATE: 19920615
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/718,302
FILING DATE: June 18, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/869,911
FILING DATE: April 14, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: None
INFORMATION FOR SEQ. ID NO.: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 Nucleotides
TYPE: NUCLEIC ACID
STRANDEDNESS: single stranded
TOPOLOGY: linear
PCT-US92-05035-7

Query Match 96.3%; Score 26; DB 5; Length 80;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGCTCTGAG 26
|||||
DB 55 TCTGACTTTGAGCCTCAGGCTCTGAG 80

RESULT 4

US-08-013-419-1/c
Sequence 1, Application US/08013419
Patent No. 530635
GENERAL INFORMATION:
APPLICANT: Macfarlane, Donald E.
TITLE OF INVENTION: Product and Process for Isolating RNA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/013,419
FILING DATE: 19930201
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: URIF1USA


```
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-013-419-1

Query Match      81.5%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACTTGGAGCCTCAGGGCTCTGA 25
DB 22 GACTTGGAGCCTCAGGGCTCTGA 1

RESULT 5
US-08-122-795B-10/c
Sequence 10, Application US/08122795B
Patent No. 5635385
GENERAL INFORMATION:
APPLICANT: Lance H. Leopold
APPLICANT: Scott K. Shore
APPLICANT: Moole V. R. Reddy
APPLICANT: E. Premkumar Reddy
TITLE OF INVENTION: MULTI-UNIT RHODZYME
TITLE OF INVENTION: INHIBITION OF ONCOGENE EXPRESSION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Seidel, Gonda, Lavoragna
ADDRESSEE: 6 Monaco, P.C.
STREET: Two Penn Center Plaza, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/122,795B
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 122,795
FILING DATE: 15 September 1993
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-192
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: No. 5635385e
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-08-122-795B-10

Query Match      81.5%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACTTGGAGCCTCAGGGCTCTGA 25
DB 22 GACTTGGAGCCTCAGGGCTCTGA 1

RESULT 6
US-08-525-818-1/c
Sequence 1, Application US/08525818
Patent No. 5728822
GENERAL INFORMATION:
APPLICANT: Macfarlane, Donald E.
TITLE OF INVENTION: Quaternary Amine Surfactants and Methods
TITLE OF INVENTION: of Using Same in Isolation of RNA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,818
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/113,727
FILING DATE:
APPLICATION NUMBER: US 08/013,419
FILING DATE: 01-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: UIFPLUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-525-818-1

Query Match      81.5%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACTTGGAGCCTCAGGGCTCTGA 25
DB 22 GACTTGGAGCCTCAGGGCTCTGA 1

RESULT 7
US-09-028-184-1/c
Sequence 1, Application US/09028184
Patent No. 5985572
GENERAL INFORMATION:
APPLICANT: Macfarlane, Donald E.
TITLE OF INVENTION: Quaternary Amine Surfactants and
TITLE OF INVENTION: Methods of Using Same in Isolation of RNA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
```

STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028.184
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/525.818
FILING DATE: 07-SEP-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/113.727
FILING DATE: 27-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/013.419
FILING DATE: 01-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kodoff, Cathy A.
REGISTRATION NUMBER: 33,980
REFERENCE/DOCKET NUMBER: UIRFICUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-09-028-184-1

Query Match 81.5%; Score 22; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTGAGCCTCAGGCTCGA 25
DB 22 GACTTGAGCCTCAGGCTCGA 1

RESULT 8
Sequence 1, Application PC/TUS9400680
GENERAL INFORMATION:
APPLICANT: University of Iowa, Research Foundation
TITLE OF INVENTION: Quaternary Amine Surfactants and
METHOD OF INVENTION: Methods of Using Same in Isolation of RNA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00680
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/013.419
FILING DATE: 01-FEB-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/113.727
FILING DATE: 27-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: UIRFAPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
PCT-US94-00680-1

Query Match 81.5%; Score 22; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTGAGCCTCAGGCTCGA 25
DB 22 GACTTGAGCCTCAGGCTCGA 1

RESULT 9
PCT-US94-09963A-10/c
Sequence 10, Application PC/TUS9409963A
GENERAL INFORMATION:
TITLE OF INVENTION: MULTI-UNIT RIBOZYME
METHOD OF INVENTION: INHIBITION OF ONCOGENE EXPRESSION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna
ADDRESS: 6 Monaco, P.C.
STREET: Two Penn Center Plaza, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09963A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 122.795
FILING DATE: 15 September 1993
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-192
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8363
TELEFAX: (215) 568-5549
TELEX: None
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
PCT-US94-09963A-10

Query Match 81.5%; Score 22; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTGAGCCTCAGGCTCTGA 25
|||||

Db 22 GACTTGAGCCTCAGGCTCTGA 1

RESULT 10
US-07-940-652-19
Sequence 19, Application US/07940652
Patent No. 5424413
GENERAL INFORMATION:
APPLICANT: James J. Hogan et al.
TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS Version 3.30
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/940,652
FILING DATE: 19920904
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/827,021
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 199/201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 56
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear

US-07-940-652-19

Query Match 63.0%; Score 17; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTGAGCCTCA 17
|||||

Db 40 TCTGACTTGAGCCTCA 56

RESULT 11
US-08-255-553-19
Sequence 19, Application US/0825553
Patent No. 5451503
GENERAL INFORMATION:
APPLICANT: James J. Hogan et al.
TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA

ZIP: 90017

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS Version 3.30
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/255,553
FILING DATE: 07-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/940,652
FILING DATE: 04-SEP-1992
APPLICATION NUMBER: US/07/827,021
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 199/201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 56
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-255-553-19

Query Match 63.0%; Score 17; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTGAGCCTCA 17
|||||

Db 40 TCTGACTTGAGCCTCA 56

RESULT 12
US-07-872-678A-13/C
Sequence 13, Application US/07872678A
Patent No. 5541060
GENERAL INFORMATION:
APPLICANT: Bell, Graeme, et al.
TITLE OF INVENTION: DETECTION OF EARLY-ONSET
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: Post Office Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/872,678A
FILING DATE: 22-APRIL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coughlin, Daniel F.
REGISTRATION NUMBER: 36,111
REFERENCE/DOCKET NUMBER: ARCD016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
TELEX: 79-0924

;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-07-872-678A-13

Query Match 58.5%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 57;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TTGAGCCTCAGGCTCTCA 25
|||||
DB 19 TTGAGCCTCAGAACTCTCA 1

RESULT 13
-08-170-095B-35
Sequence 35, Application US/08170095B
Patent No. 5563254

GENERAL INFORMATION:
APPLICANT: Hoffman, Stephen J.
APPLICANT: Nagai, Kiyoshi
TITLE OF INVENTION: Blood Substitutes
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Somatogen, Inc.
STREET: 2545 Central Avenue
CITY: Boulder
STATE: Colorado
ZIP: 80301

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,095B
FILING DATE: December 20, 1993
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: No. 5563254ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: Hoffman 2A/CONT2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-541-3322
TELEFAX: 303-444-3013

INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 67
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown to applicant
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: beta globin sequence fragment
HYPOTHETICAL: no
US-08-170-095B-35

Query Match 57.8%; Score 15.6; DB 1; Length 67;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 18; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 TGACTTTGAGCCTCAGGCTGAG 26
|||||
DB 44 TGCTAGSAGCCTCAGAGTCTGAG 67

RESULT 14
US-08-921-887-48
Sequence 48, Application US/08921887
Patent No. 6030771

;; GENERAL INFORMATION:
;; APPLICANT: KHUDYAKOV, YURI E.
;; APPLICANT: FIELDS, HOWARD A.
;; TITLE OF INVENTION: MOSAIC PROTEIN AND RESTRICTION
;; TITLE OF INVENTION: ENDONUCLEASE ASSISTED LIGATION METHOD FOR MAKING THE SAME
;; NUMBER OF SEQUENCES: 55
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: JONES & ASKEW, LLP
;; STREET: 191 Peachtree Street, N.W., 37th Floor
;; CITY: Atlanta
;; STATE: GA
;; COUNTRY: USA

ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/921,887
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: WARREN, WILLIAM L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 03063-0380
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Hepatitis virus
US-08-921-887-48

Query Match 57.8%; Score 15.6; DB 3; Length 80;
Best Local Similarity 81.8%; Pred. No. 93;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CTGACTTTGAGCCTCAGGCTCT 23
|||||
DB 59 CTGAGTCTGAGCCTCAGGCTTGT 80

RESULT 15
US-08-761-131-7/c
Sequence 7, Application US/08761131
Patent No. 5804384

GENERAL INFORMATION:
APPLICANT: M Iler, Uwe R. et al.
TITLE OF INVENTION: DEVICES AND METHODS FOR DETECTING
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Vysis, Inc.
STREET: 3100 Woodcreek Drive
CITY: Downers Grove
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60515

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,131
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5804384val B.
REGISTRATION NUMBER: 33,595
REFERENCE/DOCKET NUMBER: 01886/064001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-271-7417
TELEFAX: 708-271-7048
TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-761-131-7

Query Match      55.6%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCTGACTTTGAGCCT 15
        |||
Db      15 TCTGACTTTGAGCCT 1

Search completed: December 21, 2002, 11:58:25
Job time : 25.2531 secs
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2
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:28:32 ; Search time 23.2531 Seconds
(Without alignments)
356,094 Million cell updates/sec

Title: US-09-121-239-23

Sequence: 1 UGACUUGAGCCUGAGCUGAGU 27

Scoring table: IDENTITY_NUC
Gap 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Issued_Patents_NA.*
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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	26	96.3	80 1	US-08-152-621-7
2	26	96.3	80 1	US-08-306-6918-38
3	26	96.3	80 5	PCT-US92-05035-7
4	22	81.5	22 1	US-08-013-419-1
5	22	81.5	22 1	US-08-122-785B-10
6	22	81.5	22 1	US-08-525-818-1
7	22	81.5	22 1	US-09-028-184-1
8	22	81.5	22 5	PCT-US94-0963A-10
9	22	81.5	22 5	PCT-US94-0963A-10
10	17	63.0	56 1	US-07-940-652-19
11	17	63.0	56 1	US-08-255-553-19
12	15.8	57.8	20 1	US-07-872-678A-13
13	15.6	57.8	67 1	US-08-170-095B-35
14	15.6	57.8	80 3	US-08-921-887-48
15	15.6	57.8	20 1	US-08-761-131-7
16	15.6	57.8	20 1	US-07-784-222-2
17	15.6	57.8	27 3	US-08-998-099-278
18	15.6	57.8	40 1	US-08-761-131-1
19	15.6	57.8	40 1	US-08-761-131-2
20	14.6	53.3	27 4	US-08-584-040-3123
21	14.4	53.3	27 4	US-08-985-162-924
22	14.4	53.3	27 4	US-08-584-040-3204
23	14.4	53.3	37 1	US-08-428-733A-7
24	14.4	53.3	37 1	US-08-428-733A-38
25	14.4	53.3	37 1	US-08-428-733A-39
26	14.4	53.3	43 3	US-08-723-708C-6
27	14.2	52.6	33 1	US-08-463-224-61

c 28	14.2	52.6	33 2	US-08-463-377-61	Sequence 61, Appl
c 29	14.2	52.6	36 2	US-08-292-620A-1109	Sequence 1109, Ap
c 30	14.2	52.6	36 3	US-09-071-845-1109	Sequence 1109, Ap
c 31	14.2	52.6	41 1	US-08-654-773-4	Sequence 4, Appl
c 32	14.2	52.6	41 2	US-08-909-768-4	Sequence 4, Appl
c 33	14.2	52.6	42 1	US-07-834-539A-17	Sequence 17, Appl
c 34	14.2	52.6	42 1	US-08-053-2513-25	Sequence 25, Appl
c 35	14.2	52.6	42 1	US-08-645-641-25	Sequence 25, Appl
c 36	14.2	52.6	42 1	US-07-853-408B-25	Sequence 25, Appl
c 37	14.2	52.6	42 1	US-08-096-762-25	Sequence 25, Appl
c 38	14.2	52.6	42 2	US-08-800-853-17	Sequence 17, Appl
c 39	14.2	52.6	42 2	US-08-308-865-25	Sequence 193, App
c 40	14.2	52.6	42 4	US-08-758-417A-41	Sequence 41, Appl
c 41	14.2	52.6	42 4	US-08-417A-41	Sequence 17, Appl
c 42	14.2	52.6	42 5	PCT-US92-06183-15	Sequence 25, Appl
c 43	14.2	52.6	42 5	PCT-US92-10983-25	Sequence 25, Appl
c 44	14.2	52.6	69 1	US-08-434-001-122	Sequence 122, App
c 45	14.2	52.6	69 1	US-08-433-585-122	Sequence 122, App

ALIGNMENTS

RESULT 1
US-08-152-621-7
Sequence 7, Application US/08152621
Patent No. 5652222
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
TITLE OF INVENTION: Selective inhibition of
TRIPLE OR INVENTION: Leukemic Cell Proliferation by ber-abl
TITLE OF INVENTION: Antisense Oligonucleotides
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: SELDEN, GONDA, LAVORGNA
ADDRESS: 1800 Two Penn Center
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08152,621
FILING DATE: No. 5652222 December 15, 1993
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/718,302
FILING DATE: June 18, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8363
TELEFAX: (215) 568-5549
TELEX: No. 5652222e
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-08-152-621-7
Query Match 96.3%; Score 26; DB 1; Length 80;
Best Local Similarity 69.2%; Pred. No. 0.001;
Matches 18; Conservative 8; Mismatches 0; Gaps 0;


```
TELECOMMUNICATION INFORMATION:
: TELEPHONE: 215-540-9206
: TELEFAX: 215-540-5818
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 22 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: DNA (genomic)
: US-08-013-419-1

Query Match      81.5%; Score 22; DB 1; Length 22;
Best Local Similarity 72.7%; Pred. No. 0.064;
Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      4 GACUUGAGCCUCGAGGUCUGA 25
Db      22 GACTTGAGCCTCAGGCTCTGA 1

RESULT 5
US-08-122-795B-10/c
Sequence 10, Application US/08122795B
Patent No. 5635385
GENERAL INFORMATION:
APPLICANT: Lance H. Leopold
APPLICANT: Scott K. Shore
APPLICANT: Nicole V. R. Reddy
APPLICANT: E. Premkumar Reddy
TITLE OF INVENTION: MUTATION-UNT RIBOZYME
TITLE OF INVENTION: INHIBITION OF ONCOGENE EXPRESSION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Seidel, Gonda, Lavorina
ADDRESSER: 6 Monaco, P.C.
STREET: Two Penn Center Plaza, Suite 1800
STATE: Philadelphia
CITY: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/122,795B
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 122,795
FILING DATE: 15 September 1993
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-192
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: No. 5635385
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-08-122-795B-10

Query Match      81.5%; Score 22; DB 1; Length 22;
Best Local Similarity 72.7%; Pred. No. 0.064;
Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      4 GACUUGAGCCUCGAGGUCUGA 25
Db      22 GACTTGAGCCTCAGGCTCTGA 1

RESULT 6
US-08-525-818-1/c
Sequence 1, Application US/08525818
Patent No. 5728822
GENERAL INFORMATION:
APPLICANT: Macfarlane, Donald E.
TITLE OF INVENTION: Quaternary Amine Surfactants and Methods
TITLE OF INVENTION: of Using Same in Isolation of RNA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Howson and Howson
STREET: Spring House Corporate Cntr., P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,818
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/113,727
FILING DATE:
APPLICATION NUMBER: US 08/013,419
FILING DATE: 01-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: UIF1AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-940-5618
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-525-818-1

Query Match      81.5%; Score 22; DB 1; Length 22;
Best Local Similarity 72.7%; Pred. No. 0.064;
Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      4 GACUUGAGCCUCGAGGUCUGA 25
Db      22 GACTTGAGCCTCAGGCTCTGA 1

RESULT 7
US-09-028-184-1/c
Sequence 1, Application US/09028184
Patent No. 5985572
GENERAL INFORMATION:
APPLICANT: Macfarlane, Donald E.
TITLE OF INVENTION: Quaternary Amine Surfactants and
TITLE OF INVENTION: Methods of Using Same in Isolation of RNA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
```

STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,184
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/525,818
FILING DATE: 07-SEP-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/113,727
FILING DATE: 27-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/013,419
FILING DATE: 01-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kodroff, Cathy A.
REGISTRATION NUMBER: 33,980
REFERENCE/DOCKET NUMBER: UIR1PCUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-09-028-184-1

Query Match 81.5%; Score 22; DB 2; Length 22;
Best Local Similarity 72.7%; Pred. No. 0.064;
Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACUUGAGCCUCAGGUCUGA 25
||||:||||:||||:||||:
Db 22 GACTTGAGCCTCAGGTCGTA 1

SUPT 8
T-US94-00680-1/c
Sequence 1, Application PC/TUS9400680
GENERAL INFORMATION:
APPLICANT: University of Iowa, Research Foundation
TITLE OF INVENTION: Quarternary Amine Surfactants and
TITLE OF INVENTION: Methods of using Same in Isolation of RNA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00680
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/013,419
FILING DATE: 01-FEB-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/113,727
FILING DATE: 27-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: UIR1APCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
PCT-US94-00680-1

Query Match 81.5%; Score 22; DB 5; Length 22;
Best Local Similarity 72.7%; Pred. No. 0.064;
Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACUUGAGCCUCAGGUCUGA 25
||||:||||:||||:||||:
Db 22 GACTTGAGCCTCAGGTCGTA 1

RESULT 9
PCT-US94-09963A-10/c
Sequence 10, Application PC/TUS9409963A
GENERAL INFORMATION:
TITLE OF INVENTION: MULTI-UNIT RIBOZYME
TITLE OF INVENTION: INHIBITION OF ONCOGENE EXPRESSION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna
ADDRESSEE: & Monaco, P.C.
STREET: Two Penn Center Plaza, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09963A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 122,795
FILING DATE: 15 September 1993
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-192
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: None
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
PCT-US94-09963A-10

Query Match 81.5%; Score 22; DB 5; Length 22;
Best Local Similarity 72.7%; Pred. No. 0.064;


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: INFORMATION FOR SEQ ID NO: 13
:
: SEQUENCE CHARACTERISTICS:
:
:   LENGTH: 20 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
:
:   MOLECULE TYPE: DNA (genomic)
:
: OS-07-872-678A-13

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Query Match	58.5%;	Score 15.8;	DB 1;	Length 20;
Best Local Similarity	57.9%;	Pred. NO. 57;		
Matches 11; Conservative	6;	Mismatches 2;	Indels 0;	Gaps 0;

```

QY      7  UUUGAGCCUCAGGGUCUGA  25
          :::|||||:| |  :|:| |
Db     19  TTGAGCCTCAGAATCTGA   1

```

RESULT 13
-08-170-095B-35
Sequence 35, Application US/08170095B
Patent No 5563254

APPLICANT: Hoffman, Stephen J.
APPLICANT: Nagai, Kiyoshi
TITLE OF INVENTION: Blood Substitutes
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Somatogen, Inc.
STREET: 2545 Central Avenue
CITY: Boulder
STATE: Colorado
ZIP: 80301

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.04
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,095B
FILING DATE: December 20, 1993
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: NO. 55632544k, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: Hoffman 2A/CONT2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-541-3322
TELEFAX: 303-444-3013
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:

LENGTH: 67
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown to applicant
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: beta globin sequence fragment
 HYPOTHEETICAL: no
 OS-08-170-0958-35

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Query Match:          57.8%; Score 15.6; DB 1; Length 67;
Best Local Similarity 54.2%; Prec. NO. 90;
Matches    13; Conservative   6; Mismatches    5; Indels     0; Gaps      0.
QY       3 UCACUUGAGCCUCGAGGCGUCUGAG 26
         :|:::||||::||::|
         44 TSCCTAGSAGCCTGAAGGTCTGAG 67

```

RESULT 14
US-08-921-887-48
; Sequence 48, Application US/08921887
; Patent No. 6030771

GENERAL INFORMATION:
APPLICANT: KHUDYAKOV, YURI E.
APPLICANT: FIELDS, HOWARD A.
TITLE OF INVENTION: MOSAIC PROTEIN AND RESTRICTION
TITLE OF INVENTION: ENDONUCLEASE ASSISTED LIGATION METHOD FOR MAKING THE SAME
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:

ADDRESSSEE: JONES & ASKEW, LLP
STREET: 191 Peachtree Street, N.W., 37th Floor
CITY: Atlanta
STATE: GA
COUNTRY: USA

ZIP: 30303-1769

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.300
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/921,887
FILING DATE:

CLASSIFICATION: 435

NAME: WARREN, WILLIAM L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 03063-0386
TELECOMMUNICATION INFORMATION:

TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799

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; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:

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LENGTH: 80 base pairs
TYPE: nucleic acid

STRANDEDNESS: sin

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;
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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; HYPOTHETICAL: NO
; ANTI-SENSE: NO

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; FRAGMENT TYPE: Internal
: ORIGINAL SOURCE:

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ORGANISM: Hepatitis virus
US-08-921-887-48

Query Match	57.8%;	Score 15.6;	DB 3;	Length 80;
Best Local Similarity	54.5%;	Pred. No. 93;		
Matches 12; Conservative	6;	Mismatches 4;	Indels 0;	Gaps 0

```
QY      2 CTGACUUUGAGCCUCAGGGUUCU 23
          |:: : |||||:|||| : :
Db     59 CTGAGTCTGAGCCTCAGGTGT 80
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RESULT 15
US-08-761-131-7/c

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; sequence /, Application US/08/61131
; Patent No. 5804384

```

```

; GENERAL INFORMATION:
; APPLICANT: M 11et

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TITLE OF INVENTION:	DEVICES AND METHODS FOR DETECTING
TITLE OF INVENTION:	MULTIPLE ANALYTES IN SAMPLES
;	

NUMBER OF SEQUENCES: 7

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ysis, Inc
;

```

STREET: 3100 Woodcreek Drive
CITY: Downers Grove

STATE: Illinois
COUNTRY: U S A

ZIP: 60515

21F: 00313
COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEO Version 2.0

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Mon Dec 23 08:48:00 2002

us-09-121-239-23.rni

Page 7

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? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/761,131
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Galloway, No. 5804384val B.
? REGISTRATION NUMBER: 33,595
? REFERENCE/DOCKET NUMBER: 01886/064001
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 708-271-7417
? TELEFAX: 708-271-7048
? TELEX: 200154
? INFORMATION FOR SEQ ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 20 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: Genomic DNA
? OS=08-761-131-7

Query Match 55.6%; Score 15; DB 1; Length 20;
Best Local Similarity 60.0%; Pred No. 1.4e+02;
Matches 9; Conservative 6; Mismatches 0; Gaps 0;
CY 1 UCUNACUUGAGGCU 15
   |||:|||||:
DB 15 TCTGACTTTGAGCCT 1

```

1
2



1
2

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:28:32 Search time 15.502 Seconds
(without alignments)
356.094 Million cell updates/sec

Title: US-09-121-239-26
Perfect score: 18
Sequence: 1 GGAATCATCGAGCGATCG 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues
Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents NA:
1: /cgn2_6/ptodata/1/lna/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/lna/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/lna/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/lna/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/lna/PCU05.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	13.8	76.7	37	1	US-08-444-231-3 Sequence 3, Appl1
2	13.8	76.7	37	1	US-08-152-443A-3 Sequence 36, Appl1
3	13.8	76.7	73	4	US-09-625-188-36 Sequence 13, Appl1
4	12.8	71.1	20	1	US-08-480-552-13 Sequence 1, Appl1
5	12.8	71.1	20	1	US-08-204-740-1 Sequence 1, Appl1
6	12.8	71.1	20	2	US-08-486-382-1 Sequence 1, Appl1
7	12.8	71.1	20	2	US-08-485-657A-1 Sequence 2, Appl1
8	12.8	71.1	20	2	US-09-258-371-22 Sequence 1, Appl1
9	12.8	71.1	20	3	US-09-258-371-22 Sequence 1, Appl1
10	12.8	71.1	20	3	US-08-923-208-13 Sequence 13, Appl1
11	12.8	71.1	20	3	US-09-081-167A-1 Sequence 1, Appl1
12	12.8	71.1	20	3	US-09-081-395-1 Sequence 22, Appl1
13	12.8	71.1	20	3	US-08-751-230-22 Sequence 22, Appl1
14	12.8	71.1	20	3	US-08-499-082-22 Sequence 1, Appl1
15	12.8	71.1	20	4	US-09-416-833-1 Sequence 22, Appl1
16	12.8	71.1	20	4	US-09-258-371-22 Sequence 1, Appl1
17	12.8	71.1	20	5	US-09-568-315-13 Sequence 13, Appl1
18	12.8	71.1	20	5	PCY-US95-02303-1 Sequence 14, Appl1
19	12.8	71.1	20	5	PCY-US95-02303-1 Sequence 14, Appl1
20	12.8	71.1	23	1	US-08-480-552-14 Sequence 2, Appl1
21	12.8	71.1	23	1	US-08-204-740-2 Sequence 2, Appl1
22	12.8	71.1	23	2	US-08-486-382-2 Sequence 2, Appl1
23	12.8	71.1	23	2	US-08-485-657A-2 Sequence 23, Appl1
24	12.8	71.1	23	2	US-09-258-371-23 Sequence 2, Appl1
25	12.8	71.1	23	3	US-09-235-546-2 Sequence 14, Appl1
26	12.8	71.1	23	3	US-08-929-208-14 Sequence 2, Appl1
27	12.8	71.1	23	3	US-09-081-167A-2 Sequence 2, Appl1

c 28	12.8	71.1	23	3	US-09-081-395-2	Sequence 2, Appl1
c 29	12.8	71.1	23	3	US-08-751-230-23	Sequence 23, Appl1
c 30	12.8	71.1	23	3	US-09-499-082-23	Sequence 2, Appl1
c 31	12.8	71.1	23	4	US-09-416-833-2	Sequence 2, Appl1
c 32	12.8	71.1	23	4	US-09-258-372-23	Sequence 14, Appl1
c 33	12.8	71.1	23	4	US-09-568-315-14	Sequence 2, Appl1
c 34	12.8	71.1	23	5	PCY-US95-02303-2	Sequence 2, Appl1
c 35	12.8	71.1	23	5	PCY-US95-02303-2	Sequence 2, Appl1
c 36	12.2	67.8	24	4	US-09-593-012-214	Sequence 16, Appl1
c 37	12.2	67.8	36	2	US-08-864-224-3	Sequence 3, Appl1
c 38	12.2	67.8	37	4	US-08-900-574-16	Sequence 21, Appl1
c 39	12	66.7	39	3	US-09-428-589-3	Sequence 61, Appl1
c 40	11.8	65.6	21	4	US-09-121-920-21	Sequence 3, Appl1
c 41	11.8	65.6	24	4	US-09-423-233-61	Sequence 62, Appl1
c 42	11.8	65.6	29	3	US-09-556-868-3	Sequence 15, Appl1
c 43	11.8	65.6	29	3	US-08-258-287B-62	Sequence 15, Appl1
c 44	11.8	65.6	29	3	US-08-368-704C-60	Sequence 15, Appl1
c 45	11.8	65.6	37	4	US-08-900-574-15	Sequence 15, Appl1

ALIGNMENTS

```

RESULT 1
US-08-444-231-3
; Sequence 3, Application US/08444231
; Patent No. 5652210
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J.
; APPLICANT: SHAPIRO, JOHN P.
; APPLICANT: KIEFER, MICHAEL C.
; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSER: MORRISON & FORRESTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,231
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/152,443
; FILING DATE: 15-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20006.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-444-231-3
Query Match 76.7%; Score 13.8; DB 1; Length 37;
Best Local Similarity 88.2%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

OY 1 GGAATCATCGAGGCATG 17
|||||
Db 14 GGAATCATCGAGGCATG 30

RESULT 2

US-08-152-443A-3
; Sequence 3, Application US/08152443A
; Patent No. 5663070

GENERAL INFORMATION:

APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,443A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-152-443A-3

Query Match

Best Local Similarity 76.7%; Score 13.8; DB 1; Length 37;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGGCATG 17
|||||
Db 14 GGAATCATCGAGGCATG 30

RESULT 3

US-09-625-188-36
; Sequence 36, Application US/09625188
; Patent No. 6307037

GENERAL INFORMATION:

APPLICANT: No. 6307037artis AG
TITLE OF INVENTION: Fungal Target Genes and Methods
FILE REFERENCE: PB/5-31285P1
CURRENT APPLICATION NUMBER: US/09/625,188
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 36
LENGTH: 73
TYPE: DNA
ORGANISM: Artificial Sequence

FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-625-188-36

Query Match

Best Local Similarity 76.7%; Score 13.8; DB 4; Length 73;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGGCATG 17
|||||
Db 44 GGAATCATCGAGGCATG 60

RESULT 4

US-08-480-552-13
; Sequence 13, Application US/08480552
; Patent No. 5665550

GENERAL INFORMATION:

APPLICANT: Gudkov, Andrei
APPLICANT: Roninson, Igor B.
TITLE OF INVENTION: Genes And Genetic Elements Associated
TITLE OF INVENTION: With Sensitivity To Chemotherapeutic Drugs
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: Allegretti & Wilcoff, Ltd.
STREET: 75 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,552
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/033,086
FILING DATE: 09 MAR 1993
ATTORNEY/AGENT INFORMATION:
NAME: Keown, Wayne A.
REGISTRATION NUMBER: 33,923
REFERENCE/DOCKET NUMBER: 93,354
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/345-9110
TELEFAX: 617/345-9111

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-480-552-13

Query Match

Best Local Similarity 71.1%; Score 12.8; DB 1; Length 20;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AATCATCGAGGCATG 18
|||||
Db 1 AATCATCGAGGCATG 16

RESULT 5

US-08-204-740-1
; Sequence 1, Application US/08204740

Patent No. 5753432
GENERAL INFORMATION:
APPLICANT: Gudkov, Andrei
APPLICANT: Kazarov, Alexander
APPLICANT: Mazo, Ilya
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Methods for identifying Genetic
TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allgrett & Witcoff, Ltd.
STREET: 10 S. Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,740
FILING DATE: 04-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5753432nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-204-740-1
Query Match 71.1%; Score 12.8; DB 1; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY 3 AATCATCGAGCATG 18
DB 1 AATCATCGAGCATG 16
RESULT 6
US-08-486-382-1
Sequence 1, Application US/08486382
Patent No. 5866327
GENERAL INFORMATION:
APPLICANT: Gudkov, Andrei
APPLICANT: Roninson, Igor B.
TITLE OF INVENTION: Association of Kinesin with Sensitivity
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 75 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,382
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/177,571
FILING DATE: 05 JAN 1994
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5866327nan, Kevin E.
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/715-1000
TELEFAX: 312/715-1234
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-486-382-1
Query Match 71.1%; Score 12.8; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY 3 AATCATCGAGCATG 18
DB 1 AATCATCGAGCATG 16
RESULT 7
US-08-485-657A-1
Sequence 1, Application US/08485657A
Patent No. 5942389
GENERAL INFORMATION:
APPLICANT: Kirschling, Deborah J
APPLICANT: Gudkov, Andrei
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Genes and Genetic Elements Associated
TITLE OF INVENTION: with Sensitivity to Cisplatin
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,657A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5942389nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-485-657A-1

Query Match 71.1%; Score 12.8; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AATCATCGAGCATGG 18
|||||
Db 1 AATCATCGATGATGG 16

RESULT 8
US-09-258-371-22
; Sequence 22, Application US/09258371
; Patent No. 5986078

GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,371
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mool, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-09-258-371-22

Query Match 71.1%; Score 12.8; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AATCATCGAGCATGG 18
|||||
Db 1 AATCATCGATGATGG 16

RESULT 9
US-09-235-546-1
; Sequence 1, Application US/09235546
; Patent No. 6043340

GENERAL INFORMATION:
APPLICANT: Gudkov, Andrei
APPLICANT: Roninson, Igor B.
TITLE OF INVENTION: Association of Kinesin with Sensitivity
TITLE OF INVENTION: To Chemotherapeutic Drugs
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 75 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/235,546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,382
FILING DATE:
APPLICATION NUMBER: US 08/177,571
FILING DATE: 05 JAN 1994
ATTORNEY/AGENT INFORMATION:
NAME: No. 6043340nan, Kevin E.
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/715-1000
TELEFAX: 312/715-1234

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-235-546-1

Query Match 71.1%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AATCATCGAGCATGG 18
|||||
Db 1 AATCATCGATGATGG 16

RESULT 10
US-08-929-208-13
; Sequence 13, Application US/08929208
; Patent No. 6060244

GENERAL INFORMATION:
APPLICANT: Gudkov, Andrei
APPLICANT: Roninson, Igor B.
TITLE OF INVENTION: Genes And Genetic Elements Associated
TITLE OF INVENTION: With Sensitivity To Chemotherapeutic Drugs
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 75 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

RESULT 13
US-08-751-230-22
; Sequence 22, Application US/08751230
; Patent No. 6117633
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Radoowl, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE INGI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,230
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569721
; FILING DATE: 08-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mool, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-08-751-230-22

Query Match 71.1%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AATCATCGAGCATGG 18
||||||| |
DB 1 AATCATCGATGATGG 16

RESULT 14
US-09-499-082-22
; Sequence 22, Application US/09499082
; Patent No. 6143522
; GENERAL INFORMATION:
; APPLICANT: Helbing, Caren C.
; APPLICANT: Radoowl, Karl
; APPLICANT: Johnston, Randall N.
; APPLICANT: Garkavtsev, Igor
; TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/499,082
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,158
; FILING DATE: 27-MAR-1997
; APPLICATION NUMBER: US 08/751230
; FILING DATE: 15-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569721
; FILING DATE: 08-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mool, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-854-7400
; TELEFAX: 650-854-8275
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-09-499-082-22

Query Match 71.1%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AATCATCGAGCATGG 18
||||||| |
DB 1 AATCATCGATGATGG 16

RESULT 15
US-09-416-833-1
; Sequence 1, Application US/09416833
; Patent No. 6197521
; GENERAL INFORMATION:
; APPLICANT: Gudkov, Andrei
; APPLICANT: Kazarov, Alexander
; APPLICANT: Mazo, Ilya
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: Methods for Identifying Genetic
; TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
; TITLE OF INVENTION: Growth in Cancer Cells
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Allgretti & Witcoff, Ltd.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/416,833
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,740

Mon Dec 23 08:48:01 2002

us-09-121-239-26.rni

Page 7

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6197521nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-416-833-1

Query Match 71.1%; Score 12.8; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 AATCATCGAGGCATGG 18
|||||||
Db 1 AATCATCGATGATGG 16

Search completed: December 21, 2002, 11:58:26
Job time : 16.502 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:28:32 : Search time 22.3918 seconds
(without alignments)
356.094 Million cell updates/sec

Title: US-09-121-239-27
Perfect score: 26
Sequence: 1 CACTGACGACCTGGATTAGCAGAG 26

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: /cgn2.6/p/odata/1/ina/5B.COMB.seq:*
3: /cgn2.6/p/odata/1/ina/5A.COMB.seq:*
4: /cgn2.6/p/odata/1/ina/5B.COMB.seq:*
5: /cgn2.6/p/odata/1/ina/pctus.COMB.seq:*
6: /cgn2.6/p/odata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	56	1	US-07-940-652-16
2	26	100.0	56	1	US-08-255-553-16
3	26	100.0	90	5	PCT-US93-06251-4
4	25	96.2	40	4	US-09-358-972-125
5	25	96.2	41	4	US-09-358-972-126
6	25	96.2	66	1	US-07-940-652-13
7	25	96.2	66	1	US-08-255-553-13
8	21.4	82.3	40	1	US-07-940-652-131-2
9	18	69.2	18	1	US-08-761-131-4
10	16	61.5	88	4	US-09-171-759-17
11	15	57.7	22	4	US-09-358-972-127
12	15	57.7	22	4	US-09-358-972-128
13	15	57.7	22	4	US-09-406-064-97
14	15	57.7	22	4	US-09-406-064-98
15	15	57.7	22	4	US-08-761-131-5
16	15	57.7	22	4	US-08-761-131-5
17	14.4	55.4	28	1	US-08-479-852-12
18	14.4	55.4	28	1	US-08-479-852-14
19	14.4	55.4	28	1	US-08-479-852-78
20	14.4	55.4	28	1	US-08-479-852-92
21	14.4	55.4	28	2	US-08-462-646-12
22	14.4	55.4	28	2	US-08-462-646-14
23	14.4	55.4	28	2	US-08-462-646-16
24	14.4	55.4	28	2	US-08-462-646-18
25	14.4	55.4	28	2	US-09-013-406-12
26	14.4	55.4	28	4	US-09-013-406-14
27	14.4	55.4	28	4	US-09-013-406-16

28	14.4	55.4	28	4	US-09-013-406-92	Sequence 92, Appl
29	14.4	55.4	30	1	US-08-171-389-486	Sequence 486, App
30	14.4	55.4	30	1	US-08-171-389-487	Sequence 487, App
31	14.4	55.4	50	1	US-08-123-936-486	Sequence 486, App
32	14.4	55.4	50	1	US-08-123-936-487	Sequence 487, App
33	14.4	55.4	50	2	US-08-475-228A-486	Sequence 486, App
34	14.4	55.4	50	2	US-08-475-228A-487	Sequence 487, App
35	14.4	55.4	50	3	US-08-482-080A-486	Sequence 486, App
36	14.4	55.4	50	3	US-08-482-080A-487	Sequence 487, App
37	14.4	55.4	50	4	US-09-354-947-486	Sequence 486, App
38	14.4	55.4	50	4	US-09-354-947-487	Sequence 487, App
39	14.4	55.4	50	5	PCT-US93-12388-486	Sequence 486, App
40	14.4	55.4	50	5	PCT-US93-12388-487	Sequence 487, App
41	14.4	55.4	35	1	US-08-343-682-12	Sequence 12, Appl
42	14	53.8	47	4	US-09-641-638-1213	Sequence 1213, Appl
43	14	53.8	49	1	US-08-343-682-11	Sequence 11, Appl
44	13.6	51.5	20	1	US-08-259-745A-46	Sequence 46, Appl
45	13.4	51.5	24	2	US-08-474-450A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-07-940-652-16
Sequence 16, Application US-07-940652
Patent No. 542413
GENERAL INFORMATION:
APPLICANT: James J. Hogan et al.
TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS Version 3.30
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-07-940, 652
FILING DATE: 19920904
CLASSIFICATION: 433
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US-07-827, 021
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Waiburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 199/201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 56
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: Linear
US-07-940-652-16
Query Match 100.0% Score 26; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CACTGACGACCTGGATTAGCAGAG 26
DB 10 CACTGACGACCTGGATTAGCAGAG 35

RESULT 2
US-08-255-553-16
Sequence 16, Application US/0825553
Patent No. 5451503
GENERAL INFORMATION:
APPLICANT: James J. Hogan et al.
TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS Version 3.30
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/255,553
FILING DATE: 07-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/940,652
FILING DATE: 04-SEP-1992
APPLICATION NUMBER: US/07/827,021
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Walburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 199/201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 56
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-255-553-16

Query Match 100.0%; Score 26; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTGAGCCACTGATTTAAGCAGAG 26
DB 10 CACTGAGCCACTGATTTAAGCAGAG 35

RESULT 3
PCT-US93-06251-4
Sequence 4, Application PC/TUS9306251
GENERAL INFORMATION:
APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivial Synthesis of Oligonucleotides Containing
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCUDLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
FILING DATE: 19930630
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-4

Query Match 100.0%; Score 26; DB 5; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTGAGCCACTGATTTAAGCAGAG 26
DB 45 CACTGAGCCACTGATTTAAGCAGAG 70

RESULT 4
US-09-358-972-125/C
Sequence 125, Application US/09358972
Patent No. 6235480
GENERAL INFORMATION:
APPLICANT: Shultz, John W.
APPLICANT: Lewis, Martin K.
APPLICANT: Lieppe, Donna
APPLICANT: Mandrekar, Michelle
APPLICANT: Kephart, Daniel
APPLICANT: Rhodes, Richard B.
APPLICANT: Andrews, Christine A.
APPLICANT: Hartnett, James R.
APPLICANT: Gu, Trent
APPLICANT: Olson, Ryan J.
APPLICANT: Wood, Keith W.
APPLICANT: Welch, Roy
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: Pro-103 6868/75528
CURRENT APPLICATION NUMBER: US/09/358,972
CURRENT FILING DATE: 1999-07-22
EARLIER APPLICATION NUMBER: 09/252,436
EARLIER FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: 09/042,287
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 290
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 125
LENGTH: 40
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: native bcr
US-09-358-972-125

Query Match 96.2%; Score 25; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ACTGAGCCACTGATTTAAGCAGAG 26

Db 40 ACTCAGCCACTGATTTAAGCAG 16

RESULT 5

US-09-358-972-126/c
Sequence 126, Application US/09358972
Patent No. 6235480

GENERAL INFORMATION:

APPLICANT: Shultz, John W.
APPLICANT: Lewis, Martin K.
APPLICANT: Lieppe, Donna K.
APPLICANT: Mandreker, Michelle
APPLICANT: Kephart, Daniel
APPLICANT: Rhodes, Richard B.
APPLICANT: Andrews, Christine A.
APPLICANT: Hartnett, James R.
APPLICANT: Gu, Trent
APPLICANT: Olson, Ryan J.
APPLICANT: Wood, Keith W.
APPLICANT: Welch, Roy
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: Pro-103 6868/75528
CURRENT APPLICATION NUMBER: US/09/358,972
CURRENT FILING DATE: 1999-07-22
EARLIER APPLICATION NUMBER: 09/252,436
EARLIER FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: 09/042,287
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 290
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 126
LENGTH: 41
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: bcr/dbl translocation
US-09-358-972-126

Query Match 96.2%; Score 25; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 ACTCAGCCACTGATTTAAGCAG 26
41 ACTCAGCCACTGATTTAAGCAG 17

US-07-940-652-13/c
Sequence 13, Application US/07940652
Patent No. 5424413

GENERAL INFORMATION:

APPLICANT: James J. Hogan et al.
TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS Version 3.30
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA: US/07/940,652
APPLICATION NUMBER: US/07/940,652
FILING DATE: 19920904
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/827,021
FILING DATE: 22-JAN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 199/201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 66
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-940-652-13

Query Match 96.2%; Score 25; DB 1; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 ACTCAGCCACTGATTTAAGCAG 26
66 ACTCAGCCACTGATTTAAGCAG 42

US-08-255-553-13/c
Sequence 13, Application US/08255553
Patent No. 5451503

GENERAL INFORMATION:

APPLICANT: James J. Hogan et al.
TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS Version 3.30
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA: US/08/255,553
FILING DATE: 07-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/940,652
FILING DATE: 04-SEP-1992
APPLICATION NUMBER: US/07/827,021
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 199/201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 66
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-255-553-13

Query Match 96.2%; Score 25; DB 1; Length 66;

Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ACTCAGCCACTGATTTAAGACAG 26
|||||
Db 66 ACTCAGCCACTGATTTAAGACAG 42

RESULT 8
US-08-761-131-2
; Sequence 2, Application US/08761131
; Patent No. 5804384
; GENERAL INFORMATION:
; APPLICANT: M Iler, Uwe R. et al.
; TITLE OF INVENTION: DEVICES AND METHODS FOR DETECTING
; TITLE OF INVENTION: MULTIPLE ANALYTES IN SAMPLES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Vysis, Inc.
; STREET: 3100 Woodcreek Drive
; CITY: Downers Grove
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60515
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,131
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: Galloway, No. 5804384val B.
; REGISTRATION NUMBER: 33,595
; REFERENCE/DOCKET NUMBER: 01886/064001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-271-7417
; TELEFAX: 708-271-7048
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
US-08-761-131-2

Query Match 82.3%; Score 21.4; DB 1; Length 40;
Best Local Similarity 95.7%; Pred. No. 0.034; 1; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 ACTCAGCCACTGATTTAAGACAG 24
|||||
Db 1 ACTCAGCCACTGATTTAAGTAG 23

RESULT 9
US-08-761-131-4/c
; Sequence 4, Application US/08761131
; Patent No. 5804384
; GENERAL INFORMATION:
; APPLICANT: M Iler, Uwe R. et al.
; TITLE OF INVENTION: DEVICES AND METHODS FOR DETECTING
; TITLE OF INVENTION: MULTIPLE ANALYTES IN SAMPLES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Vysis, Inc.

STREET: 3100 Woodcreek Drive
CITY: Downers Grove
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60515
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,131
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Galloway, No. 5804384val B.
; REGISTRATION NUMBER: 33,595
; REFERENCE/DOCKET NUMBER: 01886/064001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-271-7417
; TELEFAX: 708-271-7048
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
US-08-761-131-4

Query Match 69.2%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ACTCAGCCACTGATTTA 19
|||||
Db 18 ACTCAGCCACTGATTTA 1

RESULT 10
US-09-171-759-17
; Sequence 17, Application US/09171759
; Patent No. 6346415
; GENERAL INFORMATION:
; APPLICANT: Feldhaus, Andrew
; TITLE OF INVENTION: TRANSCRIPTIONALLY-ACTIVATED
; AAV INVERTED TERMINAL REPEATS (ITRS) FOR USE WITH RECOMB
; AAV VECTORS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/171,759
; FILING DATE: 20-Oct-1998
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <unknown>
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:

```

NAME: Dylan, Tyler M
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 22627-20038.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-171-759-17

Query Match
61.5% Score 16; DB 4; Length 88;
Best Local Similarity 79.2%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CTCAGCCACTGGATTAAACAGAG 26
DB 43 CCCACCCCGCTGATATACAGAG 66

RESULT 11
US-09-171-759-18/c
Sequence 18, Application US/09171759
Patent No. 6346415
GENERAL INFORMATION:
APPLICANT: Feldhaus, Andrew
TITLE OF INVENTION: TRANSCRIPTIONALLY-ACTIVATED
AAV INVERTED TERMINAL REPEATS (ITRS) FOR USE WITH RECOMBINANT
AAV VECTORS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,759
FILING DATE: 20-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Dylan, Tyler M
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 22627-20038.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-171-759-18

Query Match
61.5% Score 16; DB 4; Length 88;
Best Local Similarity 79.2%; Pred. No. 26;

```

```

Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CTCAGCCACTGGATTAAACAGAG 26
DB 50 CCCACCCCGCTGATATACAGAG 27

RESULT 12
US-09-358-972-127
Sequence 127, Application US/09358972
Patent No. 6235480
GENERAL INFORMATION:
APPLICANT: Shultz, John W.
APPLICANT: Lewis, Martin K.
APPLICANT: Lieppe, Donna
APPLICANT: Mandrekar, Michelle
APPLICANT: Kephart, Daniel
APPLICANT: Rhodes, Richard B.
APPLICANT: Andrews, Christine A.
APPLICANT: Hartnett, James R.
APPLICANT: Gu, Trent
APPLICANT: Olson, Ryan J.
APPLICANT: Wood, Keith W.
APPLICANT: Welch, Roy
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: Pro-103 6868/75528
CURRENT APPLICATION NUMBER: US/09/358,972
EARLIER FILING DATE: 1999-07-22
EARLIER APPLICATION NUMBER: 09/042,287
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 290
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 127
LENGTH: 22
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: probe for native bcr
US-09-358-972-127

Query Match
57.7% Score 15; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TCGATTTAACAGAG 26
DB 1 TCGATTTAACAGAG 15

RESULT 13
US-09-358-972-128
Sequence 128, Application US/09358972
Patent No. 6235480
GENERAL INFORMATION:
APPLICANT: Shultz, John W.
APPLICANT: Lewis, Martin K.
APPLICANT: Lieppe, Donna
APPLICANT: Mandrekar, Michelle
APPLICANT: Kephart, Daniel
APPLICANT: Rhodes, Richard B.
APPLICANT: Andrews, Christine A.
APPLICANT: Hartnett, James R.
APPLICANT: Gu, Trent
APPLICANT: Olson, Ryan J.
APPLICANT: Wood, Keith W.
APPLICANT: Welch, Roy
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: Pro-103 6868/75528
CURRENT APPLICATION NUMBER: US/09/358,972
EARLIER FILING DATE: 1999-07-22
EARLIER APPLICATION NUMBER: 09/252,436

```

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; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 09/042,287
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 128
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: probe for bcr/abl translocation
US-09-358-972-128

```

```

Query Match          57.7%; Score 15; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 12 TCGATTTAAGCAGAG 26
      |||
DB 1 TCGATTTAAGCAGAG 15

```

```

RESULT 14
US-09-406-064-97
; Sequence 97, Application US/09406064
; Patent No. 6270973
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Leippe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel B
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Wood, Keith V.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: MULTIPLEX METHOD FOR NUCLEIC ACID DETECTION
; FILE REFERENCE: PRO-107.0 (6868/75532)
; CURRENT APPLICATION NUMBER: US/09/406,064
; EARLIER FILING DATE: 1999-09-27
; EARLIER APPLICATION NUMBER: 09/358,972
; EARLIER FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: 09/252,436
; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 09/042,287
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 97
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-406-064-97

```

```

Query Match          57.7%; Score 15; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 12 TCGATTTAAGCAGAG 26
      |||
DB 1 TCGATTTAAGCAGAG 15

```

```

RESULT 15
US-09-406-064-98
; Sequence 98, Application US/09406064
; Patent No. 6270973
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Leippe, Donna

```

```

; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel B
; APPLICANT: Rhodes, Richard B
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Wood, Keith V.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: MULTIPLEX METHOD FOR NUCLEIC ACID DETECTION
; FILE REFERENCE: PRO-107.0 (6868/75532)
; CURRENT APPLICATION NUMBER: US/09/406,064
; EARLIER FILING DATE: 1999-09-27
; EARLIER APPLICATION NUMBER: 09/358,972
; EARLIER FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: 09/252,436
; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 09/042,287
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 98
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-406-064-98

```

```

Query Match          57.7%; Score 15; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 12 TCGATTTAAGCAGAG 26
      |||
DB 1 TCGATTTAAGCAGAG 15

```

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Search completed: December 21, 2002, 11:58:27
Job time : 23.3918 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:20:00 : Search time 1664.08 Seconds
(without alignments)
525.549 Million cell updates/sec

Title: US-09-121-239-1

Perfect score: 54
Sequence: 1 TAAATTAATACGACTCACTA.....CCCTGAGGCTCAACTCAGA 54

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estbm:*
3: em_estlin:*
4: em_estlun:*
5: em_estcov:*
6: em_estlpl:*
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9: gb_estl:*
10: gb_estl2:*
11: gb_estc:*
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13: gb_estl4:*
14: gb_estl5:*
15: em_estfun:*
16: em_estlom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
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21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23.4	43.3	79	9	AJ282930 4A3A-PIE1
2	23.2	43.0	75	9	AJ282930 4A3A-PIE1
3	23	42.6	30	17	AQ797214 RPI-22-4
4	23	42.6	69	17	BH217910 1006061D0
5	22.6	41.9	100	9	A1353756 zeh0940.s
6	22.4	41.5	46	9	A1096189 SWAMCACC26

C	7	22.4	41.5	50	10	AM160061	AM160061 SWLACAK06
C	8	22.4	41.5	50	10	AM172194	AM172194 SWLACAK08
C	9	22.4	41.5	53	10	AM160055	AM160055 SWLACAK06
C	10	22.4	41.5	53	10	AM041922	AM041922 SWLACAK02
C	11	22.4	41.5	60	10	AM172242	AM172242 SWLACAK08
C	12	22.4	41.5	62	9	A1096287	A1096287 SWAMCACC24
C	13	22.4	41.5	62	10	AM159998	AM159998 SWLACAK05
C	14	22.4	41.5	64	10	AM159945	AM159945 SWLACAK04
C	15	22.4	41.5	66	10	AM172179	AM172179 SWLACAK07
C	16	22.4	41.5	68	9	A1218795	A1218795 SWOVARCAP
C	17	22.4	41.5	69	9	A1096196	A1096196 SWAMCACC26
C	18	22.4	41.5	70	9	AA273106	AA273106 SWMCA193
C	19	22.4	41.5	73	9	AA680645	AA680645 LMFYAM009
C	20	22.4	41.5	74	10	AM159913	AM159913 SWLACAK04
C	21	22.4	41.5	75	10	AM160023	AM160023 SWLACAK05
C	22	22.4	41.5	75	10	AM160023	AM160023 SWOVARCAP
C	23	22.4	41.5	76	10	AM160031	AM160031 SWLACAK06
C	24	22.4	41.5	76	10	AM160031	AM160031 SWOVARCAP
C	25	22.4	41.5	80	9	AJ494595	AJ494595 AJ494595
C	26	22.4	41.5	80	9	A1066878	A1066878 SWMCA143
C	27	22.4	41.5	91	9	AM203873	AM203873 SWMCA143
C	28	22.4	41.5	93	10	AM172121	AM172121 SWLACAK07
C	29	22.4	41.5	95	10	AM172121	AM172121 SWLACAK07
C	30	22.4	41.5	95	10	R29179	R29179 F1-287D 22
C	31	22.4	41.5	97	9	AM051907	AM051907 SWMCA143
C	32	22.4	41.5	97	9	AM051907	AM051907 SWMCA143
C	33	22.4	41.5	97	9	AM051907	AM051907 SWMCA143
C	34	22.4	41.5	98	10	AM041925	AM041925 SWLACAK06
C	35	22.4	41.5	98	10	AM160064	AM160064 SWLACAK06
C	36	22.4	41.5	100	9	A1239372	A1239372 SWOVARCAP
C	37	22.2	40.4	100	13	BM027537	BM027537 G17000102
C	38	21.8	40.4	89	14	N28043	N28043 EST000247 S
C	39	21.8	40.4	91	14	R29262	R29262 F1-382D 22
C	40	21.8	40.4	92	14	N28040	N28040 EST000177 S
C	41	21.8	40.4	95	9	A1353162	A1353162 zeh0113.s
C	42	21.8	40.4	95	9	A1353583	A1353583 zeh0701.s
C	43	21.8	40.4	96	9	A1616894	A1616894 zeh0783.
C	44	21.8	40.4	96	9	A1617314	A1617314 zeh01391.
C	45	21.8	40.4	96	10	AM455598	AM455598 zeh11725

ALIGNMENTS

RESULT 1	AJ282930	79 bp	mRNA	linear	EST 30-JUN-2000
LOCUS	4A3A-PIE1-R	Anopheles gambiae	immune competent	4A3A Anopheles	
DEFINITION	gambiae cDNA clone 4A3A-PIE1, mRNA sequence.				
ACCESSION	AJ282930				
VERSION	AJ282930.1	GI:6930809			
KEYWORDS	EST.				
SOURCE	African malaria mosquito.				
ORGANISM	Anopheles gambiae				
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.				
AUTHORS	1 (bases 1 to 79) Dimopoulos, G., Casavant, T.L., Chang, S., Scheetz, T., Roberts, C., Donohue, M., Schultz, J., Benes, V., Bork, P., Anstorge, W., Soares, M.B. and Kafatos, F.C.				
TITLE	Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)				
MEDLINE	20300950				
COMMENT	Contact: Dimopoulos G Fotis C. Kafatos Laboratory European Molecular Biology Laboratory Meyerhofstrasse 1, 69117 Heidelberg, Germany. Location/Qualifiers 1..79 /organism="Anopheles gambiae"				
FEATURES	source				

/strain="4A r/r"
 /db_xref="taxon:7165"
 /clone_lib="Anopheles gambiae immune competent 4A3a"
 /cell_line="Immune competent 4A3a"
 /lab_host="E. coli DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: EcoRI; Site 2: NotI; sequenced from forward priming site which reads from the 3' end of the cDNA. The 4A3a is a directionally cloned and normalized cDNA library that was constructed from the 4A3a cell line oligo-T primed cDNA according to: Bonaldo, Lennon & Soares (1996) : Normalization and Subtraction: Two approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."

BASE COUNT 26 a 16 c 18 g 18 t 1 others

ORIGIN
 Query Match 43.3%; Score 23.4; DB 9; Length 79;
 Best Local Similarity 96.0%; Pred. No. 1.2e+02;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 AATTATATACGACTCATATAGGGA 26
 ||||||||||||||||||||
 DB 28 AATTATATACGACTCATATAGGGA 52

RESULT 2
 LOCUS A1087772/c 75 bp mRNA linear EST 18-AUG-1998
 DEFINITION SMOVAMCA02F02SK Onchocerca volvulus adult male cDNA (SAM98MLW-OVAM
 A1087772) Onchocerca volvulus cDNA clone SMOVAMCA02F02 5', mRNA sequence.
 ACCESSION A1087772.1 GI:3426748
 VERSION EST.
 KEYWORDS Onchocerca volvulus.
 SOURCE Onchocerca volvulus.
 ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidae; Onchocercidae; Onchocerca.
 REFERENCE 1 (bases 1 to 75)
 AUTHORS Lizotte-Waniewski, M. and Williams, S.A.
 TITLE Genes expressed in adult male stage of Onchocerca volvulus
 JOURNAL Unpublished (1998)
 COMMENT Contact: Steven A. Williams
 Molecular Parasitology
 Smith College Department of Biological Sciences
 Department of Biological Sciences, Clark Science Center, Smith
 College, Northampton, MA, 01063, USA
 Tel: 4135853826
 Fax: 4135853786
 Email: genomesmith.edu
 Seq primer: pBluescript SK.
 Location/Qualifiers
 1.75
 /organism="Onchocerca volvulus"
 /db_xref="taxon:6282"
 /clone="SMOVAMCA02F02"
 /clone_lib="Onchocerca volvulus adult male cDNA (SAM98MLW-OVAM)"
 /sex="male"
 /dev_stage="adult"
 /lab_host="XLI-Blue MRF"
 /note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2: Kho I; Filarial nematode parasite of humans, six adult male worms of Onchocerca volvulus were isolated from converted patients and quick frozen. Adult male mRNA was transcribed to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 2 x 10⁵ independent recombinants and the average insert size is ~1100bp. The library was constructed by Michelle Lizotte-Waniewski with worms provided by Dr. Sara Lustigman. The library is available from Dr. Steven A. Williams, email: genomesmith.edu."

BASE COUNT 13 a 19 c 24 g 19 t

ORIGIN
 Query Match 43.0%; Score 23.2; DB 9; Length 75;
 Best Local Similarity 70.5%; Pred. No. 1.4e+02;
 Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Oy 2 AATTATATACGACTCATATAGGGA 45
 ||||||||||||||||||||
 DB 67 AATTATATACGACTCATATAGGGA 24

RESULT 3
 LOCUS A0797214/c 30 bp DNA linear GSS 26-JAN-2001
 DEFINITION RPCI-22-458D11-T7 RPCI-22 Mouse (129S6/SvEvTac) genomic library Mus
 musculus genomic clone RPCI-22-458D11-T7 similar to Catalase (Cat)
 gene; Mouse Chr 2.57, DNA sequence.
 ACCESSION A0797214
 VERSION A0797214.1 GI:5705683
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 30)
 AUTHORS Osoegawa, K., Tateo, M., Woon, P. Y., Frengen, E., Mammoser, A. G.,
 Catalanese, J. J., Hayashizaki, Y., and de Jong, P. J.
 TITLE Bacterial artificial chromosome libraries for mouse sequencing and
 JOURNAL functional analysis
 MEDLINE Genome Res. 10 (1), 116-128 (2000)
 COMMENT Contact: de Jong, P. J.
 Children's Hospital Oakland Research Institute
 747 Fifty Second Street, Oakland, CA 94609-1809, USA
 Tel: 510 450 7911
 Fax: 510 450 7924
 Email: pdejong@mail.cho.org
 BAC end sequences. For clone availability please contact Pieter de
 Jong (pdejong@mail.cho.org). BACPAC Resources WWW site:
 www.choi.org/bacpac
 Seq primer: T7
 Class: BAC ends.
 Location/Qualifiers
 1.30
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="RPCI-22-458D11-T7"
 /clone_lib="RPCI-22 Mouse (129S6/SvEvTac) genomic library"
 /sex="Female"
 /cell_type="Spleen"
 /note="Vector: pBAC3.6; BAC clones in E. coli DH10B"

BASE COUNT 6 a 8 c 7 g 9 t

ORIGIN
 Query Match 42.6%; Score 23; DB 17; Length 30;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 TAATACGACTCATATAGGGA 28
 ||||||||||||||||||||
 DB 24 TAATACGACTCATATAGGGA 2

RESULT 4
 LOCUS BH217910 69 bp DNA linear GSS 08-NOV-2001
 DEFINITION 1006061D02.2EL_x1 1006 - Rescueu Gtid G zea mays genomic, DNA
 sequence.
 ACCESSION BH217910
 VERSION BH217910.1 GI:16810050
 KEYWORDS GSS.
 SOURCE zea mays.
 ORGANISM zea mays

REFERENCE

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

AUTHORS

Malbot, V.

TITLE

Maize genomic sequences found using engineered Rescemu transposon

JOURNAL

Unpublished (2001)

COMMENT

Contact: Malbot, V.
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: malbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1006061 row: 21
Class: transposon-tagged.
Location/Qualifiers

FEATURES

source

1..69
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone.lib="1006 - Rescemu Grid G"
/tissue.type="leaf"
/dev.stage="adult"
/lab.host="DH10B"
/note="Organ: leaf; Vector: Rescemu (engineered from Bluescript backbone); Site.1: BamHI; Site.2: BglII; Rescemu is a 4.9 kb, modified maize mu transposon designed to allow plasmid rescue from total genomic DNA elements insert preferentially into transcription units. For more information on Rescemu, go to the web site 'www.zmld.laistate.edu' and follow the links for 'Rescemu'. Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT

16 a 18 c 21 g 14 t

ORIGIN

Query Match 42.6%; Score 23; DB 17; Length 69;
Best Local Similarity 83.9%; Pred. No. 1.5e+02;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY

6 TAAATGACGACTATAGGAGGAGGAGC 36

DB

2 TAAATGACGACTATAGGAGGAGGAGC 32

RESULT 5

AI353756 100 bp mRNA linear EST 04-JAN-1999

LOCUS

ze09040.seq.F zebrafish Embryonic Heart cDNA Library Danio rerio

DEFINITION

cDNA 5', mRNA sequence.

ACCESSION

AI353756 GI:4093909

VERSION

EST.

KEYWORDS

zebrafish.

SOURCE

Danio rerio

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes

AUTHORS

1 (bases 1 to 100)
Ton, C., Mably, J.D., Dempsey, A.A., Hwang, D.M., Fishman, M.C. and Liew

TITLE

Identification and Characterization of Expressed Sequence Tags from

JOURNAL

Unpublished (1999)
Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School

75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 6179750995
Email: ctlew@rics.bwh.harvard.edu

PCR Primers
FORWARD: 5' GCCAGGCTCGAATTAACCTCCTCAATAGG 3'
BACKWARD: 5' CCAGTGAATGTATATGCGACTACATATAGGCG 3'

Seq primer: 5' GAAATTAACCTCCTCAATAGG 3'.
Location/Qualifiers

FEATURES

source

1..100
/organism="Danio rerio"

/db_xref="taxon:7955"
/clone.lib="zebrafish Embryonic Heart cDNA Library"

/dev.stage="Embryonic day 3 post-fertilization"

/lab.host="E.coli XL1-Blue MRF"

/note="Organ: heart; Vector: Lambda ZAP Express; Site.1:

EcoRI; Site.2: XhoI; mRNA was purified from embryonic

zebrafish hearts (3 day post-fertilization). cDNA was

synthesized using a XhoI-oligo dT adaptor-primer. EcoRI

adaptors were ligated, followed by digestion with XhoI,

for directional cloning into pre-digested lambda ZAP

Express vector."

BASE COUNT

20 a 27 c 27 g 26 t

ORIGIN

Query Match 41.9%; Score 22.6; DB 9; Length 100;
Best Local Similarity 86.2%; Pred. No. 2.7e+02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY

2 AATTAATGACGACTATAGGAGGAGC 30

DB

98 AATGTAATGACGACTATAGGAGGAGC 70

RESULT 6

AI096189 46 bp mRNA linear EST 19-AUG-1998

LOCUS

SNAMCNC26D04SK Brugia malayi adult male cDNA (SNW94NL-BmAM) Brugia

DEFINITION

malayi cDNA clone SNAMCNC26D04 5', mRNA sequence.

ACCESSION

AI096189 GI:3445100

VERSION

EST.

KEYWORDS

Brugia malayi.

SOURCE

Brugia malayi.

ORGANISM

Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;

REFERENCE

Onchocercidae; Brugia.

AUTHORS

1 (bases 1 to 46)
Williams, S.A.

TITLE

Genes expressed in adult males of Brugia malayi

JOURNAL

Unpublished (1995)

COMMENT

Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu

FEATURES

source

1..46
/organism="Brugia malayi"

/strain="R5 labs"

/db_xref="taxon:6279"

/clone.lib="SNAMCNC26D04"

/lab.host="XLI-Blue MRF"

/note="Vector: lambda Unizap X; Site.1: EcoR I; Site.2:

Xho I; Lymphatic filarial nematode parasite of humans.

mRNA was prepared from adult males of Brugia malayi

isolated from jirds and converted to double stranded cDNA

using reverse transcriptase and oligo(dT) followed by

Rnase H and DNase I. The library had 4.6 x 10E6

independent recombinants and average insert size was 800 base pairs. The library was constructed by Noelle Ling. The library is available from Dr. S.A. Williams, email genome@smith.edu."

BASE COUNT 9 a 12 c 15 g 10 t

Query Match 41.5%; Score 22.4; DB 9; Length 46;
Best local similarity 72.5%; Pred. No. 2e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 6 TAATACGACTCACTATAGGAGACTCAGACCTGAGGCTC 45
|||||
DB 44 TAATACGACTCACTATAGGAGGCAATGGGTACCGGCCCC 5

RESULT 7

AM160061/c 50 bp mRNA linear EST 05-NOV-1999
LOCUS SW14CAK0605SK Brugia malayi L4 cDNA (SAM99MLM-Bml4) Brugia malayi
DEFINITION CDNA clone SW14CAK0605 5', mRNA sequence.
ACCESSION AM160061
VERSION AM160061.1 GI:6272090
KEYWORDS EST.
SOURCE Brugia malayi.
ORGANISM Brugia malayi.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.
1 (bases 1 to 50)
/db_xref="taxon:6279"
/clone="SW14CAK0605"
/dev_stage="larval stage four"
/lab_host="XLI-Blue MRF"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from L4s isolated from the peritoneal cavity of jirds and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 2.7 x 10⁵ independent recombinants and the average insert size is approx. 1050bp. The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr. S.A. Williams, email: genome@smith.edu

REFERENCE 1
AUTHORS Williams, S.A.
TITLE Genes expressed in fourth stage larvae of Brugia malayi
JOURNAL Unpublished (1999)
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
1..50

FEATURES
source

BASE COUNT 10 a 13 c 17 g 10 t

Query Match 41.5%; Score 22.4; DB 10; Length 50;
Best local similarity 72.5%; Pred. No. 2.1e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 6 TAATACGACTCACTATAGGAGACTCAGACCTGAGGCTC 45
|||||
DB 44 TAATACGACTCACTATAGGAGGCAATGGGTACCGGCCCC 5

RESULT 8
AM172194/c

LOCUS AM172194 50 bp mRNA linear EST 15-NOV-1999
DEFINITION SW14CAK08A08SK Brugia malayi L4 cDNA (SAM99MLM-Bml4) Brugia malayi
ACCESSION AM172194
VERSION AM172194
KEYWORDS EST.
SOURCE Brugia malayi.
ORGANISM Brugia malayi.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.
1 (bases 1 to 50)
/db_xref="taxon:6279"
/clone="SW14CAK08A08"
/dev_stage="larval stage four"
/lab_host="XLI-Blue MRF"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from L4s isolated from the peritoneal cavity of jirds and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 2.7 x 10⁵ independent recombinants and the average insert size is approx. 1050bp. The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr. S.A. Williams, email: genome@smith.edu

REFERENCE 1
AUTHORS Williams, S.A.
TITLE Genes expressed in fourth stage larvae of Brugia malayi
JOURNAL Unpublished (1999)
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
1..50

FEATURES

BASE COUNT 9 a 14 c 17 g 10 t

Query Match 41.5%; Score 22.4; DB 10; Length 50;
Best local similarity 72.5%; Pred. No. 2.1e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 6 TAATACGACTCACTATAGGAGACTCAGACCTGAGGCTC 45
|||||
DB 44 TAATACGACTCACTATAGGAGGCAATGGGTACCGGCCCC 5

RESULT 9

AM160055/c 53 bp mRNA linear EST 05-NOV-1999
LOCUS SW14CAK0605SK Brugia malayi L4 cDNA (SAM99MLM-Bml4) Brugia malayi
DEFINITION CDNA clone SW14CAK0605 5', mRNA sequence.
ACCESSION AM160055
VERSION AM160055.1 GI:6272084
KEYWORDS EST.
SOURCE Brugia malayi.
ORGANISM Brugia malayi.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.
1 (bases 1 to 53)
/db_xref="taxon:6279"
/clone="SW14CAK0605"
/dev_stage="larval stage four"
/lab_host="XLI-Blue MRF"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from L4s isolated from the peritoneal cavity of jirds and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 2.7 x 10⁵ independent recombinants and the average insert size is approx. 1050bp. The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr. S.A. Williams, email: genome@smith.edu

REFERENCE 1
AUTHORS Williams, S.A.
TITLE Genes expressed in fourth stage larvae of Brugia malayi
JOURNAL Unpublished (1999)
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith

College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genomesmith.edu

Seg primer: pBluescript SK.
Location/Qualifiers

FEATURES

source

1..53

/organism="Brugia malayi"

/db_xref="taxon:6279"

/clone="SML4CAK06D05"

/clone_1lb="Brugia malayi L4 CDNA (SAM99MLM-Bml4)"

/dev_stage="larval stage four"

/lab_host="X11-Blue MRF"

/note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from L4s isolated from the peritoneal cavity of birds and converted to double-stranded cDNA using reverse transcriptase and oligo(dT), followed by RNase H and DNA pol I. The library has 2.7 x 10⁵ independent recombinants and the average insert size is approx. 1050bp. The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr. S.A. Williams, email: genomesmith.edu."

BASE COUNT

12 a 14 c 17 g 10 t

Query Match 41.5%; Score 22.4; DB 10; Length 53;
Best Local Similarity 72.5%; Pred. No. 2.2e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 6 TAATAGACTCACTATAGGAGACGACACCTGAGGCTC 45
|||||
Db 51 TAATAGACTCACTATAGGAGACGATTTGGTACCGGCCCC 12

RESULT 10

AM041922/c

LOCUS SML4CAK02D06SK Brugia malayi L4 CDNA (SAM99MLM-Bml4) Brugia malayi
DEFINITION CDNA clone SML4CAK02D06 5', mRNA sequence.
ACCESSION AM041922
VERSION AM041922.1 GI:5900822
KEYWORDS EST.
SOURCE Brugia malayi.
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.
REFERENCE 1 (bases 1 to 59)
Williams, S.A.
Genes expressed in fourth stage larvae of Brugia malayi
Unpublished (1999)
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genomesmith.edu
Seg primer: pBluescript SK.
Location/Qualifiers
1..59

FEATURES

source

/organism="Brugia malayi"

/db_xref="taxon:6279"

/clone="SML4CAK02D06"

/clone_1lb="Brugia malayi L4 CDNA (SAM99MLM-Bml4)"

/dev_stage="larval stage four"

/lab_host="X11-Blue MRF"

/note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from L4s isolated from the peritoneal cavity of birds and converted to double-stranded cDNA using reverse transcriptase and oligo(dT), followed by RNase H and DNA pol I. The library has 2.7 x 10⁵ independent recombinants and the average insert size is approx. 1050bp. The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr. S.A. Williams, email: genomesmith.edu."

BASE COUNT

9 a 20 c 19 g 12 t

Query Match 41.5%; Score 22.4; DB 10; Length 60;
Best Local Similarity 72.5%; Pred. No. 2.3e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 6 TAATAGACTCACTATAGGAGACGACACCTGAGGCTC 45
|||||
Db 54 TAATAGACTCACTATAGGAGACGATTTGGTACCGGCCCC 15

RESULT 12

AM172242/c

LOCUS SML4CAK06D06SK Brugia malayi L4 CDNA (SAM99MLM-Bml4) Brugia malayi
DEFINITION CDNA clone SML4CAK06D06 5', mRNA sequence.
ACCESSION AM172242
VERSION AM172242.1 GI:6432038
KEYWORDS EST.
SOURCE Brugia malayi.
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.
REFERENCE 1 (bases 1 to 60)
Williams, S.A.
Genes expressed in fourth stage larvae of Brugia malayi
Unpublished (1999)
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genomesmith.edu
Seg primer: pBluescript SK.
Location/Qualifiers
1..60

FEATURES

source

/organism="Brugia malayi"

/db_xref="taxon:6279"

/clone="SML4CAK06D06"

/clone_1lb="Brugia malayi L4 CDNA (SAM99MLM-Bml4)"

/dev_stage="larval stage four"

/lab_host="X11-Blue MRF"

/note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from L4s isolated from the peritoneal cavity of birds and converted to double-stranded cDNA using reverse transcriptase and oligo(dT), followed by RNase H and DNA pol I. The library has 2.7 x 10⁵ independent recombinants and the average insert size is approx. 1050bp. The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr. S.A. Williams, email: genomesmith.edu."

BASE COUNT

9 a 20 c 19 g 12 t

Query Match 41.5%; Score 22.4; DB 10; Length 59;
Best Local Similarity 72.5%; Pred. No. 2.2e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 6 TAATAGACTCACTATAGGAGACGACACCTGAGGCTC 45
|||||
Db 50 TAATAGACTCACTATAGGAGACGATTTGGTACCGGCCCC 11

AI096267/c
 LOCUS AI096267 62 bp mRNA linear EST 19-AUG-1998
 DEFINITION SWAMCACC24C05SK Brugia malayi adult male cDNA (SAM94NL-BmAM) Brugia
 malayi cDNA clone SWAMCACC24C05 5', mRNA sequence.
 ACCESSION AI096267
 VERSION AI096267.1 GI:3445056
 KEYWORDS EST.
 SOURCE Brugia malayi.
 ORGANISM Brugia malayi.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 Onchocercidae; Brugia.
 REFERENCE 1 (bases 1 to 62)
 AUTHORS Williams, S.A.
 TITLE Genes expressed in adult males of Brugia malayi
 JOURNAL Unpublished (1995)
 COMMENT Contact: Steven A. Williams
 Molecular Parasitology
 Smith College Department of Biological Sciences
 Department of Biological Sciences, Clark Science Center, Smith
 College, Northampton, MA, 01063, USA
 Tel: 4135853826
 Fax: 4135853786
 Email: genome@smith.edu
 Seq primer: Bluescript SK.
 Location/Qualifiers
 1..62
 /organism="Brugia malayi"
 /strain="TRS labs"
 /db_xref="taxon:6279"
 /clone="SWAMCACC24C05"
 /clone_1lb="Brugia malayi adult male cDNA (SAM94NL-BmAM)"
 /lab_host="XLI-Blue MRF"
 /note="Vector: lambda UniZAP XR; Site 1: EcoR I; Site 2:
 Xho I; Lymphatic filarial nematode parasite of humans.
 mRNA was prepared from adult males of Brugia malayi
 isolated from jirds and converted to double stranded cDNA
 using reverse transcriptase and oligo(dT) followed by
 RNase H and DNAPol I. The library had 4.6 x 10⁶
 independent recombinants and average insert size was 800
 base pairs. The library was constructed by Noelle Ling.
 The library is available from Dr. S.A. Williams, email
 genome@smith.edu."

BASE COUNT 15 a 15 c 19 g 13 t
 ORIGIN
 Query Match 41.5%; Score 22.4; DB 9; Length 62;
 Best Local Similarity 72.5%; Pred. No. 2.4e+02;
 Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 Oy 6 TAATACGACTCATTAGGAGACTCAGACCCCTGAGGCTC 45
 |||||||||||||||||||
 Db 60 TAATACGACTCATTAGGAGACTGATGGGGAATGGTACCGGGCCCC 21

RESULT 13
 AM159998/c 63 bp mRNA linear EST 05-NOV-1999
 LOCUS AM159998
 DEFINITION SWL4CAK05E03SK Brugia malayi l4 cDNA (SAM99MLW-Bml4) Brugia malayi
 cDNA clone SWL4CAK05E03 5', mRNA sequence.
 ACCESSION AM159998
 VERSION AM159998.1 GI:6272027
 KEYWORDS EST.
 SOURCE Brugia malayi.
 ORGANISM Brugia malayi.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 Onchocercidae; Brugia.
 REFERENCE 1 (bases 1 to 63)
 AUTHORS Williams, S.A.
 TITLE Genes expressed in fourth stage larvae of Brugia malayi
 JOURNAL Unpublished (1999)
 COMMENT Contact: Steven A. Williams
 Molecular Parasitology
 Smith College Department of Biological Sciences

Department of Biological Sciences, Clark Science Center, Smith
 College, Northampton, MA, 01063, USA
 Tel: 4135853826
 Fax: 4135853786
 Email: genome@smith.edu
 Seq primer: Bluescript SK.
 Location/Qualifiers
 1..63
 /organism="Brugia malayi"
 /db_xref="taxon:6279"
 /clone="SWL4CAK05E03"
 /clone_1lb="Brugia malayi l4 cDNA (SAM99MLW-Bml4)"
 /dev_stage="larval stage four"
 /lab_host="XLI-Blue MRF"
 /note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:
 Xho I; Lymphatic filarial nematode parasite of humans.
 mRNA was prepared from l4s isolated from the peritoneal
 cavity of jirds and converted to double-stranded cDNA
 using reverse transcriptase and oligo(dT) followed by
 RNase H and DNA pol I. The library has 2.7 x 10⁵
 independent recombinants and the average insert size is
 approx. 1050bp. The library was constructed by Michelle
 Lizotte-Waniewski. The library is available from Dr. S.A.
 Williams, email: genome@smith.edu."

BASE COUNT 15 a 15 c 20 g 13 t
 ORIGIN
 Query Match 41.5%; Score 22.4; DB 10; Length 63;
 Best Local Similarity 72.5%; Pred. No. 2.4e+02;
 Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 Oy 6 TAATACGACTCATTAGGAGACTCAGACCCCTGAGGCTC 45
 |||||||||||||||||||
 Db 60 TAATACGACTCATTAGGAGACTGATGGGGAATGGTACCGGGCCCC 21

RESULT 14
 AM159945/c 64 bp mRNA linear EST 05-NOV-1999
 LOCUS AM159945
 DEFINITION SWL4CAK04F11SK Brugia malayi l4 cDNA (SAM99MLW-Bml4) Brugia malayi
 cDNA clone SWL4CAK04F11 5', mRNA sequence.
 ACCESSION AM159945
 VERSION AM159945.1 GI:6271974
 KEYWORDS EST.
 SOURCE Brugia malayi.
 ORGANISM Brugia malayi.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 Onchocercidae; Brugia.
 REFERENCE 1 (bases 1 to 64)
 AUTHORS Williams, S.A.
 TITLE Genes expressed in fourth stage larvae of Brugia malayi
 JOURNAL Unpublished (1999)
 COMMENT Contact: Steven A. Williams
 Molecular Parasitology
 Smith College Department of Biological Sciences
 Department of Biological Sciences, Clark Science Center, Smith
 College, Northampton, MA, 01063, USA
 Tel: 4135853826
 Fax: 4135853786
 Email: genome@smith.edu
 Seq primer: Bluescript SK.
 Location/Qualifiers
 1..64
 /organism="Brugia malayi"
 /db_xref="taxon:6279"
 /clone="SWL4CAK04F11"
 /clone_1lb="Brugia malayi l4 cDNA (SAM99MLW-Bml4)"
 /dev_stage="larval stage four"
 /lab_host="XLI-Blue MRF"
 /note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:
 Xho I; Lymphatic filarial nematode parasite of humans.
 mRNA was prepared from l4s isolated from the peritoneal
 cavity of jirds and converted to double-stranded cDNA

using reverse transcriptase and oligo(dT), followed by RNase H and DNA pol. I. The library has 2.7 x 10⁵ independent recombinants and the average insert size is approx. 1500bp. The library was constructed by Michelle Licotte-Mandlowski. The library is available from Dr. S.A. Williams, email: genome@anal.smith.edu."

15 a	15 c	21 g
------	------	------

13 f

Query Match	41.5%	Score 22.4;	DB 10;	Length 64;
Best Local Similarity	72.5%;	Pred. No. 2.4e+02;		
Matches 29; Conservative	0;	Mismatches 11;	Indels 0;	Gaps 0;

Qy 6 TAATACGACTCATTAGGAGACTCAGACCCCTAGGCTC 45
 |||||
 Db 62 TAATACGACTCATTAGGAGCGAATTGGTATCCGGGCC 23

RESULT 15					
AM172179/c					
LOCUS					
DEFINITION					
AM172179	66 bp	mRNA	linear	EST 15-NOV-1998	
SMILCA07G11SK	Brugia malayi L4 CDNA (SANGMUTW-Bml4)				Brugia malayi
NCBI accession: F070711.5; mRNA sequence					

ACCESSION	AW172179	GI:6431975
VERSION	AW172179.1	
KEYWORDS	EST.	
SOURCE	Brugia malayi.	
ORGANISM	Brugia malayi	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 66)	Williams, S. A.	Genes expressed in fourth stage larvae of <i>Brugia malaya</i>	Unpublished (1999)	Contact: Steven A. Williams

Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135833826
Fax: 4135833786

Email: genome@smith.edu
 Seq primer: bluescript SK.
 Location/Qualifiers
 1. . 66
 * source
 /organism="Brugia r

```

/organism="Brugia malayi"
/db_xref="taxon:6279"
/clone.lib="Brugia malayi L4 CDNA (SAM99MLW-BmtL4)"
/db_stages="larval stage four"
/seq_host="Y11-nlue Mpp7"

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/note=vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
 Xho I; Lymphatic filarial nematode parasite of humans.
 mRNA was prepared from l4s isolated from the peritoneal
 cavity of jirds and converted to double-stranded cDNA
 using reverse transcriptase and oligo(dT) followed by

RNAse H and DNA pol I. The library has 2.7 x 10⁵ independent recombinants and the average insert size is approx. 1050bp. The library was constructed by Michelle Litotze-Waniewski. The library is available from Dr. S.A. Williams, email: genomel@smith.edu."

BASE COUNT	17 a	15 c	21 g	13 t
ORIGIN				

Query Match	41.58;	Score 22.4;	DB 10;	Length 66;
Best Local Similarity	72.58;	Pred. No. 2.5e+02;		
Matches 29; Conservative	0;	Mismatches 11;	Indels 0;	Gaps 0;

OY 6 TATACGACTCACTATATGGGAGACTGAGACCCGAGGGTC 45
 |||||
 DB 63 TATACGACTCACTATATGGGCGAATTGGGTACCGGGCCCC 24

Search completed: December 21, 2002, 19:25:02
Job time : 1673.08 secs

100

Mon Dec 23 08:48:06 2002

us-09-121-239-5.rst

Page 1

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:20:00 ; Search time 739.592 Seconds
(without alignments)
525.549 Million cell updates/sec

Title: US-09-121-239-5
Perfect score: 24
Sequence: 1 GACCACTGCTGTGTAACCTCA 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mem:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	66.7	50	9	AU104202
2	15.8	65.8	100	12	BE767056
3	15	60.5	97	13	BM139696
4	14.6	60.8	58	14	N23403
5	14.6	60.8	99	10	BP057655
6	14.4	60.0	95	17	BH857328

7	14.2	59.2	52	9	AT938077	sc41f11.x
8	14.2	59.2	69	17	AZ767038	IM0566B01
9	14	58.3	68	14	B0539757	PTAM0065
10	14	58.3	73	12	BG820653	602782957
11	14	58.3	75	17	AL767207	Arabidops
12	14	58.3	90	17	AZ584799	IM0389M11
13	13.8	57.5	48	10	AV844988	AV844988
14	13.8	57.5	48	17	BE322561	NE0060D51
15	13.8	57.5	75	10	BH848620	SALK_0686
16	13.6	56.7	73	10	AM241397	AM241397
17	13.6	56.7	73	10	AM243548	km40f09.x
18	13.6	56.7	94	17	BH216327	1006041H0
19	13.4	55.8	58	9	AT856074	sc31c06.x
20	13.4	55.8	81	10	BE323827	NF008F03P
21	13.4	55.8	82	17	BH218003	BH218003
22	13.4	55.8	88	9	AA952812	SMTECEA00
23	13.4	55.8	92	14	T63384	vc07b12.r1
24	13.4	55.8	92	17	AZ483748	IM0309M09
25	13.4	55.8	97	13	B1400183	MI-P-AV1-
26	13.2	55.0	40	9	A1180630	uc67f04.x
27	13.2	55.0	57	9	A0255880	A0255880
28	13.2	55.0	60	17	B03761	csRL-186F7-
29	13.2	55.0	63	17	AQ254801	EP(2)0574
30	13.2	55.0	86	9	AA682708	z187a06.s
31	13.2	55.0	90	10	AM712002	f8a08ne.r
32	13.2	55.0	92	14	BQ763409	EBF002-SQ
33	13.2	55.0	94	9	AA647390	vc77c09.s
34	13.2	55.0	99	12	BF224750	uz10e03.x
35	13.2	55.0	99	14	T73709	W96947
36	13	54.2	70	14	W96947	mt88c03.r1
37	13	54.2	76	17	BH887468	LB00557a.
38	13	54.2	78	17	BH886048	LA00557a.
39	13	54.2	81	17	AZ916566	Ps1-7.f1
40	13	54.2	82	9	AA562265	v13404.r
41	13	54.2	84	17	BH759199	KG00155-3
42	13	54.2	87	13	B1493713	d104f06.
43	13	54.2	87	17	AZ495829	IM0331U19
44	13	54.2	88	17	BH626218	1007112B0
45	13	54.2	90	17	BH893996	3526_1.27

ALIGNMENTS

RESULT 1
LOCUS AU104202 50 bp mRNA linear EST 30-ANG-2001
DEFINITION AU104202 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP05745, mRNA sequence.
ACCESSION AU104202
VERSION AU104202.1 GI:13553723
KEYWORDS
SOURCE
ORGANISM
human.
REFERENCE
AUTHORS
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
1 (bases 1 to 50)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE
JOURNAL
MEDLINE
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and Characterization of a Full Length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers

FEATURES

```

source
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP05743"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated u937 cells"
BASE COUNT
17 a 14 c 10 g 9 t
ORIGIN

Query Match
Best Local Similarity 66.7%; Score 16; DB 9; Length 50;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 GACCAACTGCTGTGTAACCTCA 24
1 ||||| ||||| |||||
Db 7 GCCCAAGCGTGTGTAACCTCA 30

RESULT 2
BE767056 100 bp mRNA linear EST 19-SEP-2000
LOCUS RC4-NT0115-180500-011-c06 NT0115 Homo sapiens cDNA, mRNA sequence.
DEFINITION BE767056
ACCESSION BE767056.1 GI:10196980
VERSION BE767056.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 100)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
PROC. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL MEDLINE
20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=622-RC4-NT0115-180
500-011-c06&ts=2000-05-18&ta=1)
Seq primer: puc 18 forward
High quality sequence stop: 100.
Location/Qualifiers
1. .100
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT0115"
/dev_stage="Adult"
/note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT
26 a 27 c 23 g 24 t
ORIGIN

Query Match
Best Local Similarity 65.8%; Score 15.8; DB 12; Length 100;
Matches 89.5%; Pred. NO. 4e+03;

FEATURES
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1. .100
/organism="Glycine max"
/cultivar="PI 437654"
/db_xref="taxon:3847"
/clone="Gm-40-7A"
/dev_stage="10 hours after soybean cyst nematode's
infection"
/note="Organ: Root; Vector: pGEM-T.; Prepared by
suppression subtractive hybridization using root mRNA, 10
hours after soybean cyst nematode's infection as a tester,
and the non-infected root mRNA as a driver."
BASE COUNT
28 a 20 c 26 g 23 t
ORIGIN

Query Match
Best Local Similarity 62.5%; Score 15; DB 13; Length 97;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 2 ACCAAGCTGCTGTGTAACCTCA 24
1 ||||| ||||| |||||
Db 62 ACCAATCTCTGTGTAACCTCA 40

RESULT 4
N23403 58 bp mRNA linear EST 28-DEC-1995
LOCUS yx83h12.s1 Soares melanocyte ZNDHM Homo sapiens cDNA clone
DEFINITION IMAGE:268391.3' similar to SP:SI6967; NADH DEHYDROGENASE ;,
N23403
ACCESSION N23403
VERSION N23403.1 GI:1137553
KEYWORDS EST.

```

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Riklin, L., Rohlfing, T., Soares, M., Ten, F., Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.
TITLE The Mashu-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson R.
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL.
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Insert Length: 728 Std Error: 0.00
Seq primer: m3 40 forward
High quality sequence stop: 1.
Location/Qualifiers
1..58
/organism="Homo sapiens"
/db_xref="GDB:387803"
/db_xref="taxon:9606"
/clone="IMAGE:268391"
/clone_id="Soares melanocyte 2NBHM"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT73D (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5', TGTTACCACTCGTGTGTGAACCTC 3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."

BASE COUNT 16 a 11 c 9 g 19 t 3 others
ORIGIN
Query Match 60.8%; Score 14.6; DB 14; Length 58;
Best Local Similarity 73.9%; Pred. No. 1.2e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 GACCACTCGTGTGTGAACCTC 23
DB 49 GACNANNTGGCTTGAATTC 27
|||||
|||||

RESULT 5
LOCUS BE057655 99 bp mRNA linear EST 03-DEC-2001
DEFINITION sn05c12.y1 Gm-c1015 glycine max cDNA clone GENOME SYSTEMS CLONE ID:
ACCESSION BE057655
VERSION BE057655.1 GI:8402021
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 99)
AUTHORS Shoemaker, R., Kelm, P., Vodkin, L., Eipelting, J., Corvelli, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., Mccann, R., Waterston, R., and Wilson, R.
TITLE Public Soybean EST Project
JOURNAL Unpublished (1999)
COMMENT Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccuteresgen.com
Seq primer: 40RP from Gibco.
Location/Qualifiers
1..99
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1015-8687"
/clone_id="Gm-c1015"
/tissue_type="Mature flowers, field grown plants"
/lab_host="X110-Gold"
/note="Vector: pBluescript II Xr; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from mature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II Xr cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into X110-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Eipelting."

BASE COUNT 38 a 18 c 18 g 25 t
ORIGIN
Query Match 60.8%; Score 14.6; DB 10; Length 99;
Best Local Similarity 81.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 ACCAAGCTGCTGTGAACCTC 22
DB 46 ACCAAGCTGCTGTGAATTC 66
|||||
|||||

RESULT 6
LOCUS BH857328 95 bp DNA linear GSS 08-JUL-2002
DEFINITION SALK_076431.39.10.x Arabidopsis thaliana JDNA insertion lines
ACCESSION BH857328
VERSION BH857328.1 GI:21708108
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 95)
AUTHORS Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadgil, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Preditsis, L., Shinn, P., Zimmermann, J., and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL
COMMENT

Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu
This is single pass sequence recovered from the left border of
TDNA.

FEATURES
Source

Class: TDNA tagged.
Location/Qualifiers
1..95
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_076431.39.10.X"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at <http://signal.salk.edu/tdna-protocols.html>"
BASE COUNT 27 a 14 c 21 g 33 t
ORIGIN

Query Match 60.0%; Score 14.4; DB 17; Length 95;
Best Local Similarity 75.0%; Pred. No. 1.7e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Gy 1 GACCACTCGTGTGTAACCTCA 24
Db 70 CTCGACCCGGGATGTAACCTCA 93

RESULT 7 52 bp mRNA linear EST 30-NOV-2001
A1938077
LOCUS sc41f11.x1 Gm-cl014 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
DEFINITION Gm-cl014-1702 3' similar to TR:064505 064505 PUTATIVE SER/THR
ACCESSION A1938077
VERSION A1938077
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolae;
Glycine.
1 (bases 1 to 52)

REFERENCE
AUTHORS Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna
A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wille, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schuck
R., Riltter, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann
R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R./Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu

TITLE
JOURNAL
COMMENT Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand This clone is
available through: Resgen, Invitrogen Corp. 2130 South Memorial
Parkway Huntville, AL 35801 For further information call: (800
)-533-4363 or contact via email: ccu@resgen.com

FEATURES
Source

Seq primer: primer name ambiguous
High quality sequence stop: 1.
Location/Qualifiers
1..52

/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl014-1702"
/clone_id="Gm-cl014"
/tissue_type="leaves, 2-3 week old seedlings, greenhouse
grown"
/lab_host="DH10B"
/note="Vector: pT73Pac (PT73, Pharmacia); Site 1: EcoRI;
Site 2: HindIII. This cDNA library was constructed from
mRNA isolated from leaves of 2-3 week old greenhouse grown
plants. Complementary DNA was synthesized from mRNA using
a 3' anchored poly (dT) primer. EcoRI adapters were
ligated to the blunt-ended cDNA fragments followed by
digestion with EcoRI and HindIII. The cDNA fragments were
directionally cloned into the EcoRI-HindIII restriction
site of the PT73-Pac vector. The ligated cDNA fragments
were transformed into DH10B host cells (Gibco BRL). This
library was constructed by Dr. Randy Shoemaker and Dr.
John Erpelting."

BASE COUNT 14 a 10 c 10 g 18 t
ORIGIN
Query Match 59.2%; Score 14.2; DB 9; Length 52;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Gy 1 GACCACTCGTGTGTAACCTCA 19
Db 28 GACCACTCGTGTGTAACCTCA 46

RESULT 8 69 bp DNA linear GSS 16-FEB-2001
A2767038
LOCUS 1M056B01F Mouse 10kb plasmid UUCGM library Mus musculus genomic
DEFINITION clone UUCGM1M056B01 F, DNA sequence.
ACCESSION A2767038
VERSION A2767038
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 69)

REFERENCE
AUTHORS Dunn, D., Koyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0566 row: B column: 01
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 69.

FEATURES
Source

Location/Qualifiers
1..69
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"

University of Utah Genome Center
University of Utah

5-705-1113

Rm. 308, Biomedical Polymers Research Bldg., 220 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0389 row: M column: 11
Seq primer: CACACAGGAAACGCTATGACC
Class: Plasmid ends
High quality sequence stop: 90.
Location/Qualifiers
1. 90
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0389M11"
/clone_11b="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-rephased with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g1147321149b1AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

30 a 19 c 11 g 30 t

ch 58.3%; Score 14; DB 17; Length 90;
11 Similarity 77.3%; Pred. No. 2.6e+04;
17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CCAACTCGTGTGTGAACCTCCA 24
111 111111111 11
CCAAAGAGTGGGTGAACCTACA 49

AV844988 48 bp mRNA EST 08-NOV-2001
AV844988 Nori Satoh unpublished cDNA library; cleavage stage embryo
Ciona intestinalis cDNA clone rc1c109f08 3', mRNA sequence.
AV844988.1 GI:16822964
EST.
Ciona intestinalis.
Ciona intestinalis
Ektaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterozona;
Phlebobranchia; Clonidae; Ciona.
1 (bases 1 to 48)
Satoh,N., Satou,Y., Kohara,Y. and Shin-I,T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

```

FEATURES
  source
    Location/Qualifiers
      1..48
        /organism="Clona intestinalis"
        /db_xref="taxon:7719"
        /clone="rcic109f08"
        /clone_lib="Nori Satoh unpublished cDNA library, cleavage
        stage embryo"
        /tissue_type="whole animal"
        /dev_stage="cleavage stage embryo"
        /note="Vector: pBluescript SK"
BASE COUNT      8 a      11 c      18 g      9 t      2 others
ORIGIN
Query Match      57.5%; Score 13.8; DB 10; Length 48;
Best Local Similarity 88.2%; Pred. No. 2.5e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 CTCGTGTGTAACCTCC 23
Db 3 CTCGTGTGTAACCTCC 19

RESULT 14
LOCUS      BE322561
DEFINITION NP006D05IN1F1043 Insect herbivory Medicago truncatula cDNA clone
VERSION    BE322561
KEYWORDS   EST.
SOURCE     Medicago truncatula
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
REFERENCE  1 (bases 1 to 75)
AUTHORS   Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores
          , H.R., Inman, J.T., Weller, J.W., and May, G.D.
TITLE      Expressed Sequence Tags from the Samuel Roberts Noble Foundation
          Medicago truncatula insect herbivory library
JOURNAL    Unpublished (2000)
COMMENT    On Jul 14, 2000 this sequence version replaced gi:9196338.
          Contact: Korth K
          Dept. of Plant Pathology
          University of Arkansas
          217 Plant Science Building, Fayetteville, AR 72701, USA
          Tel.: 501 575 5191
          Fax: 501 575 7601
          Email: korth@comp.uark.edu
          Medicago Genome Initiative accession: MGI:S:25300
          Insert Length: 910 Std Error: 0.00
          Plate: 006 row: D column: 05
          Seq primer: TCACACAGGAAACGCTATGAC.
          Location/Qualifiers
            1..75
              /organism="Medicago truncatula"
              /db_xref="taxon:3880"
              /clone="NF006D05IN"
              /clone_lib="Insect herbivory"
              /tissue_type="local and systemic leaves"
              /dev_stage="mature"
              /note="Vector: Lambda zap; Library was produced from fully
              expanded M. truncatula leaves of plants fed upon by
              Spodoptera exigua (beet armyworm) for 24 hours. Systemic
              (undamaged leaves from injured plants) and wounded leaves
              were harvested and pooled."
BASE COUNT      24 a      18 c      14 g      19 t
ORIGIN
Query Match      57.5%; Score 13.8; DB 10; Length 75;
Best Local Similarity 88.2%; Pred. No. 3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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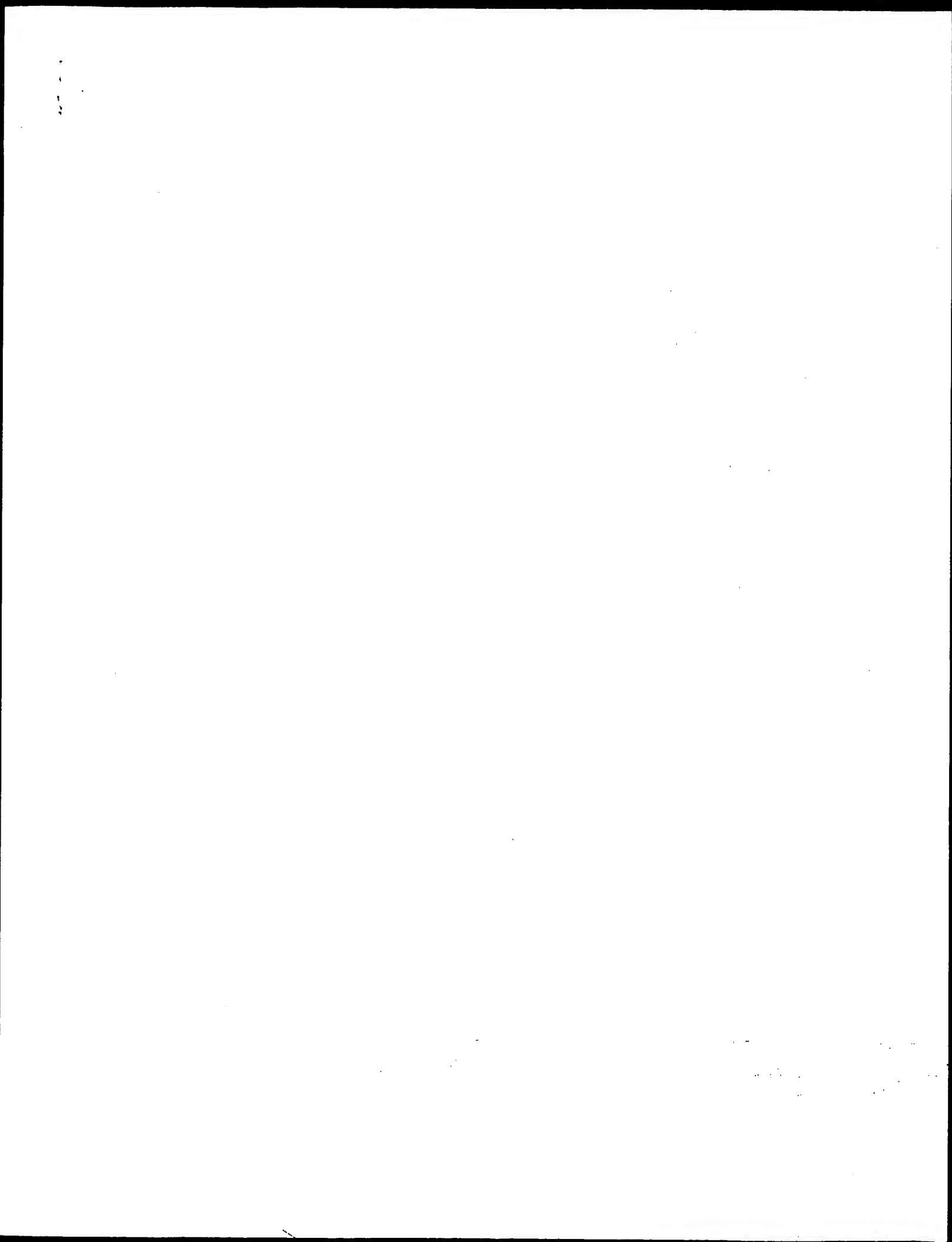
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Qy 8 TCGTGTGTAACCTCCA 24
Db 48 TCGTGTGTAACCTCCA 64

RESULT 15
LOCUS      BH848620
DEFINITION BH848620 20.30 x Arabidopsis thaliana TDNA insertion lines
          Arabidopsis thaliana genomic clone SALK_068609.20.30.x, DNA
          sequence.
          70 bp
          DNA
          linear
          GSS
          SALK_068609.20.30.x Arabidopsis thaliana TDNA insertion lines
          Arabidopsis thaliana genomic clone SALK_068609.20.30.x, DNA
          sequence.
ACCESSION   BH848620.1 GI:21419491
VERSION     BH848620.1
KEYWORDS    t3ale cress.
SOURCE      Arabidopsis thaliana
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 70)
AUTHORS     Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadriab
          , C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,
          Zimmerman, J., and Ecker, J.R.
TITLE       A Sequence-Indexed Library of Insertion Mutations in the
          Arabidopsis Genome
JOURNAL     Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
          Salk Institute Genomic Analysis Laboratory (SIGAL)
          The Salk Institute for Biological Studies
          10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
          Tel: 858 453 4100 x1752
          Fax: 858 558 6379
          Email: ecker@salk.edu
          This is single pass sequence recovered from the left border of
          TDNA. This sequence lies within an annotated intron of At3g50700.
          Class: TDNA tagged.
          Location/Qualifiers
            1..70
              /organism="Arabidopsis thaliana"
              /strain="Columbia 0"
              /db_xref="taxon:3702"
              /clone="SALK_068609.20.30.x"
              /clone_lib="Arabidopsis thaliana TDNA insertion lines"
              /note="PCR was performed on Arabidopsis thaliana lines
              each of which contains one or more TDNA insertion
              elements. The resultant fragment for each line was
              directly sequenced to determine the genomic sequence at
              the site of insertion. Details of the protocols used can
              be found at http://signal.salk.edu/tdna\_protocols.html"
BASE COUNT      27 a      20 c      7 g      16 t
ORIGIN
Query Match      56.7%; Score 13.6; DB 17; Length 70;
Best Local Similarity 80.0%; Pred. No. 3.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 5 AACTCGTGTGTAACCTCCA 24
Db 41 AATCGTATTAAGAACTCCA 60

```

Search completed: December 21, 2002, 19:25:16
 Job time : 753.592 secs



Mon Dec 23 08:48:08 2002

us-09-121-239-9.fst

Page 1

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:20:00 ; Search time 770.408 Seconds
(without alignments)
525.549 Million cell updates/sec

Title: US-09-121-239-9

Perfect score: 25
Sequence: 1 GACGTCCACAGCATTCGCGTACGC 25

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hnc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hnc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estlum:*
16: em_estlom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pla:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	16.6	66.4	70	9	AI216035	q10e11.x	AI216035 q10e11.x
2	15.2	60.8	88	13	BJ059813	BJ059813	BJ059813 BJ059813
3	15	60.0	88	9	AI883598	fc66912.y	AI883598 fc66912.y
4	14.8	59.2	100	9	AI006829	ua74e03.r	AI006829 ua74e03.r
5	14.4	57.6	54	12	BC020892	dl16h09.x	BC020892 dl16h09.x
6	14.4	57.6	78	9	AA999832	cv04e02.s	AA999832 cv04e02.s

C	7	14.2	56.8	28	17	AZ483948	AZ483948 1M0309119
C	8	14.2	56.8	80	13	BI736494	BI736494 603360142
C	9	14.2	56.8	90	17	AZ474370	AZ474370 1M0290123
C	10	14.2	56.8	94	9	AA622040	AA622040 ng23c02.s
C	11	14.2	56.8	62	17	TA271C040	TA271C040
C	12	14.2	56.0	64	17	CNS03C5U	AL237387 Tetradon
C	13	14.2	56.0	64	17	AM423872	AM423872 Tetradon
C	14	14.2	56.0	78	17	HSNG26D02	X88221 H.sapiens D
C	15	14.2	56.0	88	17	HSNG26D02	AA572309 vl52909.r
C	16	14.2	56.0	90	9	AA572309	AA572309 2M0243J09
C	17	13.8	55.2	96	17	AZ970505	AZ970505 1007088H0
C	18	13.8	55.2	57	17	BH630515	BH630515 1007088H0
C	19	13.8	55.2	63	17	AZ310562	AZ310562 1M0025003
C	20	13.6	54.4	79	9	AA628831	AA628831 co93d10.s
C	21	13.6	54.4	74	17	AZ789998	AZ789998 2M0038F09
C	22	13.6	54.4	76	13	BMS33309	BMS33309 fvl6d01.y
C	23	13.6	54.4	82	9	AI154844	AI154844 ud80c03.r
C	24	13.6	54.4	88	12	BE719496	BE719496 mab35b05.s
C	25	13.6	54.4	95	17	AZ485646	AZ485646 1M0313M08
C	26	13.4	53.6	25	17	AZ480905	AZ480905 2M0138H09
C	27	13.4	53.6	37	9	AA488066	AA488066 ab13c10.s
C	28	13.4	53.6	37	14	H03404	H03404 y148c04.s1
C	29	13.4	53.6	60	14	H55068	H55068 CHR220007 C
C	30	13.4	53.6	84	13	BU059170	BU059170
C	31	13.4	53.6	87	9	AA429847	AA429847 z59c07.r
C	32	13.4	53.6	88	9	AI204865	AI204865 zE5EST187
C	33	13.4	53.6	90	10	BE251953	BE251953 60107633
C	34	13.4	53.6	93	17	AZ507519	AZ507519 1M0349M08
C	35	13.4	53.6	94	9	AI996082	AI996082 701549907
C	36	13.4	53.6	96	12	BF824192	BF824192 NCST53a21
C	37	13.4	53.6	97	9	AI810999	AI810999 tui10b08.x
C	38	13.4	53.6	98	17	AZ862256	AZ862256 2M0169D24
C	39	13.4	53.6	98	17	AQ254869	AQ254869 EP(2)2510
C	40	13.2	52.8	35	17	AL771545	AL771545 Arabidops
C	41	13.2	52.8	35	17	AL771545	AL771545 Arabidops
C	42	13.2	52.8	34	9	AU013434	AU013434
C	43	13.2	52.8	57	10	BE307847	BE307847 601096321
C	44	13.2	52.8	60	9	AI882516	AI882516 ub97b04.r
C	45	13.2	52.8	73	17	AZ419093	AZ419093 1M015M23

ALIGNMENTS

RESULT 1
AI216035/C 70 bp mRNA linear EST 30-NOV-1998
LOCUS q10e11.x1 Scores: NFI.T.GBC.S1 Homo sapiens CDNA clone
IMAGE:1844300 3' similar to TR:Q1513 Q1513 PROCOLAEN
C-PROTEINASE ENHANCER PROTEIN PRECURSOR. [1] : contains TAR1, t3 TAR1
repetitive element ; mRNA sequence.
ACCESSION AI216035.1 GI:3785076
VERSION AI216035.1
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS Contact: Robert Strausberg, Ph.D.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
JOURNAL
COMMENT
FEATURES
source 1..70

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:1844300"
 /clone_lib="Soares_NFL_T-CBC_S1"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: pT7TD-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCL-GAP-GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 726408-728711, and 729096-731399. Subtraction by Bento Soares and W. Fatima Bonalido." 1 others

BASE COUNT 15 a 16 c 23 g 15 t

ORIGIN

Query Match 66.4%; Score 16.6; DB 9; Length 70;
 Best Local Similarity 82.6%; Pred. No. 4e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 CTGCGACAGATTCCGCTGACC 25
 DB 59 CTGCGCAAGACACTCGCTGACC 37

RESULT 2
 BJO59813/c 88 bp mRNA linear EST 11-DEC-2001
 LOCUS BJO59813
 DEFINITION laevis cDNA clone Xl063p11 5', mRNA sequence.
 ACCESSION BJO59813
 VERSION BJO59813.1 GI:17493153
 KEYWORDS EST.
 SOURCE African clawed frog.
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae; Xenopodinae; Xenopus.
 REFERENCE 1 (bases 1 to 88)
 AUTHORS Kityayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-I, T. and Kohara, Y.
 TITLE Expressed genes in X. laevis embryo
 JOURNAL Unpublished (2001)
 COMMENT Contact: Tadao Shin-I
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.

FEATURES
 source
 1. 88
 Location/Qualifiers
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone_image="Xl063p11"
 /clone_lib="NIBB Mochii normalized Xenopus tailbud library"
 /tissue_type="whole embryo"
 /dev_stage="stage 25"
 /note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute)."

BASE COUNT 23 a 21 c 20 g 23 t 1 others
 ORIGIN

Query Match 60.8%; Score 15.2; DB 13; Length 88;
 Best Local Similarity 85.0%; Pred. No. 1.6e+04;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 6 TCCACAGATTCCGCTGACC 25
 DB 24 TTCACAGATTCCGCTGACC 5

RESULT 3
 A1883598/c 88 bp mRNA linear EST 07-JUN-2001
 LOCUS A1883598
 DEFINITION f66g12.y1 zebrafish Mashu MPIMG EST Danio rerio cDNA clone
 NATI. ; mRNA sequence.
 ACCESSION A1883598
 VERSION A1883598.1 GI:5588762
 KEYWORDS EST.
 SOURCE zebrafish.
 ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
 REFERENCE 1 (bases 1 to 88)
 AUTHORS Clark, M., Johnson, S.L., Lebrach, R., Lee, R., Li, F., Marra, M., Eddy, R., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, S., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schuck, R., Rither, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., Mccann, R., Waterston, R. and Wilson, R.
 Mashu zebrafish EST Project 1998
 Unpublished (1998)
 CONTACT: Stephen L. Johnson
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: zbrafish@wustl.edu
 CDNA Library Preparation: Matthew Clark, CDNA Library Arrayed by: Matthew Clark, DNA Sequencing by: Washington University Genome Sequencing Center Clone Distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and www.rzpd.de)
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: 13 bp from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1. 88
 Location/Qualifiers
 /organism="Danio rerio"
 /db_xref="taxon:7955"
 /clone_image="IMAGE:3726406"
 /clone_lib="zebrafish Mashu MPIMG EST"
 /sex="mixed"
 /tissue_type="26 somite embryos, adult livers, shield stage embryos"
 /lab_host="Xl1-blue MRP"
 /note="Vector: pSPOR1; Site_1: NotI; Site_2: SalI; 1st strand cDNA was primed with a Not I - oligo(dT)15 primer double-stranded cDNA was ligated to Sal I adaptors (BRL), sites of the pSPOR1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). cDNAs for EST hybridization were selected following oligonucleotide zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were

sequence.
 accession AA999832 GI:3190387
 EST.
 keywords EST.
 source human.
 organism Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 reference 1 (bases 1 to 78)
 title NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 authors National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 tumor gene index
 journal Unpublished (1997)
 comment Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA library Preparation: M. Bento Soares, Ph.D.
 CDNA library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMW at:
 www.bio.lnlnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Seq primer: -40m13 fwd. Ex from Amersham
 High quality sequence stop: 1.
 location/Qualifiers
 1. 78
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="1636346"
 /clone_id="NCI_CGAP_K1d3"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with
 a modified polylinker; Site: 1: Not 1; Site: 2: Eco RI; 1st
 strand cDNA was primed with a Not I oligo(dT) primer,
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not
 I and Eco RI sites of the modified pT73 vector. mRNA
 source: 2 pooled kidneys. Library went through one round
 of normalization. Library constructed by Bento Soares and
 M. Fatima Bonaldo."

BASE COUNT 13 a 32 c 17 g 16 t
 ORIGIN

Query Match 57.6%; Score 14.4; DB 9; Length 78;
 Best Local Similarity 75.0%; Pred. No. 3.4e+04;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ACTGTCACAGCATTCGCTGACC 25
 |||||
 Db 42 ACGCTCCTCCGACATCCGCTGAGC 65

RESULT 7
 AZ483948/c 28 bp DNA linear GSS 05-OCT-2000
 LOCUS 1M0309J19R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 DEFINITION clone UUGCIM0309J19 R, DNA sequence.
 accession AZ483948
 version AZ483948.1 GI:10648274
 keywords GSS.
 organism house mouse.
 source Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 reference 1 (bases 1 to 28)
 authors Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
 and Wright, D., Weiss, R.
 title Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 University of Utah
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0309 row: 3 column: 19
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 28.
 location/Qualifiers
 1. 28
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCIM0309J19"
 /clone_id="Mouse 10kb plasmid UUGCIM library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42ny, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi14732114|gb|AF129072.1), a copy number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 7 a 7 c 8 g 6 t
 ORIGIN

Query Match 56.8%; Score 14.2; DB 17; Length 28;
 Best Local Similarity 84.2%; Pred. No. 3.3e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CTGTCCACAGCATTCGCT 21
 |||||
 Db 25 CTGTCCACAGCATTCGAT 7

RESULT 8
 B1736494/c 80 bp mRNA linear EST 20-SEP-2001
 LOCUS 603360142P1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5367131 5',
 DEFINITION mRNA sequence.
 accession B1736494
 version B1736494.1 GI:15713507
 keywords EST.
 organism house mouse.
 source Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 reference 1 (bases 1 to 80)
 authors NIH-MGC http://mhc.ncbi.nlm.nih.gov/.
 title National Institutes of Health, Mammalian Gene Collection (MGC)
 journal Unpublished (1999)
 comment Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov

Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: TINGE Genomics
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://imgc.llnl.gov>
 plate: LAM1934 row: d column: 12
 High quality sequence stop: 80.

FEATURES
 source
 1 80
 Location/Qualifiers

/organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:5367131"
 /clone_1lb="NIH_MGC_94"
 /tissue_type="retina"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pCMV-Sport6; Site: 1; NotI;
 Site: 2; SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 3.3 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC library."

BASE COUNT
 ORIGIN
 8 a 17 c 38 g 17 t

Query Match 56.8%; Score 14.2; DB 13; Length 80;
 Best Local Similarity 84.2%; Pred. No. 4.2e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 ACTGTCACAGCATTCGCC 20
 ||||| ||||| |||||
 Db 61 ACTGGCACAGCAGCATTCGCC 43

RESULT 9
 LOCUS A2474370 90 bp DNA linear GSS 04-OCT-2000
 DEFINITION "10290L23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0290L23 R, DNA sequence."
 ACCESSION A2474370
 VERSION A2474370.1 GI:10632495
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0290 row: L column: 23
 Seq primer: CACACAGGAAACAGCATATGACC
 Class: plasmid ends
 High quality sequence stop: 90.

FEATURES
 source
 1. 90
 Location/Qualifiers

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0290L23"

BASE COUNT
 ORIGIN
 30 a 21 c 19 g 20 t

Query Match 56.8%; Score 14.2; DB 17; Length 90;
 Best Local Similarity 84.2%; Pred. No. 4.3e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 ACTGTCACAGCATTCGCC 20
 ||||| ||||| |||||
 Db 88 AATGTCACAGCATTCGCC 70

RESULT 10
 LOCUS AA622040 94 bp mRNA linear EST 31-OCT-1997
 DEFINITION "ng23c02.81 NCI-CGAP Col0 Homo sapiens cDNA clone IMAGE:1144706 3'
 similar to TR:G861464 G861464 BOVINE LEUKEMIA VIRUS CELL RECEPTOR
 ;, mRNA sequence."
 ACCESSION AA622040
 VERSION AA622040.1 GI:2525916
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
 Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
www.bio.llnl.gov/dbp/image/image.html

FEATURES
 source
 1. 94
 Location/Qualifiers

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1144706"
 /clone_1lb="NCI-CGAP_Col0"

```

/tissue_type="colon tumor RER+"
/lab_host="DH10B"
/organism="Trypanosoma brucei"
/modified_polylinker="1st strand cDNA was prepared from
RER+ colon tumor, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo (N-Soares4)."
BASE COUNT      22 a      21 c      31 g      20 t
ORIGIN
Query Match      56.8%; Score 14.2; DB 9; Length 94;
Best Local Similarity 84.2%; Pred. No. 4.3e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TGTCCACAGCATTCGGCTG 22
||||| ||| ||||| |||
Db 61 TGTCCACATCATTCGGCTG 43

RESULT 11
LOCUS TA271C04Q 62 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 271c04, reverse sequence,
genomic survey sequence.
ACCESSION AL488248 GI:11864100
VERSION AL488248.1 GI:11864100
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 62)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
McVillie, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GYrat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: neilsavedelgr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
Source
1..62
/organism="Trypanosoma brucei"
/db_xref="taxon:5691"
/clone="271c04"
BASE COUNT 15 a 13 c 19 g 15 t
ORIGIN
Query Match 56.0%; Score 14; DB 17; Length 62;
Best Local Similarity 77.3%; Pred. No. 4.8e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGGCTG 22
||||| ||| ||||| |||
Db 32 GACTGTACACACCTTCACCTG 53

```

```

RESULT 12
LOCUS CNS03C5U/64 bp DNA linear GSS 15-MAY-2000
DEFINITION Tetradodon nigroviridis genome survey sequence pCC-ori end of clone
013p19 of library G from Tetradodon nigroviridis, genomic survey
sequence.
ACCESSION AL237387 GI:7896522
VERSION AL237387
KEYWORDS GSS; genome survey sequence.
SOURCE Tetradodon nigroviridis.
ORGANISM Tetradodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthopterygii; Acanthopterygii; Percormorpha; Tetradontiformes;
Tetraodontidae; Tetradodon.
1 (bases 1 to 64)
Roest-Crolius, H., Jalllon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quettier, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
Tetradodon nigroviridis DNA sequence
Unpublished
2 (bases 1 to 64)
Roest-Crolius, H., Jalllon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quettier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradodon nigroviridis
Unpublished
3 (bases 1 to 64)
Genoscope.
Direct Submission
Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetradodon.
location/Qualifiers
1..64
/organism="Tetradodon nigroviridis"
/db_xref="taxon:99883"
/clone="013p19"
/clone_lib="G"
/note="Genoscope sequence ID : COB6013CHI0SP1-end :
pCC-ori"
BASE COUNT 8 a 18 c 22 g 15 t 1 others
ORIGIN
Query Match 56.0%; Score 14; DB 17; Length 64;
Best Local Similarity 77.3%; Pred. No. 4.8e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TGTCCACAGCATTCGGTGACC 25
||||| ||| ||||| |||
Db 63 TTTCCAAACATTCGGTGACC 42

RESULT 13
LOCUS AM423872 78 bp mRNA linear EST 03-DEC-2001
DEFINITION sb57b04.y1 Gm-c1015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1015-3848 5', mRNA sequence.
ACCESSION AM423872
VERSION AM423872.1 GI:6951804
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 78)
Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna

```

TITLE
JOURNAL
COMMENT

A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schuck, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estest@wustl.edu

FEATURES

source

1. .78
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1015-3848"
/clone_id="Gm-c1015"
/tissue_type="Mature flowers, field grown plants"
/lab_host="X110-Gold"
/note="Vector: pBluescript II XE; Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from mRNA isolated from mature flowers of field grown plants. The cDNA library was prepared using the Stratagene pluscript II XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence to the blunt ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pluscript vector. The ligated cDNA fragments were transformed into X110-gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelting."

BASE COUNT

29 a 24 g 18 t

ORIGIN

Query Match 56.0%; Score 14; DB 10; Length 78;
Best Local Similarity 77.3%; Pred. No. 5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 CTGTCCAGCATTCGCTGAC 24
||| ||||| ||| |
Db 71 CTGTCTCAGCATTCCTCTGTC 50

RESULT 14

HSWC26D02/c

LOCUS HSWC26D02 88 bp DNA linear GSS 29-MAY-1997
DEFINITION H.sapiens DNA for trapped exon (ID HWC26D02), genomic survey
sequence.

ACCESSION

X88221

VERSION

X88221.1 GI:1437838

KEYWORDS

GSS.

SOURCE

Homo sapiens.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 88)
Chen, H.M., Rossier, C., Chrafi, R. and Antonarakis, S.E.

TITLE

Cloning of trapped exons from human chromosome 21

AUTHORS

Antonarakis, S.E.

JOURNAL

Direct Submission

COMMENT

Submitted (17-MAR-1995) Stylianos E. Antonarakis, Division of

Medical Genetics, University and Cantonal Hospital of Geneva, CHU, 1 rue Michel-Servet, 1211 Geneva, SWITZERLAND
3 (bases 1 to 88)
Chen, H., Chrafi, R., Rossier, C., Morris, M.A., Lalioti, M.D. and Antonarakis, S.E.
Cloning of 559 potential exons of genes of human chromosome 21 by exon trapping
Genome Res. 6 (8), 747-760 (1996)
97011340
8858350

FEATURES

source

1. .88
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
1. .88
/note="trapped exon"
BASE COUNT 14 a 19 c 34 g 18 t 3 others
ORIGIN

Query Match 56.0%; Score 14; DB 17; Length 88;
Best Local Similarity 77.3%; Pred. No. 5.2e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 4 TGTCCAGCATTCGCTGACC 25
||| ||||| ||| |
Db 55 TGACCAGCATTCGCTGACC 34

RESULT 15

AA572309/c

LOCUS AA572309/c 90 bp mRNA linear EST 27-AUG-1997
DEFINITION v152909.r1 Stratiagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:975904 5' similar to gb:U13805 Mouse type I epidermal keratin mRNA clone pKSC-50, 3' (MUSE), mRNA sequence.

ACCESSION

AA572309

VERSION

AA572309.1 GI:2345504

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 90)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

AUTHORS

Geisler, S., Kucaba, T., Lacy, M., Le, F., Martin, J., Morris, M.,

TITLE

The Washington University School of Medicine

JOURNAL

Unpublished (1996)
Contact: Marra M/Mouse EST Project

COMMENT

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:556632
Seq primer: -28m13 rev1 5' from Amerham.

FEATURES

source

1. .90
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:975904"
/clone_id="Stratiagene mouse skin (#937313)"
/tissue_type="whole skin"
/sex="females"
/issue_type="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-, Site 1: EcoRI

; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo
 dt. Whole skin from 11 week old C57BL/6 female mice.
 Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
 adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor
 sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'

BASE COUNT 19 a 12 c 29 g 30 t

ORIGIN

Query Match 56.0%; Score 14; DB 9; Length 90;
 Best Local Similarity 77.3%; Pred. No. 5.2e+04;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GACTGTCCACAGCATTCGCTG 22
 |||||
 Db 68 GCCTCTCCCCAGCATTCCTATG 47

Search completed: December 21, 2002, 19:25:29
 Job time : 783.408 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:20:00 : Search time 616.327 Seconds
(without alignments)
525.549 Million cell updates/sec

Title: US-09-121-239-13
Perfect score: 20
Sequence: 1 CAAAGAGAGAGAGAGAGAG 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlun:*
5: em_estlun:*
6: em_estlun:*
7: em_estlun:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_hum:*
20: em_gss_hum:*
21: em_gss_hum:*
22: em_gss_hum:*
23: em_gss_hum:*
24: em_gss_hum:*
25: em_gss_hum:*
26: em_gss_hum:*
27: em_gss_hum:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	15.2	76.0	50	AU107625	AU107625 AU107625
2	14.8	74.0	82	AA888583	AA888583 of90508.s
3	14.4	72.0	83	AA888583	AA888583 of90508.s
4	14.4	72.0	99	AA888583	AA888583 of90508.s
5	14.2	71.0	52	AA888583	AA888583 of90508.s
6	14.2	71.0	53	AA888583	AA888583 of90508.s

C	7	14.2	71.0	70	9	AA255635	AA255635 z531f07.r
	8	14.2	71.0	76	17	A2497409	A2497409 1M0334E14
	9	14.2	71.0	85	9	AA495306	AA495306 fa01a07.r
	10	14.2	71.0	95	17	TA9C09P	TA9C09P T. brucei
	11	14.2	71.0	96	17	AF219048	AF219048 AF219048
	12	14.2	71.0	98	9	AI606834	AI606834 v161B08.x
	13	13.8	69.0	49	14	H53725	H53725 yu38f12.x1
	14	13.8	69.0	52	9	AA915419	AA915419 v230a10.r
	15	13.8	69.0	51	9	AA496604	AA496604 zv38f05.r
	16	13.8	69.0	70	9	AA544943	AA544943 fb69f02.y
	17	13.8	69.0	73	9	AA983411	AA983411 or45d03.s
	18	13.8	69.0	85	9	AA691847	AA691847 vt05e10.r
	19	13.8	69.0	86	13	B1764202	B1764202 603046069
	20	13.8	69.0	89	17	BH413912	BH413912 1007035C0
	21	13.8	69.0	96	9	AA257631	AA257631 MB12574H3
	22	13.8	69.0	96	14	B0758134	B0758134 ERBm01.S0
	23	13.8	69.0	100	13	B1478874	B1478874 952002E10
	24	13.6	68.0	33	17	A236372	A236372 1M0066C11
	25	13.6	68.0	46	17	A2846167	A2846167 2M0146D15
	26	13.6	68.0	76	9	AA261741	AA261741 v551f08.r
	27	13.6	68.0	82	17	A2830488	A2830488 2M0109F17
	28	13.6	68.0	86	9	AA453618	AA453618 z448D03.s
	29	13.6	68.0	89	17	A2920263	A2920263 1006019A1
	30	13.6	68.0	92	17	AA920051	AA920051 v963h10.r
	31	13.6	68.0	93	17	BH792057	BH792057 SALK_0625
	32	13.6	68.0	96	17	BH405867	BH405867 RPTC-23-8
	33	13.6	68.0	100	14	BQ250094	BQ250094 TA225009H
	34	13.6	68.0	100	17	BH877600	BH877600 h39405.b
	35	13.4	67.0	28	17	TA130B12P	TA130B12P T. brucei
	36	13.4	67.0	50	9	AU105451	AU105451 AU105451
	37	13.4	67.0	65	17	AF149510	AF149510 AF149510
	38	13.4	67.0	77	9	AA064271	AA064271 m148h12.r
	39	13.2	66.0	42	17	A2812501	A2812501 2M0079P08
	40	13.2	66.0	49	17	BH846378	BH846378 SALK_0075
	41	13.2	66.0	57	17	A2662175	A2662175 1M0541D09
	42	13.2	66.0	64	14	H53642	H53642 yu38g06.s1
	43	13.2	66.0	64	13	BT261721	BT261721 602954044
	44	13.2	66.0	68	9	AA500663	AA500663 AT500663
	45	13.2	66.0	69	17	A2487201	A2487201 1M0316B12

ALIGNMENTS

RESULT 1
AU107625
LOCUS
DEFINITION AU107625 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION REC00847, mRNA sequence.
VERSION AU107625
KEYWORDS AU107625.1 GI:13557146
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Suzuki,Y., Taira,H., Tsunoda,T., Mitsuhashi-Sugano,J., Seese,J., Hata
1 (bases 1 to 50)
'H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
JOURNAL MEDLINE
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshimoto-Nakagawa,K., Maruyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers

FEATURES

JOURNAL
COMMENT

Vascular Plants. Project: 1030
Unpublished (2002)
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.

FEATURES
source

Location/Qualifiers
1. .99
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone.lib="c. reinhardtii CC-1690. Deflagellation
(normalized). lambda zap II"
/note="Vector: pBluescript II SK-; Site1: EcoRI; Site2:
XhoI; Deflagellation library, constructed by John Davies
and Jeffrey McDermott, combines cDNAs from CC-1690 cells
which had been re-synthesizing flagella for 15, 30 and 60
min after being deflagellated by pH shock. PolyA mRNA was
purified from each sample, pooled and cDNA synthesized.
The cDNA was directionally cloned into lambda zap II
(Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
zap clones by superinfection with Exsist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldi et al., (1996) Genome Research 6: 791-806."

BASE COUNT 22 a 37 c 27 g 13 t
ORIGIN

Query Match 72.0%; Score 14.4; DB 14; Length 99;
Best Local Similarity 93.8%; Pred. No. 4.2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CAACGACGACGAGGAG 16
||||| |||||
Db 9 CAACGACGAGGAGGAG 24

RESULT 5
LOCUS A2597805 52 bp DNA linear GSS 13-DEC-2000
DEFINITION M0411F20R Mouse 10kb plasmid U08C1M library Mus musculus genomic
clone U08C1M0411F20 R, DNA sequence.
ACCESSION A2597805
VERSION A2597805.1 GI:11719995
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 52)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly
, M., Rose, M., Rose, R., Stokes, R., Thigley, A., von Niederhausen, A.
and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Department of Biology
Room 308 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: Q411 row: F column: 20
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 52.

FEATURES
source

Location/Qualifiers
1. .52

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone.lib="U08C1M0411F20"
/clone.lib="Mouse 10kb plasmid U08C1M library"
/sex="Male"
/lab.host="E. coli strain X110-Gold, T1-resistant, F-"
/note="Vector: pMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g147321419b1AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli X110-Gold (Stratagene) cells
and selected for ampicillin resistance.

BASE COUNT 19 a 1 c 22 g 10 t
ORIGIN

Query Match 71.0%; Score 14.2; DB 17; Length 52;
Best Local Similarity 84.2%; Pred. No. 4.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 AAAGGACGACGAGGAG 20
||||| |||||
Db 10 AAATGATCATGAGGAG 28

RESULT 6
LOCUS BH638963 55 bp DNA linear GSS 14-FEB-2002
DEFINITION 1008026D03.2EL_y1 1008 - RescueMu Grid I Zea mays genomic, DNA
sequence.
ACCESSION BH638963
VERSION BH638963.1 GI:18663620
KEYWORDS GSS.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 55)
Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008026 row: 10
Class: transposon-tagged.
Location/Qualifiers
1. .55
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"

```

/clone.lib="1008 - RescuenMu Grid 1"
/tissue.type="leaf"
/dev.stage="adult"
/lab.host="DH10B"
/notes="Organ: leaf; Vector: RescuenMu (engineered from
pBluescript backbone); Site_1: BamHI; Site_2: BglII;
RescuenMu is a 4.9 kb, modified maize total genomic DNA.
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescuenMu, go to the web
site www.zmld.iastate.edu and follow the links for
'RescuenMu.' Grid 1 was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

BASE COUNT      13 a      9 c      22 g      11 t
ORIGIN
Query Match      71.0%; Score 14.2; DB 17; Length 55;
Best Local Similarity 84.2%; Pred. No. 4.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      2 AAAGGACGACGGAAGAGC 20
|||||
Db      8 AAAGGACGACGACGACGAGC 26

RESULT 7
AA255635/c      70 bp mRNA linear EST 13-AUG-1997
LOCUS      zs31f07.f1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:686821 5'
DEFINITION similar to SM:YK02.YEAST P36042 HYPOPHYLLAL 21.2 KD PROTEIN IN
T0R2-PASI INTERGENIC REGION.; contains element TARI repetitive
element; , mRNA sequence.
AA255635
VERSION      AA255635.1 GI:1892570
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 70)
REFERENCE      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE      Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1914 Std Error: 0.00
Seq primer: -28ml3 rev2 fw from Amersham
High quality sequence stop: 1.

FEATURES
Source
1..70
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:686821"
/clone.lib="NCI CGAP GCBI"
/tissue.type="germinal center B cell"
/lab.host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTCACATCTGACAGTGGAGCGCCGCTCACTTTTCTTTTCTTTT-3'
1. Double-stranded cDNA was ligated to Eco RI adaptors

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(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT      0 a      32 c      0 g      38 t
ORIGIN
Query Match      71.0%; Score 14.2; DB 9; Length 70;
Best Local Similarity 84.2%; Pred. No. 4.8e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      2 AAAGGACGACGGAAGAGC 20
|||||
Db      24 AAAAGAGAAGGGAAGAGGC 6

RESULT 8
AA297409      76 bp DNA linear GSS 05-OCT-2000
LOCUS      IM0334E14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0334E14 F, DNA sequence.
AA297409
ACCESSION      AA297409
VERSION      AA297409.1 GI:10674338
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 76)
REFERENCE      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,J., Hamill,C.,
AUTHORS      Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tinger,A., von Niederhausen,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0334 Row: E Column: 14
Seq primer: CGTGTAAACGACGCGCAGT
Class: Plasmid ends
High quality sequence stop: 76.

FEATURES
Source
1..76
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0334E14"
/clone.lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab.host="E. Coli strain XL10-Gold, TI-resistant, F-"
/notes="Vector: PMD42uv. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g114732114[9b]/E129072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and

```


purified. The sheared, adapted mouse DNA was annealed to
adapored vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 26 a 10 c 29 g 11 t
ORIGIN

Query Match 71.0%; Score 14.2; DB 17; Length 76;
Best Local Similarity 84.2%; Pred. No. 4.9e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 AAAGGACGAGGAGAGAGG 20
Db 39 AGAGGAGGAGGAGAGAGG 57

RESULT 9
LOCUS AA495306 85 bp mRNA linear EST 27-JUN-1997
DEFINITION fa01807.r1 zebrafish ICRFzfls Danio rerio cDNA clone 1A3 5' similar
ACCESSION AA495306
VERSION AA495306.1 GI:2225734
KEYWORDS EST.
SOURCE zebrafish.
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 85)
AUTHORS Clark, M., Heller, H., Appel, B., Eisen, J., Johnson, S., Marra, M.,
Eddy, S., Hillier, L., Allen, M., Bowles, L., Dubuque, T., Getzel, G.,
Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marlin, J., Moore, B.,
Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie
T., Waterston, R. and Wilson, R.
WashU Zebrafish EST Project
Unpublished (1997)

TITLE JOURNAL
COMMENT Contract: Steve Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
Steve Johnson lab Internal ID - P1-13 NOTE - For this library, the
CDNA id field represents a position identifier on the original
CDNA library preparation plate. CDNA library preparation: Matthew
Clark. CDNA library Arrayed by: Matthew Clark. DNA Sequencing by:
Washington University Genome Sequencing Center Clone distribution:
Genome Systems, St. Louis, and Max Planck Institut fuer Molekulare
Genetik, Berlin Tel +49 30 84 13 1235
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: 77 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
source 1..85
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone_lib="zebrafish ICRFzfls"
/sex="mixed"
/tissue_type="pooled 26-somite embryos"
/lab_host="XLI-Blue MRF"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; 1st
strand cDNA was primed with a Not I - oligo(dT)15 primer
13' pGACTAGTCTGATCGAGCGCGCCCTTTTCTTTTCTT3'1, on
mRNA from pooled 26 somite zebrafish embryos;
Double-stranded cDNA was ligated to Sal I adaptors (BRL),
digested with Not I and cloned into the Not I and Sal I
sites of the pSPORT1 vector (BRL). Library was constructed
by Matthew Clark (Lehrach lab; ICRF, London and Max
Planck Institut fuer Molekulare Genetik, Berlin) and was
not biochemically normalised. 70,000 clones from this

library were arrayed on high density filters and
subsequently screened by oligonucleotide hybridization
fingerprinting to identify unique or minimally redundant
clones for more intensive analysis."

BASE COUNT 29 a 12 c 24 g 20 t
ORIGIN

Query Match 71.0%; Score 14.2; DB 9; Length 85;
Best Local Similarity 84.2%; Pred. No. 5e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 AAAGGACGAGGAGAGAGG 20
Db 44 AAAGGACGAGGAGAGAGG 62

RESULT 10
LOCUS TA9C09P 95 bp DNA linear GSS 13-DEC-2000
DEFINITION T. Brucei sheared genomic DNA clone 9C09, forward sequence, genomic
survey sequence.
ACCESSION AL451917
VERSION AL451917.1 GI:11861109
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE 1 (bases 1 to 95)
AUTHORS Hall, N., Bowman, S., Leonard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajadream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhs@sanger.ac.uk
constructed at the Institute for Genomic Research (TIGR).
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREM0927/4 COTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.

COMMENT

FEATURES

source

1..95
/organism="Trypanosoma brucei"
/strain="TREM0927"
/db_xref="taxon:5691"
/clone="9C09"

BASE COUNT 38 a 14 c 27 g 16 t
ORIGIN

Query Match 71.0%; Score 14.2; DB 17; Length 95;
Best Local Similarity 84.2%; Pred. No. 5e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 AAAGGACGAGGAGAGAGG 20
Db 54 AAAGGACGAGGAGAGAGG 72

RESULT 11
LOCUS AF219048 96 bp DNA linear GSS 17-APR-2000
DEFINITION AF219048 Human Homo sapiens genomic clone B05, DNA sequence.
ACCESSION AF219048
VERSION AF219048.1 GI:7581585

strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTTCACATCATGAGTGGAGCGCCGCCGTCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pUT73 vector (Pharmacia). Library constructed by Bento Soares and M.Patima Ronaldo."

BASE COUNT	12 a	15 c	15 g	6 t	1 others
Query Match	89.0%	Score 13.8:	DB 14:	Length 49:	
Best Local Similarity	88.2%	Pred No.	6.7e+04;		
Matches 15; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;	
Ox	1	CANAGGACGAGGAAGA 17			
Dn	19	CACGAGGACGAGGAAGA 35			
RESULT 14					
LOCUS	AA915419				
DEFINITION	AA915419	52 bp	mRNA	linear	EST 14-APR-1996
ACCSSION	AA915419				
VERSION	AA915419.1				
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					

Trace considered overall poor quality
Putative full length read
vector to vector length is
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..52
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1327962"
/clone_lib="Soares_lymus_2NBMF"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note=Vector: pUT73b-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cdna was primed with a Not I - oligo(dT) primer [5'-TGTTTCACATCATGAGTGGAGCGCCGCCGTCTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I

BASE COUNT	ORIGIN	Query Match	Best Local Similarity	Matches	Score	DB	Length	Indels	Gaps
28 a	3 c	69.0%;	88.2%;	0;	18 g	1 t	52;	0;	0;
OY	4	ACGAGCAGGAGAGAGC	20	11111 111111111					
Db	31	ACGAGCAAGAGAGAGG	47						
RESULT 15									
LOCUS	AA496604	61 bp	MRNA	linear	EST 12-AUG-1997				
DEFINITION	z38f05.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone								
ACCESSION	AA496604								
VERSION	AA496604.1								
KEYWORDS	EST								
SOURCE	human.								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
AUTHORS	1. (bases 1 to 61) Hillier,L., Allen,M., Bowles,L., Dubucque,T., Geisel,G., Jost,S., Kucaba,V., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wyllie,T., Wallerstein,R. and Wilson.R.								
TITLE	WashU-Merck EST Project 1997								
JOURNAL	Unpublished (1997)								
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu This clone is available royalty-free through LNLN; contact the IMAG Consortium (info@image.lnl.gov) for further information. Trace considered overall poor quality Possible reversed clone; similarity on wrong strand Seq primer: 28m13 rev2 Et from Amersham High quality sequence scop: 1. Location/Qualifiers 1. 61 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:755937" /clone_lib="Soares ovary tumor NBHOT" /sex="Female" /tissue_type="Ovarian tumor" /lab_host="DH10B (ampicillin resistant)" /note="Organ: ovary; Vector: pTR73D (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTCACATCTGAAGTGGAGGCGGCGCGGCTTTTCTTTTCTTTT 3']; double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTR73 vector (Pharmacia). Library constructed by Bento Soares and M.Felina Bonaldo."								
BASE COUNT	15 a	17 c	21 g	8 t					
ORIGIN									
Query Match	69.0%;	Score 13.8;	DB 9;	Length 61;					
Best Local Similarity	88.2%;	Pred. No. 6.9e+04;							
Matches	15;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
15;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;	

OY 1 CAAGGAGCGGGAAGA 17
11 ||||| ||||
Db 13 CACAGGAGCGGGAAGA 29

Search completed: December 21, 2002, 19:25:40
Job time : 627.327 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:20:00 ; Search time 739.592 Seconds
(without alignments)
525.549 Million cell updates/sec

Title: US-09-121-239-16

Sequence: 24
1 GGGACATGACCCCTTCAGCGG 24

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estda:*
2: em_esthm:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estol:*
7: em_estro:*
8: em_estc:*
9: gb_estl:*
10: gb_estc:*
11: gb_estg:*
12: gb_estj:*
13: gb_estk:*
14: gb_estl:*
15: em_esthm:*
16: em_esthm:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rnd:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	15.2	63.3	69 17	AZ838667 2M0134N22
2	15.2	63.3	91 9	AA754748 vuz2h06.r
3	14.8	61.7	70 9	AA754748 vuz2h06.r
4	14.6	60.8	40 17	AZ805795 2M0067F20
5	14.6	60.8	65 17	AZ842595 2M0141F08
6	14.4	60.0	79 17	BH632587 1007096B0

C	7	14.4	60.0	83 9	AT720123
C	8	14.4	60.0	84 17	BH416484
C	9	14.4	60.0	89 17	AZ932244
C	10	14.2	59.2	42 17	AZ838487
C	11	14.2	59.2	42 17	AZ924607
C	12	14.2	59.2	76 17	AL768539
C	13	14.2	59.2	89 17	AZ861128
C	14	14.2	59.2	99 17	AZ859525
C	15	14.2	59.2	99 17	AZ859525
C	16	14.2	59.2	99 17	AZ859525
C	17	14.2	59.2	99 17	AZ859525
C	18	14.2	59.2	99 17	AZ859525
C	19	14.2	59.2	99 17	AZ859525
C	20	14.2	59.2	99 17	AZ859525
C	21	14.2	59.2	99 17	AZ859525
C	22	14.2	59.2	99 17	AZ859525
C	23	14.2	59.2	99 17	AZ859525
C	24	14.2	59.2	99 17	AZ859525
C	25	14.2	59.2	99 17	AZ859525
C	26	14.2	59.2	99 17	AZ859525
C	27	14.2	59.2	99 17	AZ859525
C	28	14.2	59.2	99 17	AZ859525
C	29	14.2	59.2	99 17	AZ859525
C	30	14.2	59.2	99 17	AZ859525
C	31	14.2	59.2	99 17	AZ859525
C	32	14.2	59.2	99 17	AZ859525
C	33	14.2	59.2	99 17	AZ859525
C	34	14.2	59.2	99 17	AZ859525
C	35	14.2	59.2	99 17	AZ859525
C	36	14.2	59.2	99 17	AZ859525
C	37	14.2	59.2	99 17	AZ859525
C	38	14.2	59.2	99 17	AZ859525
C	39	14.2	59.2	99 17	AZ859525
C	40	14.2	59.2	99 17	AZ859525
C	41	14.2	59.2	99 17	AZ859525
C	42	14.2	59.2	99 17	AZ859525
C	43	14.2	59.2	99 17	AZ859525
C	44	14.2	59.2	99 17	AZ859525
C	45	14.2	59.2	99 17	AZ859525

ALIGNMENTS

RESULT 1	AZ838667	69 bp	DNA	linear	GSS 20-FEB-2001
LOCUS	2M0134N22	Mouse 10kb plasmid	UUCIM library	Mus musculus genomic	
DEFINITION	2M0134N22	Mouse 10kb plasmid	UUCIM library	Mus musculus genomic	
ACCESSION	AZ838667	GI:13008575			
VERSION	AZ838667.1				
KEYWORDS	house mouse.				
SOURCE	house mouse.				
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.				
REFERENCE	Dunn, D., Aoyagi, A., Barber, M., Beccorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, D., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.,				
AUTHORS	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
TITLE	Unpublished (2000)				
JOURNAL	Contact: Robert B. Weiss				
COMMENT	University of Utah Genome Center				
	84112, USA				
	Tel.: 801 585 5606				
	Fax: 801 585 7177				
	Email: ddunne@genetics.utah.edu				
	Insert length: 10000				
	Std Error: 0.00				

MGI:639091
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m3 rev2 ET from Amersham
High quality

1.91

BASE COUNT
ORIGIN

17 a 14 c 18 g 20 t

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/clone="UUCG2M0134N20"  
/clone_lib="Mouse 10kb plasmid UUCG1M library"  
/sex="Male"  
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
inducible derivative of plasmid R1, a copy-number  
with adaptor's complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance.
```

24 a 19 c 34 g

Query Match	63.3%	Score 15.2;	DB 9;	Length 91;
Best Local Similarity	85.0%;	Pred. No. 7.8e+03;		
Matches 17; Conservative	0;	Mismatches 3;		

```

QY      3  GGAACATGAAGCCCTTCAGC  22
          |||||  |||||  |||
Db      80  GGAACATGAGGCCCTGCATC  61

```

```

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 3 GGAACATGAAGCCCTTCAGC 22
    |||||
Db 19 GGACATGAATGCGCTTAC 38

```

RESULT 2

AA754748/C	AA754748	91 bp	RNA	linear	EST 21-JAN-1998
LOCUS	U020h06.r1	Barstead mouse	myotubes	MP1RB5	Mus musculus cDNA clone
DEFINITION	IMAGE1181243.5	Similar to	WP:ZK637.2	CE00433	; mRNA sequence.
ACCESSION	AA754748				
VERSION	AA754748				

SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE	Author
Gaisel, S., Kucaba, T., Lacey, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Webster, R.	1999

TITLE
JOURNAL
COMMENT

Contact: Maria M/Mouse EST Project
WashU-HMNI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LINC; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

```
Location/Qualifiers
1..70
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
```

```

/clone="IMAGE:1229255"
/sex="females"
/tissue="Whole skin"
/seq-strategy="11 weeks old"
/lab-host="SOLR (kanamycin resistant)"
/notes="Organ: skin; Vector: pBluescript SK-; Site: 1: EcoRI
Site 2: XhoI; Cloned unidirectionally. Primer: Oligo
dr. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; uni-ZAP XR Vector: -5'
adaptor sequence: 5' GATTCGGCAGCAG 3' -3' adaptor
sequence: 5' CTCGAGTTTCTTTTCTTTT 3'
BASE COUNT      19 a      22 c      15 g      14 t
ORIGIN
Query Match      61.7%; Score 14.8; DB 9; Length 70;
Best Local Similarity 88.9%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      4      GAAACATGAGCCTTCAG 21
Db      46      GATCTTGAGCCTTCAG 29

RESULT 4
A2805795      40 bp      DNA      linear      GSS 20-FEB-2001
LOCUS      2M0067F20F Mouse 10kb plasmid U0GC1M library Mus musculus genomic
DEFINITION
ACCESSION      A2805795
VERSION      A2805795.1 GI:12966606
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 40)
AUTHORS      Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0067 row: F Column: 20
Seq Primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 40.
Location/Qualifiers
1..40
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U0GC2M0067F20"
/clone_1kb="Mouse 10kb plasmid U0GC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/notes="Vector: PMD42HV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4

```

```

polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (911473211491AF129072.1), a copy number
inducible derivative of plasmid RL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      12 a      8 c      11 g      9 t
ORIGIN
Query Match      60.8%; Score 14.6; DB 17; Length 40;
Best Local Similarity 81.0%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY      3      GAAACATGAGCCTTCAGC 23
Db      17      GAAACATGATCCTTCAGAG 37

RESULT 5
A2842595      65 bp      DNA      linear      GSS 20-FEB-2001
LOCUS      2M0141F08F Mouse 10kb plasmid U0GC1M library Mus musculus genomic
DEFINITION
ACCESSION      A2842595
VERSION      A2842595.1 GI:13012503
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 65)
AUTHORS      Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0141 row: F Column: 08
Seq Primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 65.
Location/Qualifiers
1..65
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U0GC2M0141F08"
/clone_1kb="Mouse 10kb plasmid U0GC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/notes="Vector: PMD42HV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4

```

RESULT 8				
BH416484/c				
LOCUS	BH416484	84 bp	DNA	linear
				GSS 12-DEC-2001

DEFINITION 1007048D02.2BL.y1 1007 - Rescuemu Grid H Zea mays genomic, DNA sequence.

ACCESSION BH416484

VERSION BH416484.1 GI:17599142

KEYWORDS GSS.

SOURCE Zea mays.

ORGANISM Zea mays.

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 84)

Walbot, V.

Maize genomic sequences found using engineered Rescuemu transposon

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1007048 column: 28

Class: transposon-tagged.

Location/Qualifiers

1..84

/organism="Zea mays"

/cultivar="mixed background W23/A188/B73"

/db_xref="taxon:4577"

/clone_lib="1007 - Rescuemu Grid H"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/note="Organ: leaf; Vector: Rescuemu (engineered from Bluescript backbone); Site:1: BamHI; Site:2: BglII; Rescuemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site 'www.zmbd.laistate.edu' and follow the links for 'Rescuemu', 'Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 16 a 22 c 20 g 26 t

ORIGIN

Query Match 50.0%; Score 14.4; DB 17; Length 84;

Best Local Similarity 75.0%; Pred. No. 1.8e+04;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 GTGGAACATGAAGCCCTTCAGCGG 24

DB 74 GTGGAATTTACCCCTCAGCTG 51

RESULT 9

AZ992244

LOCUS 89 bp DNA linear GSS 27-APR-2001

DEFINITION 2M0276N13R Mouse 10kb plasmid UUGC2M library Mus musculus genomic

ACCESSION AZ992244

VERSION 2M0276N13 R, DNA sequence.

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 89)

Dunn, D., Aoyagi, A., Barber, M., Becorn, T., Duval, B., Hamll, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

JOURNAL

COMMENT

'M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert length: 10000 std error: 0.00

Plate: 0276 row: N column: 13

Seq primer: CACACGAGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 89.

Location/Qualifiers

1..89

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0276N13"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (91147321149b1AF19072.1) a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 17 a 18 c 20 g 34 t

ORIGIN

Query Match 60.0%; Score 14.4; DB 17; Length 89;

Best Local Similarity 75.0%; Pred. No. 1.8e+04;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 GTGGAACATGAAGCCCTTCAGCGG 24

DB 42 GTGGCCTTGATGCTCTTTCAGCGG 65

RESULT 10

AZ938487

LOCUS 42 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M0134N09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION AZ938487

VERSION 2M0134N09 F, DNA sequence.

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 42)

Dunn, D., Aoyagi, A., Barber, M., Becorn, T., Duval, B., Hamll, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

TITLE
'M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0134 row: N column: 09
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 42.

FEATURES
Source
1. .42
Location/Qualifiers

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCC2M0134N09"
/clone_lib="Mouse 10kb plasmid UGCC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g114732114[9b]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 12 a 7 c 12 g 11 t

Query Match 59.2%; Score 14.2; DB 17; Length 42;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 GGAACATGAAGCCCTTCAG 21
||||||| | | | | |
Db 18 GGAACATGAATCGCTTCG 36

RESULT 11
LOCUS A2954607 42 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0220B23p Mouse 10kb plasmid UGCC2M 1library Mus musculus genomic
clone UGCC2M0220B23 F, DNA sequence.
ACCESSION A2954607
VERSION A2954607.1 GI:13825834
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
1 (bases 1 to 42)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

TITLE
'M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0220 row: B column: 23
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 42.

FEATURES
Source
1. .42
Location/Qualifiers

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCC2M0220B23"
/clone_lib="Mouse 10kb plasmid UGCC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g114732114[9b]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 11 a 7 c 10 g 14 t

Query Match 59.2%; Score 14.2; DB 17; Length 42;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 GGAACATGAAGCCCTTCAG 21
||||||| | | | | |
Db 19 GGAACATGAATCGCTTCG 37

RESULT 12
LOCUS AL768539 76 bp DNA linear GSS 19-JUN-2002
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GR-075H10-011890,
genomic survey sequence.
ACCESSION AL768539
VERSION AL768539.1 GI:21521658
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE
1
AUTHORS Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., Sedler, H.

REFERENCE	AUTHORS	TITLE	JOURNAL
1	And Weisshaar, B.	A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines	Unpublished
2	Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B.	A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics	Unpublished
3	Li, Y., Strizhov, N., Rosso, M. and Weisshaar, B.	(bases 1 to 76)	Direct Submission
4	Submitted (17-JUN-2002)	Weisshaar, B., Max-Planck-Institut fuer Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany	
5	This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone T4D2. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:	http://www.mpiz-koeln.mpg.de/GABI-Kat/.	
6	Location/Qualifiers		
7	1. /76		
8	/organism="Arabidopsis thaliana"		
9	/strain="Columbia 0"		
10	/db_xref="taxon:3702"		
11	/clone="GK-075H10-011890"		
12	/clone="lib-Arabidopsis thaliana T-DNA insertion lines"		
13	/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragments" resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"		
14	BASE COUNT	15 a 19 c 8 g 34 t	
15	ORIGIN		
16	Query Match	59.28; Score 14.2; DB 17; Length 76;	
17	Best Local Similarity	84.28; Fred. NO. 2.1e+04;	
18	Matches	16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
19	QY	3 GGAACATGAAGCCCTTCAG 21	
20	DB	34 GAAACTTGGAAGGCTTCAG 16	
21	RESULT 13		
22	LOCUS	AZ861128	
23	DEFINITION	2M0167M19F Mouse 10kb Plasmid UNGC1M library Mus musculus genomic clone UNGC2M0167M19 F, DNA sequence.	
24	ACCESSION	AZ861128	
25	VERSION	AZ861128.1 GI:13057138	
26	KEYWORDS	GSS.	
27	SOURCE	house mouse.	
28	ORGANISM	Mus musculus	
29	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.	
30	AUTHORS	1 (bases 1 to 89)	
31	TITLE	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.	
32	JOURNAL	Mouse whole genome scaffolding with paired end reads from 10kbp Plasmid inserts	
33	COMMENT	Unpublished (2000)	
34	CONTACT:	Robert B. Weiss	
35	UNIVERSITY OF UTAH	Genome Center	

	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLU, UT
	84112, USA
	Tel.: 801 585 5606
	Fax: 801 585 7177
	Email: dunn@genetics.utah.edu
	Insert Length: 10000 Std Error: 0.00
	Plate: 0167 row: M column: 19
	Seq primer: CGTGTGTAAGACGGCCAGC
	Class: plasmid ends
FEATURES	High quality sequence stop: 89.
SOURCE	1. 89 location/Qualifiers
	/organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="U06C2M0167M19" /clone_1ib="Mouse 10kb plasmid U06CIM library" /sex="Male" /lab_host="E. Coli strain XL10-Gold, pI-resistant, F-" /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1147321149b/AP12072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E.coli XL10-gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT	29 a 25 c 20 g 15 t
ORIGIN	
Query Match	59.2% Score 14.2; DB 17; Length 89;
Best Local Similarity	84.2%; Pred. No. 2.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
OY 3 GGAAATGAAGCCCTTCAG 21	
Db 17 GGAAATGAATGCCTTCAG 35	
RESULT 14	
AZ859525	99 bp DNA linear GSS 21-FEB-2001
LOCUS	ZM016510F Mouse 10kb plasmid U06CIM library Mus musculus genomic
DEFINITION	C clone U06C2M016510 F, DNA sequence.
ACCESSION	AZ859525
VERSION	AZ859525.1 GI:1305932
KEYWORDS	GSS.
SOURCE	house mouse.
ORGANISM	Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.	
REFERENCE	1 (bases 1 to 99)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Kelly, M., Rose,M., Reese,R., Stokes,K., Tingey,A., von Niederhausern,A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center
JOURNAL	
COMMENT	

1000

Search completed: December 21, 2002, 19:25:49
Job time : 748.592 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:20:00 : Search time 832.041 Seconds
without alignments)
525.549 Million cell updates/sec

Title: US-09-121-239-22

Sequence: 1 TCTGACCTTGAGCCCTGAGGCTGAGT 27

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

EST:
1: em_estba.*
2: em_estlum.*
3: em_estlum.*
4: em_estlum.*
5: em_estlum.*
6: em_estlum.*
7: em_estlum.*
8: em_estlum.*
9: gb_estl.*
10: gb_estl.*
11: gb_estl.*
12: gb_estl.*
13: gb_estl.*
14: gb_estl.*
15: em_estfun.*
16: em_estfun.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_hum.*
20: em_gss_hum.*
21: em_gss_hum.*
22: em_gss_hum.*
23: em_gss_hum.*
24: em_gss_hum.*
25: em_gss_hum.*
26: em_gss_hum.*
27: em_gss_hum.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	16	59.3	59	17	AZ800849 2M0059602
2	16	59.3	100	10	BE587181 WHE0519_D
3	15.6	57.8	72	17	FR0010427 F_rubrip
4	15.6	57.8	97	12	BG535415 602563077
5	15.4	57.0	52	17	AZ597394 1M0411823
6	15.2	56.3	97	9	AA973016 op25603.s

7	15.2	56.3	98	14	B0566275
8	15	55.6	61	17	AZ81308
9	14.8	54.8	83	12	BE581859 602099323
10	14.8	54.1	89	9	AA485016
11	14.6	54.1	76	9	AI594823
12	14.6	54.1	87	14	N72966
13	14.6	54.1	93	17	BH229029
14	14.6	54.1	97	14	W82482
15	14.6	53.3	97	14	AI215770
16	14.4	53.3	62	17	AZ655830
17	14.4	53.3	66	17	AZ424287
18	14.4	53.3	70	9	AZ602165
19	14.4	53.3	70	9	AI000791
20	14.4	53.3	77	14	D19089
21	14.4	53.3	79	9	AA535865
22	14.4	53.3	85	10	AM089043
23	14.4	53.3	93	9	AA637489
24	14.4	53.3	96	13	BI787905
25	14.4	53.3	97	9	AU259143
26	14.4	53.3	43	9	AA604155
27	14.2	52.6	46	17	AA656590
28	14.2	52.6	76	17	AZ789070
29	14.2	52.6	77	17	AZ508174
30	14.2	52.6	83	17	AZ777224
31	14.2	52.6	85	17	AZ944510
32	14.2	52.6	88	9	AI337691
33	14.2	52.6	88	9	AI654562
34	14.2	52.6	88	9	AI654562
35	14.2	52.6	88	17	AZ461077
36	14.2	52.6	94	17	AZ815511
37	14.2	52.6	96	17	AA880881
38	14.2	52.6	98	17	AZ481031
39	14.2	52.6	100	12	BF944293
40	14.2	51.9	24	17	AZ807619
41	14	51.9	50	9	AU106947
42	14	51.9	96	14	W76234
43	14	51.9	100	9	AA544623
44	13.8	51.1	38	17	AZ806846
45	13.8	51.1	48	17	AZ514368

ALIGNMENTS

RESULT 1
LOCUS AZ800849
DEFINITION 2M0059002F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0059002 F, DNA sequence.
ACCESSION AZ800849
VERSION AZ800849.1 GI:12953172
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE
1 (bases 1 to 59)
Dunn, D., Loy, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Kelly,
M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A.,
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
41112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0059 row: 0 column: 02
 Seq primer: CGTGTGTAACGACGCGCAGT
 Class: Plasmid ends
 High quality sequence stop: 59.
 Location/Qualifiers
 1..59
 source

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="TUGC2M0059002"
 /clone_1lb="Mouse 10kb plasmid TUGC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (9114732114[9b]AF129072.1) a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN

Query Match 59.3%; Score 16; DB 17; Length 59;
 Best Local Similarity 79.2%; Pred. No. 4.9e+03;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCTCAGGCTCTG 24
 |||||
 Db 7 TGTGCTTCTAGCTCAAGCTCTG 30

RESULT 2
 BE587181
 LOCUS BE587181 100 bp mRNA linear EST 17-ANG-2000
 DEFINITION WHE0519.D07.H132R Secale cereale aluminum-stressed root tip cDNA
 accession BE587181
 VERSION BE587181.1 GI:9840213
 KEYWORDS EST.
 SOURCE rye.
 ORGANISM Secale cereale
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 1 (bases 1 to 100)
 Anderson,O.D., Butler,E., Chao,S., Gustafson,J.P., Han,P.S., Hsia,
 C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and
 Tong,J.C.
 The structure and function of the expressed portion of the wheat
 genomes - Aluminum-stressed root tip cDNA library from rye (Secale
 cereale)
 Unpublished (2000)
 Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105555773
 Fax: 5105555818
 Email: oanderson@pw.usda.gov
 Sequence have been trimmed to remove vector sequence and low

JOURNAL COMMENT

quality sequence with phred score less than 20
 Seq primer: M13 reversed primer.
 Location/Qualifiers
 1..100
 source

/organism="Secale cereale"
 /cultivar="Bianco"
 /db_xref="taxon:4550"
 /clone="WHE0519.D07.H13"
 /clone_1lb="Secale cereale aluminum-stressed root tip cDNA library"
 /tissue_type="Root tip"
 /dev_stage="Seedling"
 /lab_host="E. coli DH2S"
 /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; Seeds were germinated aseptically on filter paper and transferred to a hydroponic growth system in a growth chamber when the primary root was 1 cm in length. After a 2-day establishment period, seedlings were subjected to a 5 ppm aluminum stress prior to tissue harvest. Plants were grown in an environmental chamber. The tissue, total RNA, and poly(A) RNA were prepared, and a cDNA library was made (Butler and Gustafson) at University of Missouri, Columbia. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 21 a 19 c 33 g 27 t
 ORIGIN

Query Match 59.3%; Score 16; DB 10; Length 100;
 Best Local Similarity 79.2%; Pred. No. 6.2e+03;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 TGACTTTGAGCTCAGGCTCTGAG 26
 |||||
 Db 45 TGCGCTTGAAGCTCAGGCTGTGAG 68

RESULT 3
 FR0010427
 LOCUS FR0010427 72 bp DNA linear GSS 18-SEP-1997
 DEFINITION F. rubripes GSS sequence, clone 041K13ba2, genomic survey sequence.
 accession AL0011704
 VERSION AL0011704.1 GI:2447274
 KEYWORDS GSS; genome survey sequence.
 SOURCE Takifugu rubripes.
 ORGANISM Takifugu rubripes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontidae; Takifugu.
 1 (bases 1 to 72)
 Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umranta,Y.,
 Williams,G. and Brenner,S.
 Direct Submision
 Submitted (09-SEP-1997) MRC Human Genome Mapping Project Resource
 Centre Hinxton, Cambridge, CB10 1SB. Email: biobelp@hmp.mrc.ac.uk
 V type: phagemid
 PRIMER: KS

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

DESCR: One pass dye-terminator sequencing of cosmid cloned genomic sequence.

FEATURES
 source

Location/Qualifiers
 1..72
 /organism="Takifugu rubripes"
 /db_xref="taxon:31033"
 /clone="041K13ba2"
 /clone_1lb="cosmid 041K13"
 BASE COUNT 11 a 17 c 21 g 21 t 2 others
 ORIGIN

Query Match 57.8%; Score 15.6; DB 17; Length 72;
 Best Local Similarity 81.8%; Pred. No. 8e+03;

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

1 (bases 1 to 97)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

FEATURES

Source

This clone is available royalty-free through LMAN; contact the IMAGE Consortium (infoimage@lmn.gov) for further information.
Seq primer: 40m13 fwd. Ex from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..97

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1577884"
/clone_1lb="Soares_NFL-T_GBC_S1"
/lab_host="DH10B"

BASE COUNT

27 a 20 c 26 g 24 t

ORIGIN

Query Match 56.3%; Score 15.2; DB 9; length 97;
Best Local Similarity 85.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCTGACCTTGAGCGTCGACGG 20
||||| ||||| ||||| |||||

Db 8 TCTGCGTTTGACCTTCAGGG 27

RESULT 7

BO566275/c

LOCUS

98 bp mRNA linear EST 19-JUN-2002
g156g02.y1 Mouse Organ of Corti cDNA pluescript Mus musculus cDNA

DEFINITION

clone g156g02 5', mRNA sequence.

ACCESSION

BO566275
BO566275.1 GI:21469592

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

house musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

1 (bases 1 to 98)
Kachar, B.

TITLE

EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

JOURNAL

Unpublished (2002)

COMMENT

Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 56 row: 9 column: 02
Seq primer: M13RPI reverse primer (ABI).
Location/Qualifiers

source

1..98
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="g156g02"
/clone_1lb="Mouse Organ of Corti cDNA pluescript"
/sex="male and female"
/dev_stage="post natal day 5 to 13".

/note="Organ: Organ of Corti. Vector: pluescript. The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bulla capsule of the cochlea was clipped away, stria vascularis epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dGTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with Xho I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Palo Alto, CA) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with giga-pack III Gold and, upon filtration on XL1 Blue MRF' cells the recombinants. Stratagene's Exassist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. The 5' end of the cDNA clones were generated with the universal M13 reverse primer (CACGACACCTATAC) and 25 Biosystems, Foster City, CA). Sequencing reactions were performed on M13 tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have known function; 23% have hits in Genbank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT

23 a 20 c 29 g 26 t

ORIGIN

Query Match 56.3%; Score 15.2; DB 14; length 98;
Best Local Similarity 85.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 TTGAGCCTTGAGCGTCGACGT 27
||| ||||| ||||| |||||

FEATURES

1..97

Db 94 TTCATCCTCAGGGTCTGAAT 75

[illegible]

REFERENCE AUTHORS

TITLE

JOURNAL
COMMENT

FEATURES

BASE COUNT
ORIGIN

Query Match	55.6%	Score 15;	DB 17;	Length 61;
Best Local Similarity	78.3%	Pred. No. 1.4e+04;		
Matches 18;	Conservative	0;	Mismatches 5;	Indels 0;
			Gaps	0;
QY	1 TCTGACTTTGAGCCTCAGGCTCT	23		

Db 6 TCTGACAGTGAGGATCAGGCTCT 28

RESULT 9	BF581859/c	BF581859	83 bp	linear	EST 12-DEC-2000
LOCUS					
DEFINITION		602099323r1 NC1-CGAF-Co24	Mus musculus cDNA clone	IMAGE:4219204	5'
ACCESSION		BF581859.1	GI:11655675		
VERSION					
KEYWORDS					
SOURCE		house mouse,			

COMMENT

FEATURES
SOURCE

BASE COUNT
ORIGIN

Query Match	54.88;	Score 14.8;	DB 12;	Length 83;
Best Local Similarity	73.18;	Pred. No. 1.9e+04;		
Matches 19; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0

Db 42 TCTGGCCAGGAGTCTCATGGCCTGAG 17

RESULT	10
LOCUS	AA485016/c
DEFINITION	AA485016 aa29f08..1 NCI_CGAP_GCB1 Homo sapiens CDNA clone IMAGE:815655 5' , mrna sequence.
ACCESSION	AA485016
VERSION	AA485016.1 GI:2214235
KEYWORDS	EST .
SOURCE	human. Homo sapiens
ORGANISM	Homo sapiens

JOURNAL
COMMENT

Tissue Procurement: Louis M. Staedt, M.D., Ph.D., David Allman Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
Statistical Analysis: Margaret W. Coe, Ph.D.

CDNA LIBRARY ATLAS by: Craig Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnlnl.gov/brpr/image/image.html
Seq primer: -28ml3 rev1 RT from Amersham
High quality sequence stop: 73.

FEATURES
source

```

1. 89
/organism="Homo sapiens"
/db_xref="GDB:6035132"
/db_xref="taxon:9606"
/clone_image:815655
/clone_id="NCI CGAP GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10b"
/notes="Vector: pP73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, 1D-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTCAAGAGGAGCGGCGCTCATTTTTTTTTTTTTTTT-3']
and double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia) digested with Not I and cloned into the Not I
and Eco RI sites of the modified pP73D vector. Library
went through one round of normalization, and was
constructed by Sento Soares and M. Fatima Bonaldo."

```

BASE COUNT	27 a	24 c	22 g	16 t
ORIGIN				

ORIGIN

Query Match	54.8%;	Score 14.8;	DB 9;	length 89;
Best Local Similarity	88.9%;	Pred. No. 2e+04;		
Matches	16;	Conservative	0;	Mismatches 2;
			Indels	0;
			Gaps	0;
OY	7	TTTGACGCTCAGGGCTCTG	24	
db	61	TTTGAGCCGCGACAGTGTCTG	44	

[illegible]

ACCESSION	AI594823
VERSION	AI594823.1
KEYWORDS	GI:4603871
EST.	

SOURCE ORGANISM

REFERENCE

AUTHORS

3333

TITLE
JOURNAL
COMMENT

Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LINT ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:648382
This clone was previously sequenced on the 5' end only, this new data is from the 3' end
Trace considered overall poor quality
High quality sequence stop: 1.
Location/Qualifiers

Source

```

          /strain="NIH Swiss"  

          /ID_xref="taxon:10090"  

          /clone_image="IMAGE:1227790"  

          /clone_lib="Stratagene mouse heart (#937316)"  

          /sex="pooled"  

          /tissue_type="heart"  

          /dev_stage="13 day embryos"  

          /lab_host="SOLR (kanamycin resistant)"  

          /note="Organ: heart; Vector: plusscript SK-; Site_1:  

          ECoRI; Site_2: XhoI; Cloned unidirectionally. Primer:  

          Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts.  

          Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'  

          adaptor sequence: 5' GAATTCGACACGAG 3' ~3' adaptor  

          sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'."

```

BASE COUNT
ORIGIN

ORIGIN

Query Match	54.1%;	Score 14.6;	DB 9;	Length 76;
Best Local Similarity	81.0%;	Pred. No. 2.3e+04;		
Matches 17; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;
QY	6	CTTGAAGCCTCAGGCTGTGAG	26	
Db	49	CTTCTCCTCTCAGACTCTGAG	69	

RESULT	LOCUS	DEFINITION
12 N72966/c	N72966	87 bp mRNA linear EST 28-JAN-1997 yy48hl1.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:246021 5' similar to gb:K02765 COMPLEMENT C3 PRECURSOR (HUMAN)

ACCESSION	N/2908
VERSION	N72966.1
KEYWORDS	EST.
SOURCE	human.

ORGANISM

REFERENCE AUTHORS

ATTN:

LIFE
JOURNAL
MEDLINE

COMMENT

FEATURES

```
1. .8/
/organism="Homo sapiens"
source
```


Query Match 54.1%; Score 14.6; DB 14; Length 97;
 Best Local Similarity 81.0%; Pred. No. 2.5e+04;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 GACTTGAGCTCAGGCTCG 24
 1 ||||| ||||| ||||
 Db 67 GCTTTGAACTCAGCTCTCG 47

RESULT 15

AI215770

LOCUS

58 bp

mRNA

linear

EST 02-DEC-1998

DEFINITION

gm39c08.x1 NCI-CGAP_Lu5 Homo sapiens CDNA clone IMAGE:1884206 3'
 similar to SW:POR2.HUMAN P45880 VOLTAGE-DEPENDENT ANION-SELECTIVE
 CHANNEL PROTEIN 2; contains element MER35 repetitive element;;
 mRNA sequence.

ACCESSION

AI215770

VERSION

AI215770.1 GI:3784811

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 58)

AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

www.bio.lnl.gov/dbtp/image/image.html

www.bio.lnl.gov/dbtp/image/image.html

Trace considered overall poor quality

Insert Length: 1424 Std Error: 0.00

Seq primer: -40UP from GIBCO

High quality sequence stop: 1.

FEATURES

Location/Qualifiers

1..58

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1884206"

/clone_1lb="NCI-CGAP_Lu5"

/tissue_type="carcinoid"

/lab_host="DH10B"

/note="Organ: lung; Vector: pRT3D-Pac (Pharmacia) with a

modified polylinker; 1st strand cDNA was prepared from a

neuroendocrine lung carcinoid, and was then primed with a

Not I - oligo(dT) primer. Double-stranded cDNA was ligated

to Eco RI adaptors (Pharmacia), digested with Not I and

cloned into the Not I and Eco RI sites of the modified

pRT3 vector. Library is normalized. Library was

constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT

ORIGIN

15 a 15 c 13 g 15 t

Query Match

53.3%; Score 14.4; DB 9; Length 58;

Best Local Similarity

93.8%; Pred. No. 2.4e+04;

Matches 15; Conservative

0; Mismatches 1; Indels 0; Gaps 0;

OY 12 GCCTCAGGCTCTGAGT 27

||||| ||||| |||||

Db 13 GCCTCAGGCTCTGAGT 28

||||| ||||| |||||

Search completed: December 21, 2002, 19:26:00
 Job time : 843.041 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:20:00 ; Search time 832.041 seconds
(without alignments)
525.549 Million cell updates/sec

Title: US-09-121-239-23

Perfect score: 1 UGACUUCUAGCCUCAGGUCUGAGU 27

Sequence: 1 UGACUUCUAGCCUCAGGUCUGAGU 27

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em.esthum:*
2: em.esthum:*
3: em.esthum:*
4: em.esthum:*
5: em.esthum:*
6: em.esthum:*
7: em.esthum:*
8: em.esthum:*
9: em.esthum:*
10: em.esthum:*
11: em.esthum:*
12: em.esthum:*
13: em.esthum:*
14: em.esthum:*
15: em.esthum:*
16: em.esthum:*
17: em.esthum:*
18: em.esthum:*
19: em.esthum:*
20: em.esthum:*
21: em.esthum:*
22: em.esthum:*
23: em.esthum:*
24: em.esthum:*
25: em.esthum:*
26: em.esthum:*
27: em.esthum:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	16	59.3	59	17	AZ800849	AZ800849 2M0059002
2	16	59.3	100	10	BE587181	BE587181 WH0519_D
3	15.6	57.8	72	17	FR0010427	AL001704 F.rubrip
4	15.6	57.8	97	12	BG535415	BG535415 602563077
5	15.4	57.0	52	17	AZ597394	AZ597394 1M0411B23
6	15.2	56.3	97	9	AA973016	AA973016 op25e03.s

c	7	15.2	56.3	98	14	B0566275	B0566275 915602.y
c	8	15	55.6	61	17	AZ781308	AZ781308 2M0019F04
c	9	14.8	54.8	83	12	BF581859	BF581859 602099323
c	10	14.8	54.8	89	9	AA485016	AA485016 aa39f08.r
c	11	14.6	54.1	76	9	A1594823	A1594823 vv18e08.x
c	12	14.6	54.1	87	14	N72966	N72966 yv48h11.r1
c	13	14.6	54.1	93	17	BH229029	BH229029 100614960
c	14	14.6	54.1	97	14	W82482	W82482 mf04d03.r1
c	15	14.4	53.3	58	9	A1215770	A1215770 qm3c08.x
c	16	14.4	53.3	62	17	AZ655830	AZ655830 1M0531G04
c	17	14.4	53.3	66	17	AZ424287	AZ424287 1M0203M17
c	18	14.4	53.3	66	17	AZ602165	AZ602165 1M0420J16
c	19	14.4	53.3	70	9	A1000791	A1000791 ov11q12.s
c	20	14.4	53.3	77	14	D19088	D19088 MDG501296
c	21	14.4	53.3	84	9	AA535865	AA535865 rf90b03.s
c	22	14.4	53.3	85	10	AA089043	AA089043 cm93a06.s
c	23	14.4	53.3	85	10	AA089043	AA089043 x672912.x
c	24	14.4	53.3	93	13	AA637489	AA637489 v132d10.t
c	25	14.4	53.3	96	13	BI787905	BI787905 s8q77b01.
c	26	14.4	53.3	97	9	A0259143	A0259143 A0259143
c	27	14.2	52.6	43	9	AA604155	AA604155 n059c01.s
c	28	14.2	52.6	66	17	AZ665590	AZ665590 1M0548P14
c	29	14.2	52.6	76	17	AZ789070	AZ789070 2M0036004
c	30	14.2	52.6	77	17	AZ508174	AZ508174 1M0350C18
c	31	14.2	52.6	83	17	AZ777224	AZ777224 2M0011D02
c	32	14.2	52.6	85	17	AZ944510	AZ944510 2M0205C24
c	33	14.2	52.6	88	9	A1937691	A1937691 wp82d11.x
c	34	14.2	52.6	88	9	AL645462	AL645462 AL645462
c	35	14.2	52.6	88	17	AZ461077	AZ461077 1M0266H14
c	36	14.2	52.6	94	17	AZ812511	AZ812511 2M0079B13
c	37	14.2	52.6	96	9	AA880881	AA880881 vx33b09.r
c	38	14.2	52.6	98	17	AZ481031	AZ481031 1M0303E01
c	39	14.2	52.6	100	12	BP944293	BP944293 CM0-NN115
c	40	14.2	52.6	24	17	AZ807619	AZ807619 2M0070001
c	41	14	51.9	50	9	AU106947	AU106947 AU106947
c	42	14	51.9	96	14	W76234	W76234 zds0c10.r1
c	43	14	51.9	100	9	AA544623	AA544623 vx34b02.t
c	44	13.8	51.1	38	17	AZ806846	AZ806846 2M0059K10
c	45	13.8	51.1	48	17	AZ514368	AZ514368 1M0361D04

ALIGNMENTS

RESULT 1	AZ800849	59 bp	DNA	linear	GSS 16-FEB-2001
LOCUS	2M0059002F	Mouse 10kb plasmid UGCLM	library	Mus musculus genomic	
DEFINITION	clone UGCLM0059002 F, DNA sequence.				
ACCESSION	AZ800849				
VERSION	AZ800849.1	GI:12953172			
KEYWORDS	GSS.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Dunn,D., Moyagl,A., Barber,M., Beaconn,T., Duval,B., Hamil,C., Islem,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D., Weiss,R.				
AUTHORS	Mouse whole genome scaffolding with paired end reads from 10kb				
TITLE	Plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: dunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00				

Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 3 UGACUUGAGCCUCCAGGUCUG 24
 Db 39 TGACTTTCAGCCCTGGGTGCG 60

RESULT 4

BG535415 97 bp mRNA linear EST 03-APR-2001
 BG535415
 DEFINITION 602563077F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4687962 5',
 mRNA sequence.
 BG535415
 VERSION BG535415.1 GI:13526960
 KEYWORDS EST
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs.fda.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1501 row: 1 column: 19
 High quality sequence stop: 97.
 Location/Qualifiers

FEATURES

1..97
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4687962"
 /clone_1b="NIH_MGC_77"
 /lab_host="DH10B (TI phage-resistant)"
 /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site: 1:
 5' (ggcgctcgcc); Site 2: 5' (ggcgctcgcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-ATCTAGAGCGCGAGCGCGCGCGACG-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.9
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."
 BASE COUNT 14 a 26 c 46 g 11 t
 ORIGIN

Query Match 57.8%; Score 15.6; DB 12; Length 97;
 Best Local Similarity 63.6%; Pred. No. 9; 1e+03;
 Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 UGACUUGAGCCUCCAGGUC 22
 Db 64 TCGACTTTCAGCCCTGGGTGCG 43

RESULT 5
 A2597394 52 bp DNA linear GSS 13-DEC-2000
 LOCUS A2597394
 DEFINITION IM0411B23F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
 IMAGE:1577884 3' similar to SW-TCF2_HUMAN P40227 T-COMPLEX PROTEIN
 ACCESSION A2597394.1 GI:11719584
 VERSION A2597394
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 52)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly
 M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhauser,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE

JOURNAL

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 Rm 308 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112 USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0411 row: B column: 23
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 52.
 Location/Qualifiers

FEATURES

1..52
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG1M0411B23"
 /clone_1b="Mouse 10kb plasmid UUCG1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: pMD42ny; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g147321419b1AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptor complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."
 BASE COUNT 19 a 8 c 6 g 19 t
 ORIGIN

Query Match 57.0%; Score 15.4; DB 17; Length 52;
 Best Local Similarity 58.8%; Pred. No. 8; 4e+03;
 Matches 10; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 QY 1 UGACUUGAGCCUCCAG 17
 Db 10 TCGACTTTCAGACCTCA 26

RESULT 6
 AA973016 97 bp mRNA linear EST 20-MAY-1998
 LOCUS AA973016
 DEFINITION op25e03.81 Soares_NFL_T_GBC.S1 Homo sapiens cDNA clone
 IMAGE:1577884 3' similar to SW-TCF2_HUMAN P40227 T-COMPLEX PROTEIN
 ACCESSION AA973016
 VERSION AA973016
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 97)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (infoimage.lnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: -40ml3 fwd. EP from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..97
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1577884"
 /clone_id="Soares_NFL_T_GBC_S1"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not 1; Site_2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NDH19W, testis NHT, and B-cell
 NCI-CGAP-GCB1) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 I.M.A.G.E. clones 297480-302087, 682632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo."
 BASE COUNT 27 a 26 g 24 t
 ORIGIN
 Query Match 56.3%; Score 15.2; DB 9; Length 97;
 Best Local Similarity 55.0%; Pred. No. 1.4e+04;
 Matches 11; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 UUGAGCUUGAGCCUCGAGG 20
 :||:|||||:|||||
 Db 8 TCTGGCTTGGACCTCAGGG 27
 RESULT 7
 BO566275/c 98 bp mRNA linear EST 19-JUN-2002
 LOCUS g156902.y1 Mouse Organ of Corti cDNA Bluescript Mus musculus cDNA
 DEFINITION clone g156902 5', mRNA sequence.
 ACCESSION BO566275
 VERSION BO566275.1 GI:21469592
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 98)
 AUTHORS Kachar,B.
 TITLE EST analysis of gene expression in the mouse Organ of Corti at the
 onset of hearing
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kachar,B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kachar@nidcd.nih.gov
 Plate: 56 row: 9 column: 02
 Seq primer: M13RPI reverse primer (ABI).
 Location/Qualifiers

source
 1..98
 /organism="Mus musculus"
 /strain="BALB/c"
 /db_xref="taxon:10090"
 /clone="g156902"
 /clone_id="Mouse Organ of Corti cDNA bluescript"
 /sex="male and female"
 /dev_stage="Post natal day 5 to 13"
 /note="Organ: Organ of Corti; Vector: pBluescript; The
 organ of Corti (OC) was fine dissected from a total of 386
 OC as follows: 102 samples from post-natal (P) day 5; 72
 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
 14 from P12 and 24 from P13. After killing animals by
 cervical dislocation followed by decapitation, the bulla
 was removed and opened in Leibowitz medium. The bony
 capsule of the cochlea was chipped away, stria vascularis
 and spiral ligament were removed and the sensory
 epithelium was carefully dissected out of the modiolus.
 Total RNA was extracted using the micro Fasttrack kit
 (catalog # K1593-02; Invitrogen, Carlsbad, CA), according
 to manufacturer's instructions. Reverse transcription and
 library construction were carried out with the Uni-Zap XR
 vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
 GigaPack III Gold Cloning kit (catalog # 237612), both
 from Stratagene (La Jolla, CA, USA), according to
 manufacturer's instructions. Briefly: 1.5 ug mRNA was
 reverse transcribed using a hybrid oligo(dT) linker-primer
 that contains an Xho I site. First strand synthesis was
 primed with the linker-primer and transcribed using
 Moloney murine leukemia virus reverse transcriptase
 (MMuLV-RT) and 5-methyl dCTP. The second strand was
 synthesized with DNA polymerase and RNase H. Complementary
 DNA was blunt ended with Pfu DNA polymerase, ligated with
 EcoR I adapters in the presence of ligase and digested
 with Xho I. The cDNA was sequentially size fractionated
 over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)
 and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)
 columns to enrich for cDNAs greater than 400bp and 1000 bp
 , respectively. The cDNA was then directionally ligated to
 the Uni-Zap XR vector, which had been predigested with
 EcoR I and Xho I. The phagemid was packaged with GigaPack
 III Gold and, upon titration on XL1 Blue MRF' cells, the
 yield of the phage library was estimated to be 11,100,000
 recombinants. Stratagene's EXASist interference
 resistance helper phage (catalogue # 211203) was adopted
 to rescue plasmid DNA from the phages. Upon plating of the
 rescued library, individual cDNA clones were selected and
 grown in 96-well, 2 ml growth plate. Plasmid DNA was
 purified from 200 ul of saturated culture with the
 Concert96(TM) plasmid purification kit (Invitrogen,
 Carlsbad, CA) as instructed by the manufacturer. ESTs from
 the 5' end of the cDNA clones were generated with the
 universal M13 reverse primer (CAGGAAGCATGACC) and 25%
 strength BigDye terminator sequencing chemistry (Applied
 Biosystems, Foster City, CA). Sequencing reactions were
 performed on MJ Tetrad thermal cyclers (MJ Research,
 Watlham, MA), and analyzed on 3700 automated capillary
 sequencers using POP5 polymer (Applied Biosystems, Foster
 City, CA). The frequency distribution of the library is
 as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10;
 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of
 genes are present in GenBank and have known function; 23%
 have hits in GenBank, but do not have assigned function;
 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 23 a 29 g 26 t
 ORIGIN
 Query Match 56.3%; Score 15.2; DB 14; Length 98;
 Best Local Similarity 55.0%; Pred. No. 1.4e+04;
 Matches 11; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 Oy 8 UUGAGCCUCGAGGCGUGAGU 27
 ::|||:|||||:|||||

D8 94 TTCATCTCAGGTCGAT 75

RESULT 8
LOCUS A2781308
DEFINITION 61 bp DNA linear GSS 16-FEB-2001
ACCESSION ZK0019P04R Mouse 10kb plasmid UNGCIM library Mus musculus genomic
VERSION clone UNGCZM0019F04 R, DNA sequence.
KEYWORDS A2781308.1 GI:12913872
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS I (bases 1 to 61)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
'M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10Kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Room 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0019 row: F column: 04
Seq primer: CACACGGAAACAGCATGACC
Class: plasmid ends
High quality sequence stop: 61.

FEATURES
SOURCE location/Qualifiers
1..61
/organism="Mus musculus"
/strain="C57Bl/6J"
/db_xref="taxon:10090"
/clone="UNGZM0019F04"
/clone_lib="Mouse 10Kb plasmid UNGCIM library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD2mV; Purified genomic DNA from M.
musculus C57Bl/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivativess
of pMW42 (g14732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
Chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 12 a 6 c 21 g 22 t
ORIGIN
Query Match 55.6%; Score 15; DB 17; Length 61;
Best Local Similarity 52.28; Prid. No. 14e+04;
Matches 12; Conservative 6; Mismatches 5; Indels 0; Gaps 0
QY 1 UCUGACUUUGAGCCUCACGSGUCU 23
:::||||::|| ::|||:::

RESULT 9	83 bp	mRNA	linear	EST 12-DEC-2000
LOCUS BF581859/c	602099323F1	NCI_CGAP_Co24	Mus musculus cDNA clone IMAGE:4219204 5',	
DEFINITION	mRNA sequence.			
ACCESSION	BF581859			
VERSION	BF581859.1	GI:11655675		
KEYWORDS	EST.			
SOURCE	house mouse			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
TITLE	1 (bases 1 to 83)			
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: L1AM9800 row: n column: 05 High quality sequence stop: 83. Location/Qualifiers 1. 83 /organism="Mus musculus" /strain="FVB/N" /db_xref="taxon:10090" /clone_1ib="NCI_CGAP_Co24" /clone_1ib="NCI_CGAP_Co24" /lab_host="DH10B (T1 phage-resistant)" /note="Organ: colon; Vector: PCWV-SPOrt6; Site:1; NotI; Site:2; SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."			
BASE COUNT	24 a	26 c	19 g	14 t
ORIGIN				
Query Match	54.8%	Score 14.8;	DB 12;	Length 83;
Best Local Similarity	57.7%	Pred No.1,9e+04;		
Matches 15;	Conservative 4;	Mismatches 7;	Indels 0;	Gaps 0
QY 1	UCGACCTUGGACCCGACGAGCTCGAG	26		
Db 42	TCTGGCCAGGAGCTCATGGCTTAG	17		
RESULT 10	89 bp	mRNA	linear	EST 15-AUG-1999
LOCUS AA485016/c	aa339f08.r1	NCI_CGAP_GCB1	Homo sapiens cDNA clone IMAGE:815635 5',	
DEFINITION	mRNA sequence.			
ACCESSION	AA485016			
VERSION	AA485016.1	GI:2214235		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
TITLE	1 (bases 1 to 89)			
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .			
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov			

Tissue Procurement: Louis M. Staedt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldi, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/brrp/image/image.html
 Seq primer: -28m13 rev1 ET from Amersham
 High quality sequence stop: 73.
 Location/Qualifiers
 1. 89

FEATURES
 source
 /organism="Homo sapiens"
 /db_xref="GDB:6035132"
 /db_xref="taxon:9606"
 /clone="IMAGE:815655"
 /clone_lib="NCI-CCAP_GCB1"
 /issue_type="germinal center B cell"
 /lab_host="DH10B"
 /note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, 19D-), provided by Dr. Louis M. Staedt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer
 5'-TGTTACCATCTGATGAGGAGGCGGCGCTATTTTCTTTT-3'
 1. Double-stranded cDNA was ligated to Eco RI adaptors and Eco RI sites of the modified pRT3D vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldi."
 BASE COUNT 27 a 24 c 22 g 16 t
 ORIGIN

Query Match 54.8%; Score 14.8; DB 9; Length 89;
 Best Local Similarity 61.1%; Pred. No. 2e+04;
 Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 Oy 7 UUGAGCCUCAGGUCUG 24
 ::::||||| ||| :|||
 Db 61 TTGAGCCGACAGTCTG 44

RESULT 11
 A1594823 76 bp mRNA linear EST 21-Apr-1999
 LOCUS
 DEFINITION
 IMAGE:1222790 3' similar to gb:D42040 RIN3 PROTEIN (HUMAN); mRNA
 sequence.
 ACCESSION
 A1594823.1 GI:4603871
 KEYWORDS
 EST.
 SOURCE
 house mouse.
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
 1 (bases 1 to 76)
 Marti, M., Hillier, L., Kucaba, T., Martin, D., Beck, C., Wylie, T.,
 Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person,
 B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter,
 E., Kohn, S., Shio, T., Jackson, Y., Cardenas, M., McCann, R.,
 Waterston, R., and Wilson, R.
 The WashU-NCI Mouse EST Project 1999
 Unpublished (1999)
 CONTACT: Maria M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:648382
 This clone was previously sequenced on the 5' end only, this new
 data is from the 3' end
 Trace considered overall poor quality
 High quality sequence stop: 1.
 Location/Qualifiers
 1. 76

FEATURES
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 /organism="Mus musculus"
 /strain="NIH Swiss"
 /db_xref="taxon:10090"
 /clone="IMAGE:1222790"
 /clone_lib="Stratagene mouse heart (#937316)"
 /sex="pooled"
 /issue_type="heart"
 /dev_stage="13 day embryos"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: heart; Vector: phuscript SK-; Site 1:
 EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
 Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts.
 Average insert size: 1.0 kb; Uni-ZAP XR Vector: -5'
 adaptor sequence: 5' GAATTCGACAGAG 3' -3' adaptor
 sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."
 BASE COUNT 12 a 27 c 16 g 21 t
 ORIGIN

Query Match 54.1%; Score 14.6; DB 9; Length 76;
 Best Local Similarity 52.4%; Pred. No. 2.3e+04;
 Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 Oy 6 CUUUGAGCCUCAGGUCUG 26
 :::: ||: ||| ||: |||
 Db 49 CTTCCTCTCAGAGTCTG 69

RESULT 12
 N72966 87 bp mRNA linear EST 28-JAN-1997
 LOCUS
 DEFINITION
 IMAGE:246021 5' similar to gb:K02765 COMPLEMENT C3 PRECURSOR (HUMAN)
); mRNA sequence.
 ACCESSION
 N72966.1 GI:1230070
 KEYWORDS
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 87)
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chapell, B.,
 Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins,
 M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
 B., Morris, M., Parsons, J., Prange, C., Riklin, L., Rohlfing, T.,
 Schellendy, K., Soares, J.B., Tan, F., Thierry-Meg, J., Trevas, E.,
 Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)
 97044478
 CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1533 Std Error: 0.00
 Seq primer: reverse ET
 High quality sequence stop: 1.
 Location/Qualifiers
 1. 87

FEATURES
 source
 /organism="Homo sapiens"

[illegible]

BASE COUNT		14 a	37 c	25 g	17 t		
ORIGIN							
Query Match		54.1%	Score 14.6;	DB: 17:	Length 93:		
Best Local Similarity		61.9%;	Pred. No. 2.5e+04;				
Matches	13/	Conservative	4;	Mismatches	4;	Indels 0; Gaps 0;	
OY	4	GAGCTTGACGCCGTCAGGCTCUG	24				
Dn	43	GAGCTTGACGCCGTCGTCTCG	63				
RESULT 14							
w82482/c							
LOCUS							
DEFINITION							
ACCESSION							
VERSION							
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
COMMENT							

extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

```

1..397
/location/Qualifiers
1..397
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_id="IMAGE:404069"
/dev_stage="P19.5 dpc total fetus"
/note="Vector: pUT3D (Pharmacia) with a modified polylinker. Site-1: Not I; site-2: Eco RI; 1st strand CDNA was primed with a Not I - oligo(dT) primer [5' GTTTCAATCATGAAGTAGGGCCGCAGTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (pharmacica), digested with Not I and cloned into the Not I and Eco RI sites of a modified pUT3 vector (Pharmacica). Library went through one round of normalization to a Cot 5 library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."
```

BASE COUNT
ORIGIN

32 a
31 c
22 g
12 t

Qy 4 GACUUGAGCCUCAGGGUCUG 24
| : : : | | : | | : | : |
Db 67 GTCCTTGAACTCAAGTCTCTG 47

RESULT 15

LOCUS
DEFINITION

ACCESSION

VERSION
KEYWORDS
SOURCE

ORGANISM

REFERENCE
AUTHORS
TITLE

**JOURNAL,
COMMENT**

Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILMIL at: www-bio.11nl.gov/dbdrp/image/image.html

Trace considered overall poor quality
Insert Length: 1424 Std Error: 0.00
Seq primer: -400P from G1bco
High quality sequence stop: 1.

FEATURES
source

1.58

```
/organism="Homo sapiens"  
/db xref="taxon:9606"
```

```
/clone="IMAGE:1884206"
/c/one 14b="NCT CCAD TUEH
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clone_id= NC1_004712
/tissue_type="carcinoid"
```

```
/lab_host="DHLUB"  
/note="Organ: lum
```

modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoma, and was then primed with a

Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia) digested with Not I and

cloned into the Not I and Eco RI sites of the modified

pr/13 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT
ORIGIN

15 a 15 c 13 g 15 t

Query Match	Best Local
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8
9	9
10	10
11	11
12	12
13	13
14	14
15	15
16	16
17	17
18	18
19	19
20	20
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22	22
23	23
24	24
25	25
26	26
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28	28
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30	30
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77	77
78	78
79	79
80	80
81	81
82	82
83	83
84	84
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86	86
87	87
88	88
89	89
90	90
91	91
92	92
93	93
94	94
95	95
96	96
97	97
98	98
99	99
100	100

Matches : 1

QY 12 GCCUCAGGGUCUGAGU 27

Db 13 GCGTCAAGAGTCTGAGT 28

Search completed: December 21, 2002, 19:26:01
Job time : 833.041 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:20:00 : Search time 554.694 Seconds
(without alignments)
525.549 Million cell updates/sec

Title: US-09-121-239-26

Perfect score: 18

Sequence: 1 GGATTCATCGAGCGATCG 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estha:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estcl:*
9: gb_estcl:*
10: gb_estcl2:*
11: gb_estcl3:*
12: gb_estcl4:*
13: gb_estcl5:*
14: gb_estcl6:*
15: em_estlin:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	13.2	73.3	86	BH629707
2	13.2	73.3	87	BH629707
3	12.8	71.1	53	BQ239833
4	12.8	71.1	60	AL769486
5	12.8	71.1	74	BQ757618
6	12.8	71.1	80	AV565503
			17	AZ661791
				IM0540J04

C	7	12.8	71.1	81	14	BQ757211	BQ757211
C	8	12.8	71.1	93	17	AA736573	AA736573
C	9	12.8	71.1	94	17	BH811235	BH811235
C	10	12.8	71.1	97	12	BG778506	BG778506
C	11	12.8	71.1	98	17	AZ606926	AZ606926
C	12	12.8	71.1	98	17	AL761738	AL761738
C	13	12.8	71.1	99	12	BG778436	BG778436
C	14	12.4	68.9	80	17	AZ784908	AZ784908
C	15	12.2	67.8	37	17	AZ833759	AZ833759
C	16	12.2	67.8	48	17	AZ805363	AZ805363
C	17	12.2	67.8	48	17	AZ356616	AZ356616
C	18	12.2	67.8	46	17	AI155176	AI155176
C	19	12.2	66.7	90	17	AZ581309	AZ581309
C	20	11.8	65.6	38	17	AZ447531	AZ447531
C	21	11.8	65.6	51	17	B06639	B06639
C	22	11.8	65.6	61	14	W48103	W48103
C	23	11.8	65.6	68	17	AZ492365	AZ492365
C	24	11.8	65.6	73	17	AZ694238	AZ694238
C	25	11.8	65.6	75	17	BH806709	BH806709
C	26	11.8	65.6	78	9	AA786689	AA786689
C	27	11.8	65.6	85	9	AI462362	AI462362
C	28	11.8	65.6	86	17	AZ485774	AZ485774
C	29	11.8	65.6	95	17	BQ56702	BQ56702
C	30	11.8	65.6	100	9	AF21606	AF21606
C	31	11.8	65.6	100	9	AA089435	AA089435
C	32	11.8	65.6	100	14	BQ846904	BQ846904
C	33	11.6	64.4	30	17	BH814304	BH814304
C	34	11.6	64.4	30	17	TA131A020	TA131A020
C	35	11.6	64.4	43	9	AI492250	AI492250
C	36	11.6	64.4	62	17	AZ608873	AZ608873
C	37	11.6	64.4	67	13	BM021089	BM021089
C	38	11.6	64.4	68	13	BM021128	BM021128
C	39	11.6	64.4	68	13	BI966026	BI966026
C	40	11.6	64.4	68	13	BM126239	BM126239
C	41	11.6	64.4	68	17	AZ772124	AZ772124
C	42	11.6	64.4	69	9	AA168290	AA168290
C	43	11.6	64.4	77	14	BQ761092	BQ761092
C	44	11.6	64.4	81	17	AZ498215	AZ498215
C	45	11.6	64.4	82	17	AZ657340	AZ657340

ALIGNMENTS

RESULT 1
LOCUS BH629707/c 86 bp DNA linear GSS 30-JAN-2002
DEFINITION 1007075E06.2EL_x1 1007 - Rescueru Grid H Zea mays genomic. DNA
ACCESSION BH629707
VERSION BH629707.1 GI:18442958
KEYWORDS GSS.
SOURCE Zea mays.
ORGANISM Zea mays.
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
COMMENT clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 86)
Walbot, V.
Maize genomic sequences found using engineered Rescueru transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
plate: 1007675 column: 36
Class: transposon-tagged
Location/Qualifiers

FEATURES

source

1..86
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1007 - Rescuenmu Grid H"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf; Vector: Rescuenmu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII; Rescuenmu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuenmu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'Rescuenmu'. Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 11 a 35 c 23 g 17 t

ORIGIN

Query Match 73.3%; Score 13.2; DB 17; Length 86;
Best Local Similarity 83.3%; Pred. No. 8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGCGATGG 18
||||| |||||||||

Db 52 GGAAGATTCGAGCGATGG 35

RESULT 2
B0239833/c 87 bp mRNA linear EST 03-MAY-2002
LOCUS TAE05026D02R TAE05 Triticum aestivum CDNA clone TAE05026D02R, mRNA
DEFINITION
ACCESSION B0239833
VERSION B0239833.1 GI:20435696
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 87)
REFERENCE
AUTHORS Cloutier, S.
TITLE Wheat functional genomics - Glenlea developing seeds cDNA libraries
JOURNAL Unpublished (2002)
COMMENT Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-Food Canada
195 Datoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@agr.ca
was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >2.0 kb
Plate: 026 row: D column: 02
Seq primer: M13 Reverse.
location/Qualifiers
1..87
/organism="Triticum aestivum"
/cultivar="Glenlea"
/db_xref="taxon:4565"
/clone_lib="TAE05026D02R"
/clone_lib="TAE05"
/tissue_type="developing seeds"
/dev_stage="5 days after anthesis"
/lab_host="E. coli DH10B"
/note="Vector: pSPOR-P (Invitrogen Technologies); Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds of cultivar Glenlea 5 days post-anthesis"

BASE COUNT 7 a 44 c 23 g 13 t

ORIGIN

Query Match 73.3%; Score 13.2; DB 14; Length 87;
Best Local Similarity 83.3%; Pred. No. 8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGCGATGG 18
||||| |||||||

Db 66 GGAATCGTCGAGCGATGG 49

RESULT 3
AL769486/c 53 bp DNA linear GSS 19-JUN-2002
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-086G01-012541,
genomic survey sequence.
ACCESSION AL769486
VERSION AL769486.1 GI:21531688
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1
Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H. and Weissshaar, B.
A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
Unpublished
2
Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weissshaar, B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
Unpublished
3 (bases 1 to 53)
REFERENCE
AUTHORS Li, Y., Strizhov, N., Rosso, M. and Weissshaar, B.
JOURNAL Direct Submission
COMMENT Submitted (17-JUN-2002) Weissshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the right border of the T-DNA. It indicates an insertion within the locus defined by clone fl5h18.
The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.
location/Qualifiers
1..53
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="GK-086G01-012541"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

BASE COUNT 13 a 14 c 19 g 7 t

ORIGIN

Query Match 71.1%; Score 12.8; DB 17; Length 53;
Best Local Similarity 87.5%; Pred. No. 1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AATCATCGAGCGATGG 18

```

Db      23 ACTCATCGAGCGCATGG 8
      1 ||||| ||||| |||||
RESULT 4
B0757618/c 60 bp mRNA linear EST 26-JUL-2002
LOCUS      Ebem10_SQ004.L03_R embryo, 2 Day germination, no treatment, cv
DEFINITION Ebem10 Hordeum vulgare cDNA clone Ebem10_SQ004.L03 5', mRNA
sequence.
ACCESSION B0757618
VERSION   B0757618.1 GI:21966090
KEYWORDS  EST.
SOURCE    Hordeum vulgare.
ORGANISM  Hordeum vulgare.
REFERENCE Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardie, L.,
AUTHORS   Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
TITLE     Development of Barley Transcriptome Resources
JOURNAL   Unpublished (2001)
COMMENT   Contact: Waugh R, Marshall DF
          Genome Dynamics/Computational Biology
          Scottish Crop Research Institute
          Invergowrie, Dundee, DD2 5DA, Scotland, UK
          Tel: 00 44 1382 562731
          Fax: 00 44 1382 562426
          Email: est@scrl.sarl.ac.uk.
          Location/Qualifiers
FEATURES
source    1..60
           /organism="Hordeum vulgare"
           /db_xref="taxon:4513"
           /clone="Ebem10_SQ004.L03"
           /clone_1lb="embryo, 2 Day germination, no treatment, cv
           Optic, Ebem10"
           /tissue_type="embryo"
           /dev_stage="2 Day germination"
           /lab_host="DH10B"
           /note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I;
           Non-normalised library, directionally cloned into pSPORT1.
           Derived from embryos dissected from germinating grains (2
           day) in glasshouse grown barley plants. Developed as part
           of the barley transcriptome resources of BSRC/SEERAD
           funded cereal iGF (Investigating Gene Function) project."
BASE COUNT 10 a 23 c 22 g 5 t
ORIGIN
Query Match 71.1%; Score 12.8; DB 14; Length 60;
Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      3 AATCATCGAGCGCATGG 18
Db      50 ACTCATCGAGCGCATGG 35
      1 ||||| ||||| |||||
RESULT 5
AV565503/c 74 bp mRNA linear EST 07-SEP-2000
LOCUS      AV565503 Arabidopsis thaliana green siliques Columbia Arabidopsis
DEFINITION thaliana cDNA clone SQ25d12f 3', mRNA sequence.
ACCESSION AV565503
VERSION   AV565503.1 GI:8736945
KEYWORDS  EST.
SOURCE    thale cress.
ORGANISM  Arabidopsis thaliana
REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          Rosidae; eucosids II; Brassicales; Brassicaceae; Arabidopsis.
          1 (bases 1 to 74)
FEATURES
source    1..80
           /organism="Mus musculus"
           /strain="C57BL/6J"
           /db_xref="taxon:10090"
           /clone="U06C1M0540J04"
           /clone_1lb="Mouse 10kb plasmid U06C1M library"

```

```

AUTHORS   Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
TITLE     A large scale analysis of cDNA in Arabidopsis thaliana: Generation
          of 12,028 non-redundant expressed sequence tags from normalized and
          size-selected cDNA libraries
JOURNAL   DNA Res. 7, 175-180 (2000)
MEDLINE   20363093
COMMENT   Contact: Erika Asamizu
          The First Laboratory for Plant Gene Research
          Kazusa DNA Research Institute
          Yata 1532-3, Kisarazu, Chiba 292-0812, Japan
          Email: asamizu@kazusa.or.jp; URL: http://www.kazusa.or.jp/en/plant/.
          Location/Qualifiers
FEATURES
source    1..74
           /organism="Arabidopsis thaliana"
           /strain="Columbia"
           /db_xref="taxon:3702"
           /clone="SQ25d12f"
           /clone_1lb="Arabidopsis thaliana green siliques Columbia"
           /tissue_type="green siliques"
           /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
           XhoI"
BASE COUNT 26 a 13 c 11 g 24 t
ORIGIN
Query Match 71.1%; Score 12.8; DB 10; Length 74;
Best Local Similarity 87.5%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      2 GAATCATCGAGCGCATG 17
Db      36 GAATCATCGAGCGCATG 21
      1 ||||| ||||| |||||
RESULT 6
AZ661791/c 80 bp DNA linear GSS 14-DEC-2000
LOCUS      AZ661791 Mouse 10kb plasmid U06C1M library Mus musculus genomic
DEFINITION clone U06C1M0540J04 R, DNA sequence.
ACCESSION AZ661791
VERSION   AZ661791.1 GI:11798937
KEYWORDS  GSS.
SOURCE    house mouse.
ORGANISM  Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
          1 (bases 1 to 80)
          Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
          Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
          M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
          and Wright, D., Weiss, R.
          Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
          Unpublished (2000)
          Contact: Robert B. Weiss
          University of Utah Genome Center
          Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 385 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0540 row: J column: 04
          Seq primer: CACACAGGAACACCTATGACC
          Class: plasmid ends
          High quality sequence stop: 80.
          Location/Qualifiers
FEATURES
source    1..80
           /organism="Mus musculus"
           /strain="C57BL/6J"
           /db_xref="taxon:10090"
           /clone="U06C1M0540J04"
           /clone_1lb="Mouse 10kb plasmid U06C1M library"

```

BASE COUNT
ORIGIN

9 a 25 c 23 g 23 t

```

/sex="Male"
/lab-host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g11473211419b1Arl29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

Query Match	71.1%	Score 12.8	DB 17	Length 80
Best Local Similarity	87.5%	Pred. No. 1,2e+04		
Matches 14; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	GCATCATCGAGGCAT	16	
Db	68	GCATCATCGAGGCAT	53	

RESULT 7				
B0757211/c				
LOCUS	B0757211	81 bp	mRNA	linear
DEFINITION	Ebm10_0_SQ003_E21_R embryo, 2 Day germination, no treatment, cv			
	Optic, Ebem10 Hordeum vulgare cDNA clone Ebem10_SQ003_E21_5', mRNA			
	sequence.			
VERSION	B0757211			
KEYWORDS	B0757211.1	GI:21965683		
SOURCE	EST.			
ORGANISM	Hordeum vulgare.			
	Hordeum vulgare			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae 1 (bases 1 to 81)			
AUTHORS	Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardie,L., Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.			
TITLE	Development of Barley Transcriptome Resources			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Waugh R, Marshall DF Genome Dynamics/Computational Biology Scottish Crop Research Institute Invergowrie, Dundee, DD2 5DA, Scotland, UK Tel: 00 44 1382 562731 Fax: 00 44 1382 562426 Email: est@scri.sari.ac.uk.			
FEATURES	Location/Qualifiers			
SOURCE	1..81			

```

/organism="Hordeum vulgare"
/cultivar="Optic"
/db_xref="taxon:4513"
/clone="EBem10-S0003_E21"
/clone_lib="embryo, 2 Day germination, no treatment, cv
Optic, EBem10"
/tissue_type="embryo"
/dev_stage="2 Day germination"
/lab_host="DH10B"
/note="Vector: pSPORT1, Site_1: Sal I; Site_2: Not I;
Non-normalised library, directionally cloned into pSPORT1
derived from embryos dissected from germinating grains (2

```

BASE COUNT	ORIGIN	Query Match	Best Local Similarity	Matches	QY	Db
16 a	29 c	29 g	7 t	71.1% Score 12.8; DB 14; Length 81; Best Local Similarity 87.5%; Pred. No. 1.3e+04; Mismatches 0; Indels 2; Gaps 0;	3 AATCATCGAGGCATGG 18 55 ACTCATCGGGGCATGG 40	

RESULT 8	AA736573	93 bp	mRNA	1linear	EST 27-JAN-1996
LOCUS	AA736573/c				
DEFINITION	AA736573 c018605.s1 NCI_CGAP_GCB1 Homo sapiens CDNA clone IMAGE:1305320 3'				
ACCESSION	AA736573				
VERSION	AA736573				
KEYWORDS	AA736573.1 GI:2767807				
SOURCE	EST.				
	human.				

REFERENCE (pages 1 to 93)
AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/nciccap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nhl.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
 Ph.D., Gerald Marti, M.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/HLNT at:
www.bio.lnli.gov/bbrp/image/image.html
 Insert length: 1054 Std Error: 0.00
 Seq primer: ~40m3 fwd. fm from Amersham
 High quality sequence stop: 74.
 Location/Qualifiers

```

SOURCE
1. 93
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1305320"
/clone_11p="NCI CGAP GC#1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/notes="Vector: pUT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAGTGAGGAGGCGCCCTCAATTTTCTTTTCTTTT-3',
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pUT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

```

Query Match	71.1%;	Score 12.8;	DB 9;	Length 93;
Best Local Similarity	87.5%;	Pred. No. 1.3e+04;		
Matches 14; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0429 row: A column: 10
 Seq primer: CGTGTAAACGACGCCACG
 Class: plasmid ends
 High quality sequence stop: 98.
 Location/Qualifiers

FEATURES

source

1. 98
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U06C1M0429A10"
 /clone_lib="Mouse 10kb plasmid U06C1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42n: Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

30 a 11 c 36 g 21 t

ORIGIN

Query Match 71.1%; Score 12.8; DB 17; Length 98;
 Best Local Similarity 87.5%; Pred. No. 1.4e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AATCATCGAGCATCG 18
 ||||| ||||| ||
 Db 13 AATCATGAGCGAGG 28

RESULT 12

AL761738 98 bp DNA linear GSS 18-JUN-2002

LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-227H11-014266,
 genomic survey sequence.

ACCESSION AL761738

VERSION AL761738.1 GI:21505030

KEYWORDS

GSS.

SOURCE

thale cress.

ORGANISM

Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 Strizhov, N., Li, Y., Rosso, M., Viehovec, P., Dekker, K., Siedler, H.

AUTHORS

TITLE

A pipeline for automated high-throughput generation of ESTs
 (flanking sequence tags) from Arabidopsis thaliana T-DNA
 transformed lines

JOURNAL

REFERENCE

2 Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B.
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
 for flanking sequence tag based reverse genetics
 Unpublished

REFERENCE

3 (bases 1 to 98)
 Li, Y., Rosso, M., Strizhov, N. and Weisshaar, B.
 Direct Submission
 Submitted (17-JUN-2002) Weisshaar, B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

COMMENT

This sequence is recovered from the left border of the T-DNA. It
 indicates an insertion within the locus defined by clone f15b18.
 The sequences are generated at the MPI for Plant Breeding Research
 in the context of the GABI-Kat project. GABI-Kat is part of the
 German Plant Genomics program designated 'GABI'. Information on
 line availability can be found at:
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES

source

1. 98
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-227H11-014266"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector pAC161. The lines contain one or more T-DNA
 insertions. The DNA fragment(s) resulting from the PCR
 were directly sequenced to determine the genomic sequence
 flanking the insertion. Sequences displaying significant
 similarity to the A. thaliana nuclear genome sequence were
 processed for submission. T-DNA derived sequences were
 removed"

BASE COUNT 21 a 27 c 37 g 13 t

ORIGIN

Query Match 71.1%; Score 12.8; DB 17; Length 98;
 Best Local Similarity 87.5%; Pred. No. 1.4e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AATCATCGAGCATCG 18
 ||||| ||||| ||
 Db 68 ACTCATCGAGCGCTCG 53

RESULT 13

BG778436 99 bp mRNA linear EST 15-MAY-2001

LOCUS 60266627F1 NIH_MGC_60 Homo sapiens CDNA clone IMAGE:4806510 5',
 mRNA sequence.

ACCESSION BG778436

VERSION BG778436.1 GI:14048753

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 99)
 NIH-MGC http://mgc.ncl.nih.gov/.

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: DCTD/DRP
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L10M1656 row: e column: 07
 High quality sequence stop: 99.
 Location/Qualifiers

FEATURES

source

1. 99
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4806510"
 /clone_lib="NIH_MGC_60"

/tissue_type="adenocarcinoma"
 /lab_host="DHL0B (T1 phage-resistant)"
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
 Site_1: Sfil (ggcccttcggcc); Site_2: Sfil (ggcccttcggcc
); Double-stranded cDNA was prepared from cell 11e RNA.
 5' and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGGCCATTTATGGCC-3' and 3' adaptor
 sequence: 5'-ATCTAGAGCCGAGGCGCCACATG-dT(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA). Note: this is a NIH-MGC
 library."

BASE COUNT 17 a 23 c 25 g 34 t
 ORIGIN
 Query Match 71.1%; Score 12.8; DB 12; Length 99;
 Best Local Similarity 87.5%; Pred. No. 1.4e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AATCATGAGCGCATG 18
 ||||| |||||
 Db 68 AATCAGCCAGCATG 53
 RESULT 14
 LOCUS AZ784908 80 bp DNA linear GSS 16-FEB-2001
 DEFINITION 2M0028F18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0028F18 F, DNA sequence.
 ACCESSION AZ784908
 VERSION AZ784908.1 GI:12921118
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 80)
 Dumm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellily
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 Plasmid Inserts
 Unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0028 row: F column: 18
 Seq primer: CGTGTAAACGACGCCACT
 Class: plasmid ends
 High quality sequence stop: 80.
 Location/Qualifiers
 80
 1
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0028F18"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42ny; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a

0.005 Inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g114732111g1AT12072.1), a copy number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 19 a 16 c 27 g 18 t
 ORIGIN
 Query Match 68.9%; Score 12.4; DB 17; Length 80;
 Best Local Similarity 92.9%; Pred. No. 2e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 AATCATGAGCGCAT 16
 ||||| |||||
 Db 80 AATCATTGAGCAT 67
 RESULT 15
 LOCUS AZ833759 37 bp DNA linear GSS 20-FEB-2001
 DEFINITION 2M0116M01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0116M01 F, DNA sequence.
 ACCESSION AZ833759
 VERSION AZ833759.1 GI:13003667
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 37)
 Dumm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellily
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 Plasmid Inserts
 Unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0116 row: M column: 01
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 37.
 Location/Qualifiers
 1
 1
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0116M01"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42ny; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 FEATURES
 source

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 FEATURES
 source

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 9 a 4 c 12 g 12 t
ORIGIN

Query Match 67.88; Score 12.2; DB 17; Length 37;
Best Local Similarity 82.48; Pred. NO. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAATCATCGAGGCATGG 18
||||| |||||||
DB 3 GAATCATCGAGGCATGG 19

Search completed: December 21, 2002, 19:26:11
Job time : 564.694 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:20:00 : Search time 801.224 Seconds
(without alignments)
525.549 Million cell updates/sec

Title: US-09-121-239-27

Sequence: 26
1 CACTCAGCCACCTGATTTAAGCAGAG 26

Scoring table: IDENTITY_NDC
Gapop 10.0, Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

EST:
1: em_estha:
2: em_esthum:
3: em_estlin:
4: em_estlun:
5: em_estlov:
6: em_estlpl:
7: em_estlro:
8: em_hic:
9: gb_estl:
10: gb_est2:
11: gb_hic:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_estfun:
16: em_estom:
17: gb_gss:
18: em_gss_hum:
19: em_gss_juv:
20: em_gss_pln:
21: em_gss_ptt:
22: em_gss_fun:
23: em_gss_mus:
24: em_gss_mus:
25: em_gss_other:
26: em_gss_pro:
27: em_gss_rtd:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	75	14	H55528
2	17	65.4	97	9	AA282576
3	16.4	63.1	92	14	H55144
4	15.2	58.5	92	9	AA460218
5	15	57.7	93	12	BF434056
6	14.8	56.9	82	17	AZ454421

Result No.	Score	Query Match	Length	DB ID	Description
7	14.6	56.2	91	17	BH790845
8	14.4	55.4	24	17	AZ866592
9	14.4	55.4	40	9	AU011413
10	14.4	55.4	84	17	AZ918464
11	14.4	55.4	91	17	AA721220
12	14.4	55.4	100	9	A1536504
13	14.4	54.6	75	12	BG408667
14	14.2	54.6	80	14	H55918
15	14.2	54.6	84	10	AM166739
16	14.2	54.6	88	9	AA780578
17	14.2	54.6	96	17	DR15M4T
18	14	53.8	46	9	AV771016
19	14	53.8	63	10	AV833914
20	14	53.8	64	10	BE638305
21	14	53.8	67	9	AA721395
22	14	53.8	73	10	AM626539
23	14	53.8	84	17	AZ315745
24	14	53.8	87	17	AZ243366
25	14	53.8	90	12	BG060109
26	13.8	53.1	72	12	BF063884
27	13.8	53.1	74	17	AZ853652
28	13.8	53.1	81	17	BH623969
29	13.8	53.1	86	14	BQ127726
30	13.8	53.1	86	17	AZ789821
31	13.8	53.1	87	13	B1493713
32	13.8	53.1	90	9	A1596246
33	13.8	53.1	98	17	BH866038
34	13.8	53.1	100	10	BE073710
35	13.8	53.1	100	12	BF908892
36	13.6	52.3	47	9	A1813483
37	13.6	52.3	51	9	AA559169
38	13.6	52.3	62	12	BG879275
39	13.6	52.3	62	12	AZ622457
40	13.6	52.3	70	9	AA777046
41	13.6	52.3	73	9	AA509351
42	13.6	52.3	73	9	AA509704
43	13.6	52.3	74	17	AZ658469
44	13.6	52.3	78	9	AA904704
45	13.6	52.3	80	9	AA484332

ALIGNMENTS

RESULT 1
H55528
LOCUS
DEFINITION
H55528
mRNA sequence.
ACCESSION
H55528
VERSION
H55528.1
KEYWORDS
EST.
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
Trofatter, J.A., Long, K.R., Murrell, J.R., Stotler, C.J., Gussella, J.F. and Buckler, A.J.
An expression-independent catalog of genes from human chromosome 22
Genome Res. 5 (3), 214-224 (1995)
6159527
COMMENT
Contact: Buckler AJ
Molecular Neurogenetics Unit
Massachusetts General Hospital
Building 149, 13th St., Charlestown MA 02129
Tel: 6177249616
Fax: 6177265736
Email: buckler@helix.mgh.harvard.edu
Seq primer: T3.
location/Qualifiers
1..75
/organism="Homo sapiens"

/db_xref="taxon:9606"
 /clone_lib="Chromosome 22 exon"
 /lab_host="E. coli DH5a"
 /note="Vector: pBluescriptIIKS+; Site_1: Sal I; Site_2: Bam HI (destroyed); Exons were isolated from human chromosome 22 specific cosmids using a modification of the method of exon amplification (Proc. Natl. Acad. Sci. USA 88:4005-4009, 1991). Amplified exons were digested with Sal I and Bgl II and subsequently cloned into pBluescriptIIKS+ at the Sal I and Bam HI sites."

BASE COUNT
 17 a 17 c 19 g 22 t

Query Match
 Best Local Similarity 100.0%; Score 26; DB 14; Length 75;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAAGCAG 26
 |||||
 DB 45 CACTCAGCCACTGGATTAAAGCAG 70

RESULT 2
 AA282576 97 bp mRNA linear EST 13-AUG-1997
 LOCUS z13c07.s1 NCI_CGAP_GCB1 Homo sapiens CDNA clone IMAGE:713004 3',
 mRNA sequence.
 AA282576
 VERSION AA282576.1 GI:1925492
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 97)
 NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL
 Unpublished (1997)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 695 Std Error: 0.00
 Seq primer: -41ml3 fwd. ET from Amersham
 High quality sequence stop: 61.
 Location/Qualifiers
 1. 97
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:713004"
 /clone_lib="NCI_CGAP_GCB1"
 /tissue_type="germinal center B cell"
 /lab_host="DH10b"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand CDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20+, IgD-),
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
 (NCI) and Dr. Gerald Marti (CBER). CDNA synthesis was
 primed with a Not I - oligo(dT) primer
 [5'-TGTTACCATCTGAGTGGAGCGCCCTCATTTTCTTTTCTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT
 38 a 13 c 12 g 34 t

Query Match
 Best Local Similarity 65.4%; Score 17; DB 9; Length 97;
 Matches 80.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAAGCAG 25
 |||||
 DB 43 CACTCAGCCACTGGATTAAAGCAG 67

RESULT 3
 H55144/c 92 bp mRNA linear EST 07-DEC-1995
 LOCUS CHR220083 Chromosome 22 exon Homo sapiens CDNA C22.110 5',
 mRNA sequence.
 DEFINITION H55144
 H55144.1 GI:1108010
 ACCESSION H55144
 VERSION H55144.1 GI:1108010
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 92)
 Trofatter, J.A., Long, K.R., Murrell, J.R., Stotler, C.J., Gusella, J.F.
 and Buckler, A.J.
 An expression-independent catalog of genes from human chromosome 22
 Genome Res. 5 (3), 214-224 (1995)
 96159527
 COMMENT
 Contact: Buckler AJ
 Molecular Neurogenetics Unit
 Massachusetts General Hospital
 Building 149, 13th St., Charlestown MA 02129
 Tel: 6177249616
 Fax: 6177265736
 Email: buckler@helix.mgh.harvard.edu
 Seq primer: T3

FEATURES
 source
 1. 92
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="C22.110"
 /clone_lib="Chromosome 22 exon"
 /lab_host="E. coli DH5a"
 /note="Vector: pBluescriptIIKS+; Site_1: Sal I; Site_2:
 Bam HI (destroyed); Exons were isolated from human
 chromosome 22 specific cosmids using a modification of
 the method of exon amplification (Proc. Natl. Acad. Sci.
 USA 88:4005-4009, 1991). Amplified exons were digested
 with Sal I and Bgl II and subsequently cloned into
 pBluescriptIIKS+ at the Sal I and Bam HI sites."

BASE COUNT
 24 a 24 c 28 g 16 t

Query Match
 Best Local Similarity 63.1%; Score 16.4; DB 14; Length 92;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAAGCAG 26
 |||||
 DB 66 CCCTCAGCCCTGGATTATGAGAG 41

RESULT 4
 AA460218/c 92 bp mRNA linear EST 09-JUN-1997
 LOCUS zx50f10.r1 Soares_testis_NHT Homo sapiens CDNA clone IMAGE:795691
 DEFINITION 5', mRNA sequence.
 AA460218
 ACCESSION AA460218
 VERSION AA460218.1 GI:2185034
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 92)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gelsel, G., Jost, S.,

BASE COUNT 6 a 2 c 9 g 7 t
 ORIGIN and selected for ampicillin resistance."

Query Match 55.4%; Score 14.4; DB 17; Length 24;
 TITLE Best Local Similarity 75.0%; Pred. No. 8.1e+03;
 COMMENT Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 ACTGACGACCTGATTACGACA 25
 DB 24 ACTGACGACCTGATTACGACA 1

RESULT 9
 LOCUS A0011413 40 bp mRNA linear EST 03-AUG-1998
 DEFINITION A0011413 Schizosaccharomyces pombe late log phase cDNA
 Schizosaccharomyces pombe cDNA clone spc11252, mRNA sequence.
 ACCESSION A0011413
 VERSION A0011413.1 GI:3356322
 KEYWORDS EST.
 SOURCE fission yeast.
 ORGANISM Schizosaccharomyces pombe
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 Schizosaccharomycetales; Schizosaccharomycetaceae;
 Schizosaccharomyces.

REFERENCE 1 (bases 1 to 40)
 AUTHORS Moriyama, M. and Mita, K.
 TITLE Identification of expressed sequence tags of Schizosaccharomyces
 pombe

JOURNAL Unpublished (1998)
 COMMENT Contact: Mitsunori Moriyama
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
 Email: moriyam@nirs.go.jp
 FEATURES Location/Qualifiers

FEATURES

Source 1..40
 /organism="Schizosaccharomyces pombe"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc11252"
 /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
 /sex="h minus"

/note="Vector: M13mp19; The cDNA library of
 Schizosaccharomyces pombe was prepared by cloning cDNA
 into the SmaI site of M13mp19 DNA and the direction of DNA
 sequences was not always from 5' to 3'. The cDNA data of
 Schizosaccharomyces pombe are available for searching on
 the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT 12 a 10 c 9 g 9 t

Query Match 55.4%; Score 14.4; DB 9; Length 40;
 Best Local Similarity 75.0%; Pred. No. 1.1e+04;
 COMMENT Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 ACTGACGACCTGATTACGACA 25
 DB 6 ACTGACGACCTGATTACGACA 29

RESULT 10
 LOCUS AZ918464 84 bp DNA linear GSS 17-DEC-2001
 DEFINITION 1006004D07.x3 1006 - RescueMu Grid G Zea mays genomic, DNA
 sequence.
 ACCESSION AZ918464
 VERSION AZ918464.1 GI:13387748
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE 1 (bases 1 to 84)
 AUTHORS Walbot, V.
 JOURNAL Unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu

Very probable ligation site of ends cut by a single endonuclease.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 1006004 row: 36
 Class: transposon-tagged.
 Location/Qualifiers

FEATURES

Source

1..84
 /organism="Zea mays"
 /cultivar="mixed background W23/Al88/B73"
 /db_xref="taxon:4577"
 /clone_lib="1006 - RescueMu Grid G"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: Leaf; Vector: RescueMu (engineered from
 pBluescript backbone); Site_1: BamHI; Site_2: BglII;
 RescueMu is a 4.9 kb, modified maize Mu transposon
 designed to allow plasmid rescue from total genomic DNA.
 Mu elements insert preferentially into transcription
 units. For more information on RescueMu, go to the web
 site 'www.zmdb.iastate.edu' and follow the links for
 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was
 extracted from leaf punches, double digested using BamHI
 and BglII, and ligated to form circular plasmids. DH10B
 cells were transformed and then screened on LB plates with
 ampicillin."

BASE COUNT 29 a 13 c 31 g 11 t

Query Match 55.4%; Score 14.4; DB 17; Length 84;
 Best Local Similarity 75.0%; Pred. No. 1.6e+04;
 COMMENT Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 CTCAGCCACTGATTACGACGAG 26
 DB 61 CTCAGCCACTGATTACGACGAG 84

RESULT 11
 LOCUS AA721220 91 bp mRNA linear EST 23-JAN-1998
 DEFINITION AA721220.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1300631 3',
 mRNA sequence.
 ACCESSION AA721220
 VERSION AA721220.1 GI:2737355
 KEYWORDS EST.
 SOURCE Human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 91)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
 Ph.D., Gerald Marti, M.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnln.gov/bdbr/image/image.html
 Insert Length: 1195 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from AmerSham
 High quality sequence stop: 87.

FEATURES

Location/Qualifiers

```
1..91
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI-CGAP-GCBI"
/clone_idb="NCI-CGAP-GCBI"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTCACATCTGAGTGGAGCGCGCCGATTTTGTGTGT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
```

BASE COUNT

15 a 24 c 35 g 17 t

ORIGIN

```
Query Match 55.4%; Score 14.4; DB 9; Length 91;
Best Local Similarity 75.0%; Pred. No. 1.7e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 CTCAGCCACTGATTTAGCAG 26
||||| | | | | |
Db 58 CTCAGCCAGCGGCTCTTAACAGTG 81
```

RESULT 12
 A1536504 100 bp mRNA linear EST 18-MAR-1999
 LOCUS
 DEFINITION
 ACCESSION A1536504
 VERSION A1536504.1 GI:4450639
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus
 house mouse.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 100)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royally-free through LNL; contact the
 IMAGE Consortium (info@image.lnln.gov) for further information.
 MGI:590083
 This read is a RESEQUENCE of a previously sequenced mouse clone
 correct orientation)
 Seq primer: -40RP from Gibco
 High quality sequence stop: 99.

FEATURES

Location/Qualifiers

```
1..100
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
```

```
/clone="IMAGE:1067723"
/clone_idb="Soares_mammary_gland_NBMWG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia)
with a modified polylinker; Site 1: Not I; Site 2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5'
TGTTCACATCTGAGTGGAGCGCGCCGATTTTGTGTGT-3'
]. Double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M. Fatima
Bonaldo."
```

BASE COUNT

19 a 23 c 40 g 18 t

ORIGIN

```
Query Match 55.4%; Score 14.4; DB 9; Length 100;
Best Local Similarity 75.0%; Pred. No. 1.8e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CACTAGCCACTGATTTAGCAG 24
||||| | | | | |
Db 28 CACACAGCTGCTGATTCACCTG 51
```

RESULT 13
 B6408667 75 bp mRNA linear EST 13-MAR-2001
 LOCUS
 DEFINITION
 ACCESSION B6408667
 VERSION B6408667.1 GI:13315016
 KEYWORDS
 SOURCE
 ORGANISM

African clawed frog.
 Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 Xenopodinae; Xenopus.
 1 (bases 1 to 75)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
 Clone distribution: Xenopus clones from this library are available
 through the I.M.A.G.E. Consortium/LNL at: info@image.lnln.gov
 Seq primer: -40RP from Gibco.

FEATURES

Location/Qualifiers

```
1..75
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:3405475"
/clone_idb="NICHD XGC 001"
/tissue_type="oocytes"
/lab_host="DH10B (phage-resistant)"
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.2 kb. Constructed by Life Technologies."
```

BASE COUNT

38 a 10 c 18 g 9 t

ORIGIN

```
Query Match 54.6%; Score 14.2; DB 12; Length 75;
Best Local Similarity 84.2%; Pred. No. 1.9e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```


GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:43:17 ; Search time 773.192 Seconds
(without alignments)
2032.551 Million cell updates/sec

Title: US-09-121-239-1
Perfect score: 54
Sequence: 1 TAAATTAATACGACGCTCACTA.....CCCTGAGGCTCAAGTCAGA 54

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl :
1: gb_da : *
2: gb_hlg : *
3: gb_in : *
4: gb_cm : *
5: gb_ov : *
6: gb_pat : *
7: gb_ph : *
8: gb_pl : *
9: gb_pr : *
10: gb_ro : *
11: gb_sts : *
12: gb_sy : *
13: gb_un : *
14: gb_vl : *
15: em_da : *
16: em_fun : *
17: em_hum : *
18: em_in : *
19: em_mu : *
20: em_mu : *
21: em_or : *
22: em_ov : *
23: em_pat : *
24: em_ph : *
25: em_pl : *
26: em_ro : *
27: em_sts : *
28: em_un : *
29: em_vl : *
30: em_hlg_hum : *
31: em_hlg_liv : *
32: em_hlg_other : *
33: em_hlg_mus : *
34: em_hlg_pin : *
35: em_hlg_rod : *
36: em_hlg_mam : *
37: em_hlg_vit : *
38: em_sy : *
39: em_higo_hum : *
40: em_higo_mus : *
41: em_higo_other : *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	31.8	58.9	51	6	AX397806	AX397806 Sequence
2	31	57.4	49	6	AR061368	AR061368 Sequence
3	31	57.4	49	6	AR108267	AR108267 Sequence
4	31	57.4	49	6	I16224	I16224 Sequence 50
5	31	57.4	49	6	I66710	I66710 Sequence 50
6	31	57.4	49	6	I84804	I84804 Sequence 50
7	31	57.4	73	6	AR061668	AR061668 Sequence
8	31	57.4	73	6	AR108567	AR108567 Sequence
9	31	57.4	73	6	I85104	I85104 Sequence 35
10	30.8	57.0	49	6	I40633	I40633 Sequence 5
11	30.8	57.0	49	6	I40634	I40634 Sequence 6
12	30.8	57.0	49	6	I40635	I40635 Sequence 8
13	30.8	55.9	49	6	I40636	I40636 Sequence 8
14	30.2	55.9	52	6	AX166846	AX166846 Sequence
15	30	55.6	55	6	AX397811	AX397811 Sequence
16	29.8	55.2	71	6	AR153317	AR153317 Sequence
17	29.6	54.8	60	6	I25073	I25073 Sequence 7
18	29.4	54.4	36	6	AX045344	AX045344 Sequence
19	29.4	54.4	49	6	AR207661	AR207661 Sequence
20	29.4	54.4	50	6	E61335	E61335 Probe for d
21	29.4	54.4	56	6	A11333	A11333 Nucleotide
22	29.4	54.4	62	6	AX019749	AX019749 Sequence
23	29.4	54.4	65	6	AX080569	AX080569 Sequence
24	29.4	54.4	67	6	AX019769	AX019769 Sequence
25	29.4	54.4	70	6	AX089393	AX089393 Sequence
26	29.4	54.4	91	6	AX019760	AX019760 Sequence
27	29.4	54.4	96	6	AX019756	AX019756 Sequence
28	29.4	54.4	99	6	AX009277	AX009277 Sequence
29	29	53.7	37	6	I25071	I25071 Sequence 5
30	29	53.7	45	6	E61325	E61325 Probe for d
31	29	53.7	47	6	AR070666	AR070666 Sequence
32	29	53.7	47	6	AR157485	AR157485 Sequence
33	29	53.7	47	6	I25930	I25930 Sequence 10
34	29	53.7	50	6	AR102985	AR102985 Sequence
35	29	53.7	79	6	I25069	I25069 Sequence 3
36	28.8	53.3	48	6	AX147895	AX147895 Sequence
37	28.8	53.3	48	6	AX147924	AX147924 Sequence
38	28.6	53.0	71	6	AX451979	AX451979 Sequence
39	28.6	53.0	71	6	AX458692	AX458692 Sequence
40	28.6	53.0	77	6	AX451980	AX451980 Sequence
41	28.6	53.0	77	6	AX458693	AX458693 Sequence
42	28.4	52.6	56	6	AX278217	AX278217 Sequence
43	28.4	52.6	88	6	BD012958	BD012958 A method
44	28.4	52.6	88	6	E37843	E37843 Process for
45	28.4	52.6	88	23	BD008384	BD008384 A method

ALIGNMENTS

RESULT 1
AX397806
LOCUS AX397806
DEFINITION Sequence 40 from Patent WO0220852.
ACCESSION AX397806
VERSION AX397806.1 GI:21260680
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
Amplification of hiv-1 sequences for detection of sequences
associated with drug-resistance mutations
Patent: WO 0220852-A 40 14-MAR-2002

Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (PR)

FEATURES
Location/Qualifiers

1. .51

/organism="synthetic construct"

/db.xref="taxon:32630"

/note="Oligonucleotide primer for Reverse Transcriptase target sequence"

Promoter

1. .29

BASE COUNT 17 a 11 c 8 g 15 t

Query Match

Best Local Similarity 58.9%; Score 31.8; DB 6; Length 51;

Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY

2 AAATTAATAGCAGCTACTATAGGAGAGACTGAGCCCTGAGGCTCAAGTCA 52

Db 1 AAATTAATAGCAGCTACTATAGGAGAGACTGAGCCCTGAGGCTCAAGTCA 51

RESULT 2

AR061368

LOCUS AR061368 49 bp DNA Linear PAT 29-SEP-1999

DEFINITION Sequence 50 from patent US 5843653.

ACCESSION AR061368

VERSION AR061368.1 GI:5989059

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 49)

AUTHORS

Gold, L. and Tuerk, C.

TITLE

Method for detecting a target molecule in a sample using a nucleic acid ligand

JOURNAL

Patent: US 5843653-A 50 01-DEC-1998;

FEATURES

Location/Qualifiers

1. .49

/organism="unknown"

BASE COUNT 18 a 10 c 8 g 13 t

Query Match

Best Local Similarity 57.4%; Score 31; DB 6; Length 49;

Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY

6 TAATAGCAGCTACTATAGGAGAGACTGAGCCCTGAGGCTCAAGTCA 52

Db 1 TAATAGCAGCTACTATAGGAGAGACTGAGCCCTGAGGCTCAAGTCA 47

RESULT 3

AR108267

LOCUS AR108267 49 bp DNA Linear PAT 14-FEB-2001

DEFINITION Sequence 50 from patent US 6110900.

ACCESSION AR108267

VERSION AR108267.1 GI:12823754

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 49)

AUTHORS

Gold, L. and Tuerk, C.

TITLE

Nucleic acid ligands

JOURNAL

Patent: US 6110900-A 50 29-AUG-2000;

FEATURES

Location/Qualifiers

1. .49

/organism="unknown"

BASE COUNT 18 a 10 c 8 g 13 t

ORIGIN

Query Match

Best Local Similarity 57.4%; Score 31; DB 6; Length 49;

Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 6 TAATAGCAGCTACTATAGGAGAGACTGAGCCCTGAGGCTCAAGTCA 52

Db 1 TAATAGCAGCTACTATAGGAGAGACTGAGCCCTGAGGCTCAAGTCA 47

RESULT 4

116224

LOCUS 116224 49 bp DNA Linear PAT 03-APR-1996

DEFINITION Sequence 50 from patent US 5475096.

ACCESSION 116224

VERSION 116224.1 GI:1251132

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 49)

AUTHORS

Gold, L. and Tuerk, C.

TITLE

Nucleic acid ligands

JOURNAL

Patent: US 5475096-A 50 12-DEC-1995;

FEATURES

Location/Qualifiers

1. .49

/organism="unknown"

BASE COUNT 18 a 10 c 8 g 13 t

ORIGIN

Query Match

Best Local Similarity 57.4%; Score 31; DB 6; Length 49;

Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY

6 TAATAGCAGCTACTATAGGAGAGACTGAGCCCTGAGGCTCAAGTCA 52

Db 1 TAATAGCAGCTACTATAGGAGAGACTGAGCCCTGAGGCTCAAGTCA 47

RESULT 5

166710

LOCUS 166710 49 bp DNA Linear PAT 29-DEC-1997

DEFINITION Sequence 50 from patent US 5670637.

ACCESSION 166710

VERSION 166710.1 GI:2724688

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 49)

AUTHORS

Gold, L. and Tuerk, C.

TITLE

Nucleic acid ligands

JOURNAL

Patent: US 5670637-A 50 23-SEP-1997;

FEATURES

Location/Qualifiers

1. .49

/organism="unknown"

BASE COUNT 18 a 10 c 8 g 13 t

ORIGIN

Query Match

Best Local Similarity 57.4%; Score 31; DB 6; Length 49;

Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY

6 TAATAGCAGCTACTATAGGAGAGACTGAGCCCTGAGGCTCAAGTCA 52

Db 1 TAATAGCAGCTACTATAGGAGAGACTGAGCCCTGAGGCTCAAGTCA 47

RESULT 6

184804

LOCUS 184804 49 bp DNA Linear PAT 04-APR-1998

DEFINITION Sequence 50 from patent US 5696249.

ACCESSION 184804

VERSION 184804.1 GI:3022324

KEYWORDS

SOURCE

ORGANISM

Unclassified.
REFERENCE 1 (bases 1 to 49)
AUTHORS Gold, L. and Tuerk, C.
TITLE Nucleic acid ligands
JOURNAL Patent: US 5696249-A 50 09-DEC-1997;
FEATURES Location/Qualifiers
source 1..49
BASE COUNT 18 a 10 c 8 g 13 t
ORIGIN

Query Match 57.4%; Score 31; DB 6; Length 49;
Best Local Similarity 78.7%; Pred. No. 0.29; 10; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 10;

QY 6 TAATAGACTCTATAGGAGACTCAGACCCCTGAAGTCA 52
|||||
Db 1 TAATAGACTCTATAGGAGACTCAGACCTTTAATCTGACATCA 47

RESULT 7
LOCUS AR061668 73 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 350 from patent US 5843653.
ACCESSION AR061668
VERSION AR061668.1 GI:5989359
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 73)
AUTHORS Gold, L. and Tuerk, C.
TITLE Method for detecting a target molecule in a sample using a nucleic acid ligand
JOURNAL Patent: US 5843653-A 350 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..73
BASE COUNT 27 a 13 c 10 g 23 t
ORIGIN

Query Match 57.4%; Score 31; DB 6; Length 73;
Best Local Similarity 78.7%; Pred. No. 0.29; 10; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 10;

QY 6 TAATAGACTCTATAGGAGACTCAGACCCCTGAAGTCA 52
|||||
Db 1 TAATAGACTCTATAGGAGACTCAGACCTTTAATCTGACATCA 47

RESULT 8
LOCUS AR108567 73 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 350 from patent US 6110900.
ACCESSION AR108567
VERSION AR108567.1 GI:12824054
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 73)
AUTHORS Gold, L. and Tuerk, C.
TITLE Nucleic acid ligands
JOURNAL Patent: US 6110900-A 350 29-AUG-2000;
FEATURES Location/Qualifiers
source 1..73
BASE COUNT 27 a 13 c 10 g 23 t
ORIGIN

Query Match 57.4%; Score 31; DB 6; Length 73;
Best Local Similarity 78.7%; Pred. No. 0.29; 10; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 10;

QY 6 TAATAGACTCTATAGGAGACTCAGACCCCTGAAGTCA 52
|||||
Db 1 TAATAGACTCTATAGGAGACTCAGACCTTTAATCTGACATCA 47

RESULT 9
LOCUS I85104 73 bp DNA linear PAT 04-APR-1998
DEFINITION Sequence 350 from patent US 5696249.
ACCESSION I85104
VERSION I85104.1 GI:3022624
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 73)
AUTHORS Gold, L. and Tuerk, C.
TITLE Nucleic acid ligands
JOURNAL Patent: US 5696249-A 350 09-DEC-1997;
FEATURES Location/Qualifiers
source 1..73
BASE COUNT 27 a 13 c 10 g 23 t
ORIGIN

Query Match 57.4%; Score 31; DB 6; Length 73;
Best Local Similarity 78.7%; Pred. No. 0.29; 10; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 10;

QY 6 TAATAGACTCTATAGGAGACTCAGACCCCTGAAGTCA 52
|||||
Db 1 TAATAGACTCTATAGGAGACTCAGACCTTTAATCTGACATCA 47

RESULT 10
LOCUS I40633 49 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 5 from patent US 5622827.
ACCESSION I40633
VERSION I40633.1 GI:2082113
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 49)
AUTHORS McAllister, D.L. and Clark, K.A.
TITLE Amplification primers and nucleic acid probes targeted to coccidioides immitis nucleic acid
JOURNAL Patent: US 5622827-A 5 22-APR-1997;
FEATURES Location/Qualifiers
source 1..49
BASE COUNT 16 a 13 c 9 g 11 t
ORIGIN

Query Match 57.0%; Score 30.8; DB 6; Length 49;
Best Local Similarity 94.1%; Pred. No. 0.35; 2; Indels 0; Gaps 0;
Matches 32; Conservative 0; Mismatches 2;

QY 2 AATTAATAGACTCTATAGGAGACTCAGAC 35
|||||
Db 1 AATTAATAGACTCTATAGGAGACTCAGAC 34

RESULT 11
LOCUS I40634 49 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 6 from patent US 5622827.
ACCESSION I40634
VERSION I40634.1 GI:2082114
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 49)
AUTHORS McAllister,D.L. and Clark,K.A.
TITLE Amplification primers and nucleic acid probes targeted to
JOURNAL coccidioides immitis nucleic acid
PATENT: US 5622827-A 6 22-APR-1997;
FEATURES Location/Qualifiers
source 1..49
/organism="unknown"
BASE COUNT 11 a 9 c 13 g 16 t
ORIGIN

Query Match 57.0%; Score 30.8; DB 6; Length 49;
Best Local Similarity 94.1%; Pred. No. 0.35;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AATTAATACGACTCCTATAGGAGACACAGAC 35
DB 49 AATTAATACGACTCCTATAGGAGACACAGAC 16

RESULT 12
LOCUS I40635 49 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 7 from patent US 5622827.
ACCESSION I40635
VERSION I40635.1 GI:2082115
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 49)
AUTHORS McAllister,D.L. and Clark,K.A.
TITLE Amplification primers and nucleic acid probes targeted to
JOURNAL coccidioides immitis nucleic acid
PATENT: US 5622827-A 7 22-APR-1997;
FEATURES Location/Qualifiers
source 1..49
/organism="unknown"
BASE COUNT 16 a 13 c 9 g 11 t
ORIGIN

Query Match 57.0%; Score 30.8; DB 6; Length 49;
Best Local Similarity 94.1%; Pred. No. 0.35;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AATTAATACGACTCCTATAGGAGACACAGAC 35
DB 1 AATTAATACGACTCCTATAGGAGACACAGAC 34

RESULT 13
LOCUS I40636 49 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 8 from patent US 5622827.
ACCESSION I40636
VERSION I40636.1 GI:2082116
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 49)
AUTHORS McAllister,D.L. and Clark,K.A.
TITLE Amplification primers and nucleic acid probes targeted to
JOURNAL coccidioides immitis nucleic acid
PATENT: US 5622827-A 8 22-APR-1997;
FEATURES Location/Qualifiers
source 1..49
/organism="unknown"
BASE COUNT 11 a 9 c 13 g 16 t
ORIGIN

Query Match 57.0%; Score 30.8; DB 6; Length 49;
Best Local Similarity 94.1%; Pred. No. 0.35;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AATTAATACGACTCCTATAGGAGACACAGAC 35
DB 49 AATTAATACGACTCCTATAGGAGACACAGAC 16

RESULT 14
LOCUS AX166846 52 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 12 from Patent WO0144510.
ACCESSION AX166846
VERSION AX166846.1 GI:14596449
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 52)
AUTHORS Brenzano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 12 21-JUN-2001;
FEATURES Gen-Probe Incorporated (US) ; Biomérieux S.A. (FR)
Location/Qualifiers
source 1..52
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer oligonucleotide"
BASE COUNT 17 a 14 c 11 g 10 t
ORIGIN

Query Match 55.9%; Score 30.2; DB 6; Length 52;
Best Local Similarity 81.4%; Pred. No. 0.59;
Matches 35; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 AATTAATACGACTCCTATAGGAGACACAGCCGAGGCT 44
DB 2 AATTAATACGACTCCTATAGGAGACACAGCAGCATCAGGCT 44

RESULT 15
LOCUS AX397811 55 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 45 from Patent WO0220852.
ACCESSION AX397811
VERSION AX397811.1 GI:21260685
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Yang,Y.Y., Brenzano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE Amplification of hiv-1 sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: WO 0220852-A 45 14-MAR-2002;
FEATURES Gen-Probe Incorporated Patent Dept (US) ; Biomérieux S.A. (FR)
Location/Qualifiers
source 1..55
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide primer for Reverse Transcriptase
target sequence"
BASE COUNT 17 a 16 c 9 g 13 t
ORIGIN

Query Match 55.6%; Score 30; DB 6; Length 55;
Best Local Similarity 86.8%; Pred. No. 0.71;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

• Mon, Dec 23 08:47:52 2002

us-09-121-239-1.rge

Page 5

OY 2 AAATTATACGACTGACTATAGGAGACTCAGACCTG 39
|||||
Db 2 AAATTATACGACTGACTATAGGAGAGACACATCCCTG 39
|||||

Search completed: December 21, 2002, 12:57:14
Job time : 781.192 secs

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:43:17 ; Search time 343.641 Seconds
(without alignments)
2032.551 Million cell updates/sec

Title: US-09-121-239-5
Perfect score: 24
Sequence: 1 GACCACTCCTGTGTGCAACTCCA 24

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 2054640 segs, 14551402878 residues
Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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17: em_hum:*

18: em_in:*

19: em_mus:*

20: em_om:*

21: em_of:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_hcg_hum:*

31: em_hcg_inv:*

32: em_hcg_other:*

33: em_hcg_mus:*

34: em_hcg_pln:*

35: em_hcg_rod:*

36: em_hcg_mam:*

37: em_hcg_vrt:*

38: em_sy:*

39: em_higo_hum:*

40: em_higo_mus:*

41: em_higo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	24	E61323	E61323 Probe for d
2	21	87.5	40	AR100696	AR100696 Sequence
3	20	83.3	20	I83631	I83631 Sequence 5
4	16	66.7	40	E16986	E16986 Sense prime
5	14	60.8	100	HSPE35A07	AL009849 H. sapiens
6	14	58.3	33	AR027112	AR027112 Sequence
7	14	58.3	60	AR139996	AR139996 Sequence
8	14	57.5	97	AGRPD32T3	268675 A. gambiiae S
9	13.8	56.7	46	AR168044	AR168044 Sequence
10	13.6	56.7	46	AR204815	AR204815 Sequence
11	13.6	56.7	48	AX221595	AX221595 Sequence
12	13.6	56.7	48	AX274567	AX274567 Sequence
13	13.6	56.7	48	AX2426270	AX2426270 Sequence
14	13.6	56.7	76	AY044144	AY044144 Syntelic
15	13.6	56.7	93	MMTCRVDJ	AX50567 Sequence
16	13.6	55.8	32	AR050567	AR050567 Sequence
17	13.4	55.8	82	HSTCRGABI	Z22683 H. sapiens T
18	13.4	55.8	93	SMSAR2	X99800 S. melanothe
19	13.4	55.8	95	AR166860	AR166860 Sequence
20	13.4	55.0	30	AX255417	AX255417 Sequence
21	13.2	55.0	31	AX255416	AX255416 Sequence
22	13.2	55.0	32	AX356256	AX356256 Sequence
23	13.2	54.2	20	AX353365	AX353365 Sequence
24	13	54.2	20	E23800	E23800 Method for
25	13	54.2	27	AR188058	AR188058 Sequence
26	13	54.2	27	AR189481	AR189481 Sequence
27	13	54.2	56	AR023824	AR023824 Sequence
28	13	54.2	56	I46850	I46850 Sequence 31
29	13	54.2	78	A59428	A59428 Sequence 21
30	13	54.2	78	HMGRBS09	AR182182 Sequence
31	13	54.2	90	AR017637	D26624 Homo sapien
32	13	54.2	98	AR094814	AR017637 Sequence
33	13	54.2	98	AR165473	AR094814 Sequence
34	13	54.2	98	AR094953	AR165473 Sequence
35	13	53.3	21	AS8045	AX094953 Sequence
36	12.8	53.3	24	AR176496	AS8045 Sequence 54
37	12.8	53.3	27	AR176496	AR176496 Sequence
38	12.8	53.3	35	AX214324	AX214324 Sequence
39	12.8	53.3	37	AR176490	AR176490 Sequence
40	12.8	53.3	37	I59456	I59456 Sequence 3
41	12.8	53.3	47	AX194760	AX194760 Sequence
42	12.8	53.3	51	AX158736	AX158736 Sequence
43	12.8	53.3	79	OE0131700	AX131700 Olea euro
44	12.8	53.3	86	AR045056	AR045056 Sequence
45	12.8	53.3	86	AR045056	AR045056 Sequence

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
E61323	E61323	Probe for detecting oligonucleotide.	E61323	E61323.1	GI:13025885	JP 1999046778-A/37.	synthetic construct.	1 (bases 1 to 24)	Daniel, L.K. and Timothy, J.F.	Probe for detecting oligonucleotide	Patent: JP 1999046778-A 37 23-FEB-1999;
											GEN-PROBE INC

24 bp DNA linear PART 18-JUN-2001

COMMENT OS Artificial Sequence
PN JP 199046778-A/37
PD 23-FEB-1999
PF 14-JAN-1998 JP 1998005607
PR 11-JUL-1989 US 379501
PI DANIEL LOUIS KASHIAN, TIMOTHY J FURUTSU
PC C12N15/09, C12Q1/68, C12N15/00
CC
FH Key Location/Qualifiers
FT source 1.24
FT Location/Qualifiers

FEATURES
source 1.24
Location/Qualifiers

BASE COUNT 7 a 7 c 5 g 5 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GACCACTCGTGTGAACTCCA 24
DB 1 GACCACTCGTGTGAACTCCA 24

RESULT 2
ARI00696 40 bp DNA linear PAT 14-FEB-2001
LOCUS
DEFINITION Sequence 16 from patent US 6080851.
ACCESSION ARI00696
VERSION ARI00696.1 GI:12811144
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 40)
AUTHORS Pachuk, C.J., Coney, L.R. and Oakes, F.T.
TITLE Ribozymes with linked anchor sequences
JOURNAL Patent: US 6080851-A 16 27-JUN-2000;
FEATURES
source 1.40
Location/Qualifiers
BASE COUNT 12 a 7 c 9 g 12 t
ORIGIN

Query Match 87.5%; Score 21; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CAACCTCGTGTGAACTCCA 24
DB 20 CAACCTCGTGTGAACTCCA 40

RESULT 3
183631 20 bp DNA linear PAT 10-AUG-1998
LOCUS
DEFINITION Sequence 5 from patent US 5714383.
ACCESSION 183631
VERSION 183631.1 GI:3407161
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Thompson, J.D.
TITLE Method and reagent for treating chronic myelogenous leukemia
JOURNAL Patent: US 5714383-A 5 03-FEB-1998;
FEATURES
source 1.20
Location/Qualifiers
/Organism="unknown"

BASE COUNT 5 a 6 c 4 g 5 t
ORIGIN

Query Match 83.3%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CAACCTCGTGTGAACTCC 23
DB 1 CAACCTCGTGTGAACTCC 20

RESULT 4
E16986 40 bp DNA linear PAT 28-JUL-1999
LOCUS
DEFINITION Sense primer for detection of major-bcr.
ACCESSION E16986
VERSION E16986.1 GI:5711669
KEYWORDS JP 1998229899-A/1.
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 40)
AUTHORS Kobayashi, M., Kawaguchi, R., Segawa, M. and Takarada, Y.
TITLE PRIMER FOR DETECTING BCR/ABL TYPE CHIMERA MESSENGER RNA AND USING THE SAME
JOURNAL Patent: JP 1998229899-A 1 08-SEP-1998;
S R L:KK, TOYOBO CO LTD
OS None
OC Artificial sequences.
PN JP 1998229899-A/1
PD 02-SEP-1998
PE 21-FEB-1997 JP 1997054092
PI KOBAYASHI MASARU, KAWAGUCHI RYUJI, SEGAWA MASAYA, PI
TAKARADA YUTAKA
PC C12Q1/68, G01N33/50//C12N15/09;
CC strandedness: Single;
CC topology: linear;
FH Key Location/Qualifiers
FH source 1.40
FT Location/Qualifiers

FEATURES
source 1.40
Location/Qualifiers
BASE COUNT 9 a 13 c 9 g 9 t
ORIGIN

Query Match 66.7%; Score 16; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 CGTGTGTGAACTCCA 24
DB 1 CGTGTGTGAACTCCA 16

RESULT 5
HSP35A07 100 bp DNA linear STS 21-MAY-1998
LOCUS
DEFINITION H. sapiens flow-sorted chromosome 1 HindIII fragment, SCIP35A07,
ACCESSION AL009849
VERSION AL009849.1 GI:2665012
KEYWORDS STS: single read.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Gregory, S., Kettleborough, R., Langford, C., Ross, M.T. and Hunt, S.E.
TITLE Direct Submission

LOCUS AR168044 46 bp DNA linear PAT 17-DEC-2001
 DEFINITION Sequence 19 from patent US 6287788.
 ACCESSION AR168044
 VERSION AR168044.1 GI:17903862
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 46)
 AUTHORS Bard,J.A., Borowsky,B., Smith,K.E., Branchek,T.A., Gerald,C.P.G.
 and Jones,K.A.
 TITLE DNA encoding galanin GALR3 receptors and uses thereof
 JOURNAL Patent: US 6287788-A 19 11-SEP-2001;
 FEATURES Location/Qualifiers
 source 1..46 /organism="unknown"
 BASE COUNT 15 a 7 c 17 g 7 t
 ORIGIN

Query Match 56.7%; Score 13.6; DB 6; Length 46;
 Best Local Similarity 80.0%; Pred. No. 8.8e+04;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

LOCUS AR204815 46 bp DNA linear PAT 20-JUN-2002
 DEFINITION Sequence 19 from patent US 6368812.
 ACCESSION AR204815
 VERSION AR204815.1 GI:21502237
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 46)
 AUTHORS Bard,J.A., Borowsky,B., Smith,K.E., Branchek,T.A., Gerald,C.P.G.
 and Jones,K.A.
 TITLE Process for determining the agonist or antagonist of galanin
 JOURNAL receptor (GALR3)
 FEATURES Patent: US 6368812-A 19 09-APR-2002;
 Location/Qualifiers
 source 1..46 /organism="unknown"
 BASE COUNT 15 a 7 c 17 g 7 t
 ORIGIN

Query Match 56.7%; Score 13.6; DB 6; Length 46;
 Best Local Similarity 80.0%; Pred. No. 8.8e+04;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

LOCUS AX221595 48 bp mRNA linear PAT 07-SEP-2001
 DEFINITION Sequence 7037 from patent WO0159103.
 ACCESSION AX221595
 VERSION AX221595.1 GI:15549319
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 48)
 AUTHORS Blatt,L., Mcswigen,J. and Chowrira,B.M.
 TITLE Method and reagent for the modulation and diagnosis of cd20 and
 nogo gene expression

JOURNAL Patent: WO 0159103-A 7037 16-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
 Mcswigen, James (US) ; Chowrira, Bharat M. (US)
 FEATURES Location/Qualifiers
 source 1..48 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Nucleic Acid"
 BASE COUNT 14 a 13 c 12 g 9 t
 ORIGIN

Query Match 56.7%; Score 13.6; DB 6; Length 48;
 Best Local Similarity 80.0%; Pred. No. 8.8e+04;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

LOCUS AX274567 48 bp mRNA linear PAT 29-OCT-2001
 DEFINITION Sequence 2136 from Patent WO0162911.
 ACCESSION AX274567
 VERSION AX274567.1 GI:16547306
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Jarvis,T., von Carlowitz,I., Mcswigen,J.A., Hamblin,P.A. and
 Ellis,J.H.
 TITLE Method and reagent for the inhibition of grid
 JOURNAL Patent: WO 0162911-A 2136 30-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
 FEATURES Location/Qualifiers
 source 1..48 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Enzymatic Nucleic Acid"
 BASE COUNT 11 a 16 c 12 g 9 t
 ORIGIN

Query Match 56.7%; Score 13.6; DB 6; Length 48;
 Best Local Similarity 80.0%; Pred. No. 8.8e+04;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

LOCUS AX426270 48 bp mRNA linear PAT 18-JUN-2002
 DEFINITION Sequence 4606 from Patent WO0186124.
 ACCESSION AX426270
 VERSION AX426270.1 GI:21529656
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Jarvis,T., von Carlowitz,I., Mcswigen,J.A., McLaughlin,F.G. and
 Randi,A.M.
 TITLE Method and reagent for the inhibition of erg
 JOURNAL Patent: WO 0186124-A 4606 22-NOV-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
 FEATURES Location/Qualifiers
 source 1..48 /organism="synthetic construct"
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BASE COUNT      10 a      15 c      15 g      8 t
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Best Local Similarity 80.0%; Pred. No. 8.8e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      4  CACATCGTGTGTGAACCTCC 23
         ||| ||||| ||||| |||
Db       1  CACCTCGTGTGAAGAACTCC 20

RESULT 14
AY044144/c
LOCUS      AY044144
DEFINITION Synthetic construct motif I cis element sequence.
ACCESSION  AY044144
VERSION     AY044144.1 GI:15625235
KEYWORDS
SOURCE      synthetic construct.
            synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 76)
AUTHORS     Peng,R., Yao,Q., Xiong,A., Li,X. and Fan,H.
TITLE       Direct Submision
JOURNAL     Submitted (06-JUL-2001) Shanghai Yong Ye Agro-Bioengineering Co.,
            Ltd, Shanghai Academy of Agricultural Sciences, Beid Road 2901,
            Shanghai 201106, China
FEATURES
    source
        1..76
            /organism="synthetic construct"
            /db_xref="taxon:32630"
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            for yeast one-hybrid system"
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Best Local Similarity 80.0%; Pred. No. 8.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2  ACCAATCGTGTGGAAC 21
         ||| ||||| ||||| |||
Db       37  ACCTACTCCTGTGTGAAT 18

RESULT 15
MMTCRVDDJ
LOCUS      MMTCRVDDJ
DEFINITION M.musculus rearranged TCR delta gene V-p-lambda-12, D-delta-1,
ACCESSION  X64902
VERSION     X64902.1 GI:54746
KEYWORDS    antigen receptor; D-region; delta gene; J-region; T cell receptor;
            V-region.
SOURCE      Mus musculus.
ORGANISM    Mus musculus.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 93)
            Chien,Y.H., Iwashima,M., Wettstein,D.A., Kaplan,K.B., Elliott,J.F.,
            Born,W. and Davis,M.M.
            T-cell receptor delta gene rearrangements in early thymocytes
            Nature 330, 24-31 (1987)
            See also X63933-9 & X64900-3.
FEATURES
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            /cell_type="thymocytes"
            /dev_stage="18-19 day fetus"

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Best Local Similarity 80.0%; Pred. No. 7.9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Job time : 353.641 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:43:17 : Search time 357.959 Seconds
(without alignments)
2032.551 Million cell updates/sec

Title: US-09-121-239-9

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Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

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2: gb_htg:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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2	25	100.0	56	114509	114509 Sequence 17
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4	24	96.0	40	E16986	E16986 Sense prime
5	18.8	75.2	39	AX003487	AX003487 Sequence 11
6	18	72.0	22	158643	158643 Sequence 11
7	18	72.0	62	AR100681	AR100681 Sequence 13
8	18	72.0	81	AR100682	AR100682 Sequence 13
9	17	68.0	60	A50293	A50293 Sequence 13
10	16	64.0	28	AR160054	AR160054 Sequence 13
11	15	60.0	15	E16784	E16784 PCR primer
12	15	60.0	54	A28014	A28014 pCD4-FVCD3
13	14.6	58.4	77	1 MMT812	1 MMT812 MYCOP1asma
14	14.6	58.4	77	1 MMT812	1 MMT812 MYCOP1asma
15	14.2	56.8	35	AX460928	AX460928 Sequence
16	14.2	56.8	86	AR081471	AR081471 Sequence
17	14.2	56.8	86	AR081480	AR081480 Sequence
18	14.2	56.8	86	AR081489	AR081489 Sequence
19	14.2	56.8	20	E16987	E16987 Sense prime
20	14	56.0	51	AX199392	AX199392 Sequence
21	14	56.0	61	AR100699	AR100699 Sequence
22	14	56.0	88	HSWC26D02	HSWC26D02 H sapiens D
23	13.8	55.2	33	AR005205	AR005205 Sequence
24	13.8	55.2	33	AR005206	AR005206 Sequence
25	13.8	55.2	33	140812	140812 Sequence 6
26	13.8	55.2	33	140812	140812 Sequence 6
27	13.8	55.2	33	140812	140812 Sequence 6
28	13.8	55.2	33	140878	140878 Sequence 7
29	13.8	55.2	33	140878	140878 Sequence 7
30	13.8	55.2	33	157348	157348 Sequence 8
31	13.8	55.2	33	157348	157348 Sequence 8
32	13.8	55.2	33	167993	167993 Sequence 5
33	13.8	55.2	33	167993	167993 Sequence 5
34	13.8	55.2	33	167994	167994 Sequence 5
35	13.8	55.2	33	168249	168249 Sequence 5
36	13.8	55.2	33	168250	168250 Sequence 5
37	13.8	55.2	33	172180	172180 Sequence 5
38	13.8	55.2	33	172181	172181 Sequence 6
39	13.8	55.2	33	181238	181238 Sequence 13
40	13.8	55.2	33	181239	181239 Sequence 13
41	13.8	55.2	33	182218	182218 Sequence 14
42	13.8	55.2	34	AR131299	AR131299 Sequence
43	13.8	55.2	34	AR173197	AR173197 Sequence
44	13.8	55.2	51	AX161939	AX161939 Sequence
45	13.8	55.2	54	AX161940	AX161940 Sequence
			9	HDMCG3A05	HDMCG3A05 Human alpha

ALIGNMENTS

RESULT 1	112447	56 bp	DNA	linear	PAT 26-JUL-1995
LOCUS	112447				
DEFINITION	Sequence 17 from patent US 5424413.				
ACCESSION	112447				
VERSION	112447.1	GI:905831			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 56)				
AUTHORS	Hogan, J.J., Arnold, L.J. Jr., Nelson, N.C. and Bezerkov, R.				
TITLE	Branching nucleic acid probes				
JOURNAL	Patent: US 5424413-A 17 13-JUN-1995;				
FEATURES	Location/Qualifiers				

source

1..56
BASE COUNT 18 a 18 c 9 g 11 t
ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 25
Db 3 GACTGTCCACAGCATTCGCGTGACC 27

RESULT 2
LOCUS 114509
DEFINITION Sequence 17 from patent US 5451503.
ACCESSION 114509
VERSION 114509.1 GI:996992
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 56)
AUTHORS Hogan,J.J., Arnold,L.J. Jr., Nelson,N.C. and Bezverkoy,R.
TITLE Method for use of branched nucleic acid probes
JOURNAL Patent: US 5451503-A 17 19-SEP-1995;
FEATURES Location/Qualifiers
source 1..56

BASE COUNT 18 a 18 c 9 g 11 t
ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 25
Db 3 GACTGTCCACAGCATTCGCGTGACC 27

RESULT 3
LOCUS 183632
DEFINITION Sequence 6 from patent US 5714383.
ACCESSION 183632
VERSION 183632.1 GI:3407162
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 26)
AUTHORS Thompson,J.D.
TITLE Method and reagent for treating chronic myelogenous leukemia
JOURNAL Patent: US 5714383-A 6 03-FEB-1998;
FEATURES Location/Qualifiers
source 1..26

BASE COUNT 6 a 10 c 5 g 5 t
ORIGIN

Query Match 96.0%; Score 24; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 24
Db 3 GACTGTCCACAGCATTCGCGTGACC 26

RESULT 4

E16986
LOCUS 40 bp DNA linear PAT 28-JUL-1999
DEFINITION Sense primer for detection of major-bcr.
ACCESSION E16986
VERSION E16986.1 GI:5711669
KEYWORDS JP 1998229899-A/1.
SOURCE unidentified.
ORGANISM unidentified

REFERENCE 1 (bases 1 to 40)
AUTHORS Kobayashi,M., Kawaguchi,R., Segawa,M. and Takarada,Y.
TITLE PRIMER FOR DETECTING BCR/ABL TYPE CHIMERA MESSENGER RNA, AND
JOURNAL DETECTION OF BCR/ABL TYPE CHIMERA MESSENGER RNA AND USING THE SAME
PATENT: JP 1998229899-A 1 02-SEP-1998;
COMMENT S R L:KK, TOYOBO CO LTD
OS None
OC Artificial sequences.
PN JP 1998229899-A/1
PD 02-SEP-1998
PF 21-FEB-1997 JP 1997054092
PI KOBAYASHI MASARU, KAWAGUCHI RYUJI, SEGAWA MASAYA, PI
TAKARADA YUTAKA
PC C1201/68, G01N33/50//C12N15/09;
CC strandedness: Single;
FH topology: Linear;
FT source 1..40

FEATURES
source Location/Qualifiers
1..40 /organism="Artificial sequences".
/db_xref="taxon:32644"

BASE COUNT 9 a 13 c 9 g 9 t
ORIGIN

Query Match 96.0%; Score 24; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 24
Db 17 GACTGTCCACAGCATTCGCGTGACC 40

RESULT 5
LOCUS AX003487/c 39 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 67 from Patent WO9928439.
ACCESSION AX003487
VERSION AX003487.1 GI:9927340
KEYWORDS
SOURCE B19 virus.
ORGANISM B19 virus.

REFERENCE 1 (bases 1 to 39)
AUTHORS Auguste,V., Garbarg-Chenon,A. and Nguyen,Q.T.
TITLE Erythrovirus and its applications
JOURNAL Patent: WO 9928439-A 67 10-JUN-1999;
ASSIST PUBL HOPITAUX DE PARIS (FR); AUGUSTE VERONIQUE (FR); GARBARG
CHENON ANTOINE (FR); NGUYEN QUANG TRI (FR)
FEATURES Location/Qualifiers
source 1..39

/organism="B19 virus"
/db_xref="taxon:10798"
BASE COUNT 8 a 11 c 13 g 7 t
ORIGIN

Query Match 75.2%; Score 18.8; DB 6; Length 39;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACTGTCCACAGCATTCGCGTGAC 23

Db 33 ACTGTCACAGCATTCGCGCA 12

RESULT 6
LOCUS 158643 22 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 11 from patent US 5652222.
ACCESSION 158643 GI:2477881
VERSION 158643.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 22)
AUTHORS Calabretta, B. and Gewirtz, A.M.
TITLE Selective inhibition of leukemic cell proliferation by bcr-abl
FEATURES
JOURNAL Patent: US 5652222-A 11 29-JUL-1997;
source Location/Qualifiers
1..22
/organism="unknown"

BASE COUNT 6 a 9 c 3 g 4 t
ORIGIN

Query Match 72.0%; Score 18; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACAGCATTCGCGTGACC 25
Db 1 CACAGCATTCGCGTGACC 18

RESULT 7
LOCUS ARI100681 62 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6080851.
ACCESSION ARI100681
VERSION ARI100681.1 GI:12811129
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 62)
AUTHORS Pachuk, C.J., Coney, L.R. and Oakes, F.T.
TITLE Ribozymes with linked anchor sequences
JOURNAL Patent: US 6080851-A 1 27-JUN-2000;
FEATURES
source Location/Qualifiers
1..62
/organism="unknown"

BASE COUNT 18 a 19 c 13 g 12 t
ORIGIN

Query Match 72.0%; Score 18; DB 6; Length 62;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACAGCATTCGCGTGACC 25
Db 1 CACAGCATTCGCGTGACC 18

RESULT 8
LOCUS ARI100682 81 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 2 from patent US 6080851.
ACCESSION ARI100682
VERSION ARI100682.1 GI:12811130
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 81)
AUTHORS Pachuk, C.J., Coney, L.R. and Oakes, F.T.
TITLE Ribozymes with linked anchor sequences
JOURNAL Patent: US 6080851-A 2 27-JUN-2000;
FEATURES
source Location/Qualifiers
1..81
/organism="unknown"

BASE COUNT 23 a 17 c 23 g 18 t
ORIGIN

Query Match 72.0%; Score 18; DB 6; Length 81;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACAGCATTCGCGTGACC 25
Db 81 CACAGCATTCGCGTGACC 64

RESULT 9
LOCUS A50293 60 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 13 from patent WO9612803.
ACCESSION A50293
VERSION A50293.1 GI:2303347
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 60)
AUTHORS Blumenfeld, M.
TITLE METHOD FOR THE EX VIVO TREATMENT OF TUMOUR CELLS FROM PATIENTS WITH
JOURNAL CM
Patent: WO 9612803-A 13 02-MAY-1996;
COMMENT Other publication FR 2726004 960426.
FEATURES
source Location/Qualifiers
1..60
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 18 a 18 c 13 g 11 t
ORIGIN

Query Match 68.0%; Score 17; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACAGCATTCGCGTGACC 25
Db 1 ACAGCATTCGCGTGACC 17

RESULT 10
LOCUS ARI160054 28 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 2 from patent US 6251690.
ACCESSION ARI160054
VERSION ARI160054.1 GI:16222959
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 28)
AUTHORS Kulmala, S., Ala-Kleime, T., Eskola, J. and Korpele, T.
TITLE Electrical excitation of label substances at insulating film-coated
conductors
JOURNAL Patent: US 6251690-A 2 26-JUN-2001;
FEATURES
source Location/Qualifiers
1..28
/organism="unknown"

BASE COUNT 5 a 5 c 8 g 10 t
ORIGIN

Query Match 64.0%; Score 16; DB 6; Length 28;
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 CAGCATTCGCGTGACC 25
 |||||
 DB 28 CAGCATTCGCGTGACC 13

RESULT 11
 E16784

LOCUS E16784 15 bp DNA linear PAT 28-JUL-1999
 DEFINITION PCR primer for detecting BCR EX3 mRNA.
 ACCESSION E16784
 VERSION E16784.1 GI:5711467
 KEYWORDS JP 1998215897-A/17.
 SOURCE unidentified.
 ORGANISM unidentified.

REFERENCE
 AUTHORS Koshimoto, H., Sato, Y. and Tsuji, A.
 TITLE DETECTION OF MUTANT CELL BY CHROMOSOMAL RECIPROCAL TRANSLOCATION,
 PROBE KIT FOR THE SAME DETECTION AND DETECTOR THEREFOR
 PATENT: JP 1998215897-A 17 18-AUG-1998;
 BUNSHI BIO PHOTONICS KENKYUSHO:KK

JOURNAL
 COMMENT OS None
 OC Artificial sequences.
 PN JP 1998215897-A/17
 PD 18-AUG-1998
 PR 05-FEB-1997 JP 1997022950
 P1 KOSHIMOTO HIROYUKI, SATO YOSHIHIRO, TSUJI AKIHIKO PC
 C1201/68, C07H21/04, C12N15/09, G01N21/78;
 CC topology: linear;
 CC strandedness: single;
 CC hypothetical: No;
 CC anti-sense: No;
 FH key
 FH Location/Qualifiers

FEATURES
 source 1.15
 Location/Qualifiers
 1.15
 /organism="unidentified"
 /db_xref="taxon:32644"

BASE COUNT 3 a 6 c 3 g 3 t
 ORIGIN

Query Match 60.0%; Score 15; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 CACAGCATTCGCGTG 22
 |||||
 DB 1 CACAGCATTCGCGTG 15

RESULT 12
 A28014/c 54 bp DNA linear PAT 03-OCT-1995
 LOCUS A28014
 DEFINITION pCD4-FVCD3 construction oligo 2139.
 ACCESSION A28014
 VERSION A28014.1 GI:1248561
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM artificial sequences.
 1 (bases 1 to 54)
 REFERENCE
 AUTHORS Karjalainen, R., Lanzavecchia, A. and Trautner, A.
 TITLE Chimeric polypeptides
 PATENT: EP 0505908-A 9 30-SEP-1992;
 F. HOFFMANN-LA ROCHE AG

FEATURES
 source 1.54
 Location/Qualifiers

BASE COUNT 11 a 9 c 22 g 12 t
 ORIGIN

Query Match 60.0%; Score 15; DB 6; Length 54;
 Best Local Similarity 78.3%; Pred. No. 1.3e+04;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 CTGTCGACAGCATTCGCGTGACC 25
 |||||
 DB 32 CAGTCGACAGCATTCGCGTGACC 10

RESULT 13
 MCTR12 77 bp mRNA linear BCT 31-MAR-1992
 LOCUS MCTR12
 DEFINITION Mycoplasma capricolum transfer RNA-ile (GAU).
 ACCESSION X16752
 VERSION X16752.1 GI:44246
 KEYWORDS transfer RNA; transfer RNA-ile.
 SOURCE Mycoplasma capricolum.
 ORGANISM Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
 Entomoplasmataceae.
 1 (bases 1 to 77)
 REFERENCE
 AUTHORS Andachi, Y., Yamao, F., Muto, A. and Osawa, S.
 TITLE Codon recognition patterns as deduced from sequences of the
 complete set of transfer RNA species in Mycoplasma capricolum.
 Resemblance to mitochondria
 JOURNAL I. Mol. Biol. 209 (1), 37-54 (1989)
 MEDLINE 90040718
 PUBMED 2478713
 COMMENT See acc# X16741-X16769 for complete set of mycoplasma transfer
 RNA's.

FEATURES
 source 1.77
 Location/Qualifiers
 1.77
 /organism="Mycoplasma capricolum"
 /strain="ATCC 27343 (Kid.)"
 /db_xref="taxon:2095"

tRNA 1.77
 modified_base 17
 /product="tRNA-ile"
 /note="dihydrouridine"
 /mod_base=d
 modified_base 20
 /note="dihydrouridine"
 /mod_base=d
 modified_base 21
 /note="dihydrouridine"
 /mod_base=d
 misc_feature 35.37
 /note="anylicodon (GAU)"
 modified_base 38
 /note="N-((9-beta-D-ribofuranosyl)purine-6-yl)
 carbamoyl)threonine"
 /mod_base=OTHER
 modified_base 47
 /note="7-methylguanosine"
 /mod_base=m7g
 modified_base 56
 /note="pseudouridine"
 /mod_base=p
 BASE COUNT 20 a 17 c 20 g 20 t
 ORIGIN

Query Match 58.4%; Score 14.6; DB 1; Length 77;
 Best Local Similarity 81.0%; Pred. No. 2.1e+04;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 CTGTCGACAGCATTCGCGTG 23
 |||||
 DB 16 CTGTCGACAGCATTCGCGTG 36

RESULT 14
 LOCUS MMTENT 77 bp mRNA linear BCT 20-APR-1994
 DEFINITION Mycoplasma mycoides sp. capri transfer RNA-ile (GAU).
 ACCSSION Y00372.1 M31334
 VERSION Y00372.1 GI:44470
 KEYWORDS transfer RNA; transfer RNA-ile.
 SOURCE Mycoplasma mycoides.
 ORGANISM Mycoplasma mycoides.
 Bacteria; Firmicutes; Mollicutes; Entomoplasmales;
 Entomoplasmatocae.
 REFERENCE 1 (bases 1 to 77)
 AUTHORS Schoen A.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-1987) Schoen A., Yale University, Dept. MB+B, 260
 White Ave., P.O. Box 6666, New Haven, CT 06511, USA
 REFERENCE 2 (bases 1 to 77)
 AUTHORS Schoen A.
 TITLE Sequence of an isolencing tRNA from Mycoplasma mycoides sp. Capri
 JOURNAL Nucleic Acids Res. 15 (13), 5488 (1987)
 MEDLINE 87260022
 PUBMED 3299273

FEATURES
 source
 1..77 Location/Qualifiers
 /organism="Mycoplasma mycoides"
 /strain="sp. capri"
 /db_xref="taxon:2102"
 1..77
 /product="tRNA-ile"
 8
 /note="4-thiouridine"
 /mod_base=s4u
 20
 /note="dihydrouridine"
 /mod_base=d
 21
 /note="dihydrouridine"
 /mod_base=d
 35..37
 /note="anticodon (GAU)"
 38
 /note="N-(9-beta-D-ribofuranosyl)purine-6-yl-(carbamoyl)threonine"
 /mod_base=OTHER
 47
 /note="7-methylguanosine"
 /mod_base=m7g
 56
 /note="pseudouridine"
 /mod_base=p
 20 a 17 c 20 g 20 t

BASE COUNT
 ORIGIN

Query Match 58.4%; Score 14.6; DB 1; Length 77;
 Best Local Similarity 81.0%; Pred. No. 2.1e+04;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 CTGTCACAGCATTCGCTGA 23
 ||| |
 Db 16 CTGCTAGACCATTCGCTGA 36

RESULT 15
 LOCUS AX460928/c 35 bp DNA linear PAT 08-JUL-2002
 DEFINITION Sequence 25 from Patent WO0238607.
 ACCSSION AX460928
 VERSION AX460928.1 GI:21726168
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.

REFERENCE 1
 AUTHORS Aparicio, S., Carlton, M., Dixon, J., Messenger, S., Russ, A. and
 Thresher, R.
 TITLE A bacn g protein coupled receptor polypeptide and polynucleotide
 JOURNAL encoding this receptor
 Patent: WO 0238607-A 25 16-MAY-2002;
 Paradigm Therapeutics Limited (GB)
 FEATURES
 source
 1..35 Location/Qualifiers
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Primer"
 7 a 7 c 13 g 8 t

BASE COUNT
 ORIGIN

Query Match 56.8%; Score 14.2; DB 6; Length 35;
 Best Local Similarity 84.2%; Pred. No. 3.1e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACTGTCACAGCATTCGCGC 20
 | |||| |
 Db 34 AGTGTCCCAAGCATTCGCGC 16

Search completed: December 21, 2002, 12:57:29
 Job time : 362.959 secs

7
1

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:43:17 : Search time 286.367 Seconds

(without alignments)
2032.551 Million cell updates/sec

Title: US-09-121-239-13

Sequence: 1 CAAAGCAGCAGCAGCAGCAGC 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Capext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_da:*
- 2: gb_hg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vl:*
- 15: em_da:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vl:*
- 30: em_hg_hum:*
- 31: em_hg_inv:*
- 32: em_hg_other:*
- 33: em_hg_mus:*
- 34: em_hg_pln:*
- 35: em_hg_rtd:*
- 36: em_hg_mam:*
- 37: em_hg_vit:*
- 38: em_sy:*
- 39: em_hgo_hum:*
- 40: em_hgo_mus:*
- 41: em_hgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.4	87.0	78	6	AR052214 Sequence
2	17.4	87.0	96	6	AR052217 Sequence
3	17.4	87.0	96	6	AR194309 Sequence
4	14.8	74.0	66	6	AR052213 Sequence
5	14.8	74.0	69	6	AR052215 Sequence
6	14.8	74.0	84	6	AR052216 Sequence
7	14.8	74.0	84	6	AR194308 Sequence
8	14.8	74.0	87	6	AR052218 Sequence
9	14.8	74.0	87	6	AR194310 Sequence
10	14.2	71.0	30	6	AX466817 Sequence
11	14.2	71.0	30	6	AR1695 Sequence
12	14.2	71.0	45	6	AR180998 Sequence
13	14.2	71.0	45	6	AR180998 Sequence
14	14.2	71.0	45	6	AR180998 Sequence
15	13.8	69.0	51	6	AR002441 Sequence
16	13.8	69.0	51	6	AR116049 Sequence
17	13.8	69.0	51	6	AX13788 Sequence
18	13.8	69.0	59	6	AX322070 Sequence
19	13.8	69.0	59	6	AX322069 Sequence
20	13.8	69.0	66	6	AX322069 Sequence
21	13.8	69.0	66	6	E06035 Sequence
22	13.8	69.0	66	6	E06644 Sequence
23	13.8	69.0	66	6	E07704 Sequence
24	13.8	69.0	66	6	AX322072 Sequence
25	13.8	69.0	68	6	AX322074 Sequence
26	13.8	69.0	68	6	AX322076 Sequence
27	13.8	69.0	68	6	AX322076 Sequence
28	13.8	69.0	68	6	AX322076 Sequence
29	13.8	69.0	68	6	AX322076 Sequence
30	13.8	69.0	68	6	AX322076 Sequence
31	13.8	69.0	75	6	AX322071 Sequence
32	13.8	69.0	75	6	AX322073 Sequence
33	13.8	69.0	75	6	AX322075 Sequence
34	13.8	69.0	75	6	E06036 Sequence
35	13.8	69.0	75	6	E06037 Sequence
36	13.8	69.0	75	6	E06038 Sequence
37	13.8	69.0	75	6	E07703 Sequence
38	13.8	69.0	75	6	E07703 Sequence
39	13.8	69.0	75	6	E07703 Sequence
40	13.8	69.0	75	6	E07703 Sequence
41	13.8	69.0	75	6	E07703 Sequence
42	13.6	68.0	28	6	AX322215 Sequence
43	13.6	68.0	30	6	E30036 Sequence
44	13.6	68.0	61	14	AF200198 Sequence
45	13.6	68.0	82	6	A62549 Sequence
			89	6	AR074468 Sequence

ALIGNMENTS

RESULT 1

AR052214 78 bp DNA 1 linear PAT 29-SEP-1999

LOCUS AR052214

DEFINITION Sequence 6 from patent US 5830866.

ACCESSION AR052214

VERSION AR052214.1 GI:5975578

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 78)

AUTHORS Redel,E. and Altd,F.

TITLE Corticotropin release inhibiting factor and methods of using same

JOURNAL Patent: US 5830866-A 6 03-NOV-1998;

FEATURES Location/Qualifiers

source 1..78 /organism="unknown"
BASE COUNT 28 a 12 c 31 g 7 t
ORIGIN

Query Match 87.0%; Score 17.4; DB 6; Length 78;
Best Local Similarity 94.7%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAAGGAGCGGAGAGAG 19
|||||
Db 19 CAAAGGAGCGTGGAGAGAG 37

RESULT 2
AR052217 AR052217 96 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 9 from patent US 5830866.
ACCESSION AR052217
VERSION AR052217.1 GI:5975581
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 96)
AUTHORS Redel,E. and Alrd,F.
TITLE Corticotropin release inhibiting factor and methods of using same
JOURNAL Patent: US 5830866-A 9 03-NOV-1998;
FEATURES
Location/Qualifiers
1..96
source /organism="unknown"

BASE COUNT 34 a 18 c 37 g 7 t
ORIGIN

Query Match 87.0%; Score 17.4; DB 6; Length 96;
Best Local Similarity 94.7%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAAGGAGCGGAGAGAG 19
|||||
Db 37 CAAAGGAGCGTGGAGAGAG 55

RESULT 3
AR194309 AR194309 96 bp DNA linear PAT 20-APR-2002
LOCUS
DEFINITION Sequence 8 from patent US 6348571.
ACCESSION AR194309
VERSION AR194309.1 GI:20240901
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 96)
AUTHORS Redel,E. and Alrd,F.
TITLE Corticotropin release inhibiting factor and methods of using same
JOURNAL Patent: US 6348571-A 8 19-FEB-2002;
FEATURES
Location/Qualifiers
1..96
source /organism="unknown"

BASE COUNT 34 a 18 c 37 g 7 t
ORIGIN

Query Match 87.0%; Score 17.4; DB 6; Length 96;
Best Local Similarity 94.7%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAAGGAGCGGAGAGAG 19
|||||
Db 37 CAAAGGAGCGTGGAGAGAG 55

RESULT 4

AR052213 AR052213 66 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 5 from patent US 5830866.
ACCESSION AR052213
VERSION AR052213.1 GI:5975577
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 66)
AUTHORS Redel,E. and Alrd,F.
TITLE Corticotropin release inhibiting factor and methods of using same
JOURNAL Patent: US 5830866-A 5 03-NOV-1998;
FEATURES
Location/Qualifiers
1..66
source /organism="unknown"

BASE COUNT 22 a 11 c 21 g 12 t
ORIGIN

Query Match 74.0%; Score 14.8; DB 6; Length 66;
Best Local Similarity 88.9%; Pred. No. 4.3e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAAGGAGCGGAGAGAG 18
|||||
Db 19 CAAAGGAGCGTGGAGAGAG 36

RESULT 5
AR052215 AR052215 69 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 7 from patent US 5830866.
ACCESSION AR052215
VERSION AR052215.1 GI:5975579
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 69)
AUTHORS Redel,E. and Alrd,F.
TITLE Corticotropin release inhibiting factor and methods of using same
JOURNAL Patent: US 5830866-A 7 03-NOV-1998;
FEATURES
Location/Qualifiers
1..69
source /organism="unknown"

BASE COUNT 22 a 11 c 24 g 12 t
ORIGIN

Query Match 74.0%; Score 14.8; DB 6; Length 69;
Best Local Similarity 88.9%; Pred. No. 4.2e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAAGGAGCGGAGAGAG 18
|||||
Db 19 CAAAGGAGCGTGGAGAGAG 36

RESULT 6
AR052216 AR052216 84 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 8 from patent US 5830866.
ACCESSION AR052216
VERSION AR052216.1 GI:5975580
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 84)
AUTHORS Redel,E. and Alrd,F.
TITLE Corticotropin release inhibiting factor and methods of using same
JOURNAL Patent: US 5830866-A 8 03-NOV-1998;
FEATURES
Location/Qualifiers
1..84
source


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BASE COUNT      27 a      17 c      27 g      13 t
ORIGIN
Query Match      74.0%; Score 14.8; DB 6; Length 84;
Best Local Similarity 88.9%; Pred. No. 4.1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CAAAGAGCAGGAGAGAA 18
       ||||| ||| ||||| |||
DB      37 CAAAGAGCTGGAGAGAA 54

RESULT 7
LOCUS      AR194308      84 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 7 from patent US 6348571.
ACCESSION  AR194308
VERSION     AR194308.1 GI:20240900
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 84)
AUTHORS    Redel,E. and Aird,F.
TITLE      Corticotropin release inhibiting factor and methods of using same
JOURNAL    Patent: US 6348571-A 7 19-FEB-2002;
FEATURES
SOURCE      1..84
            /organism="unknown"

BASE COUNT      27 a      17 c      27 g      13 t
ORIGIN
Query Match      74.0%; Score 14.8; DB 6; Length 84;
Best Local Similarity 88.9%; Pred. No. 4.1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CAAAGAGCAGGAGAGAA 18
       ||||| ||| ||||| |||
DB      37 CAAAGAGCTGGAGAGAA 54

RESULT 8
LOCUS      AR052218      87 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5830866.
ACCESSION  AR052218
VERSION     AR052218.1 GI:5975582
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 87)
AUTHORS    Redel,E. and Aird,F.
TITLE      Corticotropin release inhibiting factor and methods of using same
JOURNAL    Patent: US 5830866-A 10 03-NOV-1998;
FEATURES
SOURCE      1..87
            /organism="unknown"

BASE COUNT      26 a      17 c      31 g      13 t
ORIGIN
Query Match      74.0%; Score 14.8; DB 6; Length 87;
Best Local Similarity 88.9%; Pred. No. 4e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CAAAGAGCAGGAGAGAA 18
       ||||| ||| ||||| |||
DB      37 CAAAGAGCTGGAGAGAA 54

RESULT 9
LOCUS      AR194310
DEFINITION Sequence 9 from patent US 6348571.
ACCESSION  AR194310
VERSION     AR194310.1 GI:20240902
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 87)
AUTHORS    Redel,E. and Aird,F.
TITLE      Corticotropin release inhibiting factor and methods of using same
JOURNAL    Patent: US 6348571-A 9 19-FEB-2002;
FEATURES
SOURCE      1..87
            /organism="unknown"

BASE COUNT      26 a      17 c      31 g      13 t
ORIGIN
Query Match      74.0%; Score 14.8; DB 6; Length 87;
Best Local Similarity 88.9%; Pred. No. 4e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CAAAGAGCAGGAGAGAA 18
       ||||| ||| ||||| |||
DB      37 CAAAGAGCTGGAGAGAA 54

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LOCUS      AR194310      87 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 9 from patent US 6348571.
ACCESSION  AR194310
VERSION     AR194310.1 GI:20240902
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 87)
AUTHORS    Redel,E. and Aird,F.
TITLE      Corticotropin release inhibiting factor and methods of using same
JOURNAL    Patent: US 6348571-A 9 19-FEB-2002;
FEATURES
SOURCE      1..87
            /organism="unknown"

BASE COUNT      26 a      17 c      31 g      13 t
ORIGIN
Query Match      74.0%; Score 14.8; DB 6; Length 87;
Best Local Similarity 88.9%; Pred. No. 4e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CAAAGAGCAGGAGAGAA 18
       ||||| ||| ||||| |||
DB      37 CAAAGAGCTGGAGAGAA 54

RESULT 10
LOCUS      AX466817/c      22 bp      DNA      linear      PAT 16-JUL-2002
DEFINITION Sequence 299 from Patent WO0212343.
ACCESSION  AX466817
VERSION     AX466817.1 GI:21900176
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    synthetic construct.
REFERENCE   1
AUTHORS    Spytek,R.A., Padigaru,M., Zerhusen,B.D., Baumgartner,J.C., Li,L.,
            Casman,S.J., Vernet,C.A., Ballinger,R.A., Shenoy,S.G., Kekuda,R.,
            Burgess,G.E., Mezes,P.S., Grosse,W.M., Alsobrook,J.P., Gorman,L.,
            Larocheille,W.D., Traubier,R.J., Colman,S.D. and Szekeres,E.S.
            Proteins and nucleic acids encoding g-protein coupled receptors
            Patent: WO 0212343-A 299 14-FEB-2002;
            Curagen Corporation (US)
            Location/Qualifiers
            1..22
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="reverse primer"

BASE COUNT      3 a      7 c      3 g      9 t
ORIGIN
Query Match      71.0%; Score 14.2; DB 6; Length 22;
Best Local Similarity 84.2%; Pred. No. 1e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 AAAGAGCAGGAGAGAG 20
       ||||| ||| ||||| |||
DB      22 AAAGAGCAGCTTAAGAG 4

RESULT 11
LOCUS      AB1695      30 bp      DNA      linear      PAT 21-JAN-2000
DEFINITION Sequence 12 from Patent WO9900517.
ACCESSION  AB1695
VERSION     AB1695.1 GI:6731830
KEYWORDS
SOURCE      unidentified.
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 30)

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AUTHORS Archer, J. A. and Roland, H. J.
 TITLE BIOSENSOR MATERIALS AND METHODS
 JOURNAL Patent: WO 9900517-A 12 07-JAN-1999;
 FEATURES ARCHER JOHN ANTHON CHARLES (GB); ROLAND HERVE JACQUIAU (GB)
 SOURCE 1. .30
 /db_xref="taxon:32644"
 /organism="unidentified"

BASE COUNT 15 a 6 c 8 g 1 t
 ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 30;
 Best Local Similarity 84.2%; Pred. No. 9.4e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAAGAGCAGGAGGAGAG 19
 Db 12 CAAAGAGCAGGAGGAGAGCAG 30

RESULT 12
 LOCUS AR180998 45 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 14 from patent US 6333168.
 ACCESSION AR180998
 VERSION AR180998.1 GI:20223031
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 45)
 AUTHORS Jessell, T.M., Basler, K. and Yamada, T.
 TITLE Cloning, expression and uses of dorsalin-1
 JOURNAL Patent: US 6333168-A 14 25-DEC-2001;
 FEATURES Location/Qualifiers
 source 1. .45
 /organism="unknown"

BASE COUNT 6 a 14 c 8 g 17 t
 ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 45;
 Best Local Similarity 84.2%; Pred. No. 8.6e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAAGAGCAGGAGGAGAG 19
 Db 35 CAAAGAGCAGGAGGAGAG 17

RESULT 13
 LOCUS F222949S02/c 81 bp DNA linear ROD 05-JUL-2000
 DEFINITION Mus musculus Mtf protein (Mtf) gene, alternative exon 1h.
 ACCESSION AF222950
 VERSION AF222950.1 GI:8917536
 KEYWORDS
 SEGMENT 2 of 11
 SOURCE Mus musculus.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 81)
 Hallsson, J.H., Fawor, J., Hoddgkinson, C., Glaser, T., Lamoreux, M.L.,
 Magnusdottir, R., Gunnarsson, G.J., Sweet, H.O., Copeland, N.G.,
 Jenkins, N.A. and Steingrimsdottir, E.
 TITLE Genomic, transcriptional and mutational analysis of the mouse
 microphtalmia locus
 JOURNAL Genetics 155 (1), 291-300 (2000)
 MEDLINE 20253112
 PUBMED 10790403
 REFERENCE 2 (bases 1 to 81)
 AUTHORS Hallsson, J.H., Fawor, J., Hodgkinson, C., Glaser, T., Lamoreux, M.L.,
 Magnusdottir, R., Gunnarsson, G.J., Sweet, H.O., Copeland, N.G.,
 Magnusdottir, R., Gunnarsson, G.J., Sweet, H.O., Copeland, N.G.,

TITLE Jenkins, N.A. and Steingrimsdottir, E.
 JOURNAL Direct Submission
 Submitted (11-JAN-2000) Department of Biochemistry and Molecular
 Biology, University of Iceland, Faculty of Medicine,
 Vatnsmyrarvegur 16, Reykjavik 101, Iceland
 FEATURES Location/Qualifiers
 SOURCE 1. .81
 /organism="Mus musculus"
 /strain="129/Sv"
 /db_xref="taxon:10090"
 exon 1. .72
 /gene="Mtf"
 /note="alternatively spliced"
 /number=1h

BASE COUNT 24 a 13 c 21 g 23 t
 ORIGIN

Query Match 71.0%; Score 14.2; DB 10; Length 81;
 Best Local Similarity 84.2%; Pred. No. 7.6e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAAGAGCAGGAGGAGAG 19
 Db 59 CAAAGAGCAGGAGGAGAG 41

RESULT 14
 LOCUS AX249697/c 31 bp DNA linear PAT 28-SEP-2001
 DEFINITION Sequence 1776 from Patent W00166800.
 ACCESSION AX249697
 VERSION AX249697.1 GI:15864320
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 31)
 Caregili, M., Ireland, J.S. and Lander, E.S.
 TITLE Human single nucleotide polymorphisms
 JOURNAL Patent: WO 0166800-A 1776 13-SEP-2001;
 FEATURES Location/Qualifiers
 source 1. .31
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 5 a 9 c 6 g 10 t 1 others
 ORIGIN

Query Match 69.0%; Score 13.8; DB 6; Length 31;
 Best Local Similarity 78.9%; Pred. No. 1.4e+05;
 Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGAGCAGGAGGAGAG 20
 Db 31 AAAGAGCAGGAGGAGAG 13

RESULT 15
 LOCUS AR002441/c 51 bp DNA linear PAT 04-DEC-1998
 DEFINITION Sequence 5 from patent US 5741669.
 ACCESSION AR002441
 VERSION AR002441.1 GI:3963995
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 51)
 AUTHORS Krapcho, K. Joanne., Jackson, J. Randolph, Hunter., Johnson, J. Helen.,
 DelMar, E. George. and Kral, R. Marden, Jr.
 TITLE Insecticidally effective peptides
 JOURNAL Patent: US 5741669-A 5 21-APR-1998;

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FEATURES                               Location/Qualifiers
Source                               1. 51
BASE COUNT                          7 a 11 c 11 g 22 t
ORIGIN
Query Match                          69.0%; Score 13.8; DB 6; Length 51;
Best Local Similarity                88.2%; Pred. No. 1.3e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 AAGGAGCAGGGAAGAAG 19
Db 47 AAGGAGCAGGGAAGAAG 31

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Search completed: December 21, 2002, 12:57:33
 Job time : 290.367 secs

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:43:17 ; Search time 343.641 Seconds
(without alignments)
2032.551 Million cell updates/sec

Title: US-09-121-239-16

Sequence: 24
1 GTGGAACATGACCCCTCAGCGG 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: GenBank:
2: gb_hg:
3: gb_in:
4: gb_cm:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vt:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
21: em_or:
22: em_ov:
23: em_pat:
24: em_ph:
25: em_pl:
26: em_ro:
27: em_sts:
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30: em_hg_hum:
31: em_hg_inv:
32: em_hg_other:
33: em_hg_mus:
34: em_hg_pln:
35: em_hg_rod:
36: em_hg_mam:
37: em_hg_vrt:
38: em_sy:
39: em_hg_hum:
40: em_hg_mus:
41: em_hg_other:

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.8	65.8	56	6	112444
C 2	15.8	65.8	56	6	114506
C 3	15.6	65.0	35	6	AR105346
C 4	15.6	65.0	35	6	AX067702
C 5	15.6	65.0	42	6	AX209901
C 6	15.4	64.2	23	6	183647
C 7	15.4	64.2	23	6	183648
C 8	15.4	64.2	29	6	AA8907
C 9	15.4	64.2	44	6	AX280264
C 10	15.4	64.2	52	6	AA8906
C 11	15.4	64.2	60	6	AS0283
C 12	15.4	64.2	62	6	AR100681
C 13	15.2	63.3	61	6	AX270703
C 14	15.2	63.3	61	6	AX272234
C 15	15.2	62.5	33	6	AA9027
C 16	15.2	62.5	33	6	AA9029
C 17	15.2	62.5	34	6	AR081961
C 18	15.2	62.5	47	6	AR100692
C 19	15.2	62.5	63	6	158639
C 20	15.2	62.5	80	6	158639
C 21	15.2	62.5	80	6	158639
C 22	15.2	62.5	90	6	158639
C 23	15.2	62.5	97	10	AF177699
C 24	14.8	61.7	31	6	AB3702
C 25	14.4	60.0	23	6	158666
C 26	14.4	60.0	26	6	158661
C 27	14.4	60.0	26	6	158661
C 28	14.4	60.0	26	6	158661
C 29	14.4	60.0	26	6	158661
C 30	14.4	60.0	82	9	AF028334
C 31	14.4	60.0	82	9	AF028334
C 32	14.4	60.0	82	9	AF028334
C 33	14.4	60.0	82	9	AF028334
C 34	14.2	59.2	20	6	AR024076
C 35	14.2	59.2	23	6	BD001180
C 36	14.2	59.2	23	6	BD001180
C 37	14.2	59.2	23	6	BD001180
C 38	14.2	59.2	31	6	AX248573
C 39	14.2	59.2	31	6	AX248573
C 40	14.2	59.2	31	6	AX248573
C 41	14.2	59.2	31	6	AX248573
C 42	14.2	59.2	31	6	AX248573
C 43	14.2	59.2	31	6	AX248573
C 44	14.2	59.2	31	6	AX248573
C 45	14.2	59.2	31	6	AX248573

ALIGNMENTS

RESULT 1
112444/c 112444 56 bp DNA linear PAT 26-JUL-1995
LOCUS Sequence 14 from patent US 5424413.
DEFINITION 112444
ACCESSION 112444
VERSION 112444.1 GI:909828
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 56)
AUTHORS Hogan,J.J., Arnold,L.J., Nelson,N.C. and Bezerkov,R.
TITLE Nucleic acid probes
JOURNAL Patent: US 5424413-A 24 13-JUN-1995;
FEATURES
Location/Qualifiers

Pred. No. is the number of results predicted by chance to have a

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source 1..56
BASE COUNT 13 a 17 c 13 g 13 t
ORIGIN
Query Match 65.8%; Score 15.8; DB 6; Length 56;
Best Local Similarity 89.5%; Pred. No. 2.8e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 ACATGAGCCCTTCAGCGG 24
Db 35 ACCTAAGCCCTTCAGCGG 17

RESULT 2
LOCUS 114506 56 bp DNA linear PAT 26-SEP-1995
DEFINITION Sequence 14 from patent US 5451503.
ACCESSION 114506
VERSION 114506.1 GI:96989
KEYWORDS
SOURCE
ORGANISM
REFERENCE
Unclassified.
1 (bases 1 to 56)
AUTHORS Hogan, J.J., Arnold, L.J., Jr., Nelson, N.C. and Bezverkoy, R.
TITLE Method for use of branched nucleic acid probes
JOURNAL Patent: US 5451503-A 14 19-SEP-1995;
FEATURES
Location/Qualifiers
1..56
source /organism="unknown"

BASE COUNT 13 a 17 c 13 g 13 t
ORIGIN
Query Match 65.8%; Score 15.8; DB 6; Length 56;
Best Local Similarity 89.5%; Pred. No. 2.8e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 ACATGAGCCCTTCAGCGG 24
Db 35 ACCTAAGCCCTTCAGCGG 17

RESULT 3
LOCUS ARI05346/c 35 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 27 from patent US 6096539.
ACCESSION ARI05346
VERSION ARI05346.1 GI:12818943
KEYWORDS
SOURCE
ORGANISM
REFERENCE
Unclassified.
1 (bases 1 to 35)
AUTHORS Gomes, B., Charles, J., Kasof, G.M. and Prosser, J. Caroline.
TITLE Protein activator of apoptosis
JOURNAL Patent: US 6096539-A 27 01-AUG-2000;
FEATURES
Location/Qualifiers
1..35
source /organism="unknown"

BASE COUNT 3 a 12 c 12 g 8 t
ORIGIN
Query Match 65.0%; Score 15.6; DB 6; Length 35;
Best Local Similarity 81.8%; Pred. No. 3.8e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGACATGAGCCCTTCAGCGG 24
Db 35 GGACACCAAGCTCTTAAGCGG 14

RESULT 4

```

```

AX067702/c 35 bp DNA linear PAT 19-JAN-2001
LOCUS AX067702
DEFINITION Sequence 27 from Patent WO0077200.
ACCESSION AX067702
VERSION AX067702.1 GI:12329589
KEYWORDS
SOURCE
ORGANISM
REFERENCE
synthetic construct.
1 (bases 1 to 35)
AUTHORS Gomes, B.C., Kasof, G.M. and Prosser, J.C.
TITLE Receptor interacting protein r1p3
JOURNAL Patent: WO 0077200-A 27 21-DEC-2000;
FEATURES
Location/Qualifiers
1..35
source /organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR Primer"

BASE COUNT 3 a 12 c 12 g 8 t
ORIGIN
Query Match 65.0%; Score 15.6; DB 6; Length 35;
Best Local Similarity 81.8%; Pred. No. 3.8e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGACATGAGCCCTTCAGCGG 24
Db 35 GGACACCAAGCTCTTAAGCGG 14

RESULT 5
LOCUS AX209901 42 bp DNA linear PAT 31-AUG-2001
DEFINITION Sequence 3 from Patent WO0157240.
ACCESSION AX209901
VERSION AX209901.1 GI:15424322
KEYWORDS
SOURCE
ORGANISM
REFERENCE
synthetic construct.
1 (bases 1 to 42)
AUTHORS Melcher, T. and Kask, K.
TITLE Interaction of mdma receptor with protein tyrosine phosphatase
JOURNAL Patent: WO 0157240-A 3 09-AUG-2001;
FEATURES
Location/Qualifiers
1..42
source /organism="synthetic construct"
/db_xref="taxon:32630"
/note="antisense oligonucleotide"

BASE COUNT 9 a 19 c 6 g 8 t
ORIGIN
Query Match 65.0%; Score 15.6; DB 6; Length 42;
Best Local Similarity 81.8%; Pred. No. 3.7e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGACATGAGCCCTTCAGCGG 24
Db 10 GCACCAAGCCCTTCAGCTG 31

RESULT 6
LOCUS I83647 23 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 21 from patent US 5714583.
ACCESSION I83647
VERSION I83647.1 GI:3407177
KEYWORDS
SOURCE
ORGANISM
REFERENCE
Unclassified.

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```

REFERENCE 1 (bases 1 to 23)
AUTHORS Thompson, J.D.
TITLE Method and reagent for treating chronic myelogenous leukemia
JOURNAL Patent: US 5714383-A 21 03-FEB-1998;
FEATURES
SOURCE 1..23
Location/Qualifiers
ORGANISM /organism="unknown"
BASE COUNT 6 a 7 c 7 g 3 t
ORIGIN

Query Match 64.2%; Score 15.4; DB 6; Length 23;
Best Local Similarity 94.1%; Pred. No. 5e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ATGAAGCCTTCAGCGG 24
Db 2 AAGAAGCCTTCAGCGG 18

RESULT 7
LOCUS 183648 23 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 22 from patent US 5714383.
ACCESSION 183648
VERSION 183648.1 GI:3407178
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Thompson, J.D.
TITLE Method and reagent for treating chronic myelogenous leukemia
JOURNAL Patent: US 5714383-A 22 03-FEB-1998;
FEATURES
SOURCE 1..23
Location/Qualifiers
ORGANISM /organism="unknown"
BASE COUNT 7 a 7 c 6 g 3 t
ORIGIN

Query Match 64.2%; Score 15.4; DB 6; Length 23;
Best Local Similarity 94.1%; Pred. No. 5e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ATGAAGCCTTCAGCGG 24
Db 1 AAGAAGCCTTCAGCGG 17

RESULT 8
LOCUS A48907 29 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 3 from Patent WO9605323.
ACCESSION A48907
VERSION A48907.1 GI:2302567
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 29)
AUTHORS Sauvalgo, S., Bazin, H. and Liyache, T.
TITLE METHOD FOR THE AMPLIFICATION AND/OR DETECTION OF A NUCLEIC ACID
SEQUENCE, DETECTION REAGENT AND USES THEREOF
JOURNAL Patent: WO 9605323-A 3 22-FEB-1996;
COMMENT CTS BIO INT (FR)
FEATURES
SOURCE Other publication FR 2723591 960216.
Location/Qualifiers
1..29
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 10 a 8 c 7 g 4 t
ORIGIN

Query Match 64.2%; Score 15.4; DB 6; Length 29;

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Best Local Similarity 94.1%; Pred. No. 4.8e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ATGAAGCCTTCAGCGG 24
Db 12 AAGAAGCCTTCAGCGG 28

RESULT 9
LOCUS AX280264/c 44 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 11 from Patent WO0177383.
ACCESSION AX280264
VERSION AX280264.1 GI:16607642
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Nilsson, M.B. and Landegren, U.
TITLE Nucleic acid detection medium
JOURNAL Patent: WO 0177383-A 11 18-OCT-2001;
FEATURES
SOURCE Nilsson, Mats Bo Johan (SE); Landegren, Ulf (SE)
Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Templates for RNA synthesis"
BASE COUNT 9 a 10 c 11 g 13 t 1 others
ORIGIN

Query Match 64.2%; Score 15.4; DB 6; Length 44;
Best Local Similarity 88.9%; Pred. No. 4.5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CATGAAGCCTTCAGCGG 24
Db 21 CAANAAGCCTTCAGCGG 4

RESULT 10
LOCUS A48906 52 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 2 from Patent WO9605323.
ACCESSION A48906
VERSION A48906.1 GI:2302566
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 52)
AUTHORS Sauvalgo, S., Bazin, H. and Liyache, T.
TITLE METHOD FOR THE AMPLIFICATION AND/OR DETECTION OF A NUCLEIC ACID
SEQUENCE, DETECTION REAGENT AND USES THEREOF
JOURNAL Patent: WO 9605323-A 2 22-FEB-1996;
COMMENT CTS BIO INT (FR)
FEATURES
SOURCE Other publication FR 2723591 960216.
Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 9 a 12 c 14 g 17 t
ORIGIN

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Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ATGAAGCCTTCAGCGG 24
Db 18 AAGAAGCCTTCAGCGG 2

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RESULT 11
A50293          60 bp   DNA      linear   PAT 07-MAR-1997
DEFINITION      Sequence 13 from Patent WO9612803.
ACCESSION       A50293
VERSION         A50293.1 GI:2303347
KEYWORDS
SOURCE          unidentified.
ORGANISM        unidentified.
REFERENCE       1 (bases 1 to 60)
TITLE          Blumenfeld,M.
JOURNAL        METHOD FOR THE EX VIVO TREATMENT OF TUMOUR CELLS FROM PATIENTS WITH
COMMENT        Patent: WO 9612803-A 13 02-MAY-1996;
FEATURES       Location/Qualifiers
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               /db_xref="taxon:32644"
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Best Local Similarity 94.1%; Pred. No. 4.3e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ATGAAGCCCTTCAGCG 24
Db 28 AAGAAGCCCTTCAGCG 44

RESULT 12
A100681         62 bp   DNA      linear   PAT 14-FEB-2001
DEFINITION      Sequence 1 from patent US 6080851.
ACCESSION       A100681
VERSION         A100681.1 GI:12811129
KEYWORDS
SOURCE          Unknown.
ORGANISM        Unknown.
REFERENCE       1 (bases 1 to 62)
AUTHORS        Pachuk,C.J.; Coney,L.R. and Oakes,F.T.
TITLE          Ribozymes with linked anchor sequences
JOURNAL        Patent: US 6080851-A 1 27-JUN-2000;
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BASE COUNT     18 a 19 c 13 g 12 t
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Query Match    64.2%; Score 15.4; DB 6; Length 62;
Best Local Similarity 94.1%; Pred. No. 4.2e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ATGAAGCCCTTCAGCG 24
Db 29 AAGAAGCCCTTCAGCG 45

RESULT 13
AX270703        61 bp   DNA      linear   PAT 29-OCT-2001
DEFINITION      Sequence 1334 from Patent WO0164876.
ACCESSION       AX270703
VERSION         AX270703.1 GI:16543479
KEYWORDS
SOURCE          human.
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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REFERENCE       1
AUTHORS        Stefansson,H., Steinhorsdottir,V. and Gulcher,J.R.
TITLE          Human schizophrenia gene
JOURNAL        Patent: WO 0164876-A 1334 07-SEP-2001;
FEATURES       Decode Genetics EHF. (IS)
source         Location/Qualifiers
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               /db_xref="taxon:9606"
BASE COUNT     25 a 6 c 9 g 20 t 1 others
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Query Match    63.3%; Score 15.2; DB 6; Length 61;
Best Local Similarity 85.0%; Pred. No. 5.3e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGACATGAGCCCTTCAG 21
Db 37 TGGATATGAGCATTTTCAG 56

RESULT 14
AX272234        61 bp   DNA      linear   PAT 29-OCT-2001
LOCUS          AX272234
DEFINITION      Sequence 1334 from Patent WO0164877.
ACCESSION       AX272234
VERSION         AX272234.1 GI:16544971
KEYWORDS
SOURCE          human.
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE       1
AUTHORS        Stefansson,H., Steinhorsdottir,V. and Gulcher,J.R.
TITLE          Human schizophrenia gene
JOURNAL        Patent: WO 0164877-A 1334 07-SEP-2001;
FEATURES       Decode Genetics EHF. (IS)
source         Location/Qualifiers
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BASE COUNT     25 a 6 c 9 g 20 t 1 others
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Best Local Similarity 85.0%; Pred. No. 5.3e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGACATGAGCCCTTCAG 21
Db 37 TGGATATGAGCATTTTCAG 56

RESULT 15
A49027          33 bp   DNA      linear   PAT 07-MAR-1997
LOCUS          A49027
DEFINITION      Sequence 9 from Patent WO9606166.
ACCESSION       A49027
VERSION         A49027.1 GI:2302637
KEYWORDS
SOURCE          unidentified.
ORGANISM        unidentified.
REFERENCE       1 (bases 1 to 33)
AUTHORS        Cho,Y., Kling,A. and Garcia,I.
TITLE          IMPROVEMENTS IN OR RELATING TO BINDING PROTEINS FOR RECOGNITION OF
JOURNAL        Patent: WO 9606166-A 9 29-FEB-1996;
COMMENT        MEDICAL RES COUNCIL (GB)
FEATURES       Other publication AU 3229195 960314.
source         Location/Qualifiers
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BASE COUNT 8 a /db_xref="taxon:32644" 5 t
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Query Match 62.5%; Score 15; DB 6; Length 33;
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 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GAAGCCCTTCAGCG 24
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 Db 16 GAAGCCCTTCAGCG 30

Search completed: December 21, 2002, 12:57:37
 Job time : 347.641 secs

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:43:17 ; Search time 386.596 Seconds
(without alignments)
2032.551 Million cell updates/sec

Title:	US-09-121-239-22
Perfect score:	27

Sequence: 1 TCTGACTTTGAGCCTCAGGGTCTGAGT 27

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Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

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Minimum DB seq length: 0
Maximum DB seq length: 100

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Post-processing:	Minimum Match 0%
	Maximum Match 100%

Listing first 45 summaries

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GenEmbl1:*

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- 2: gb_hvg:*
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- 30: em_hum:*
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- 33: em_hvg:*
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- 36: em_hvg:*
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- 39: em_hvg:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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1	26	96.3	80	6	I58639	I58639 Sequence 7
2	26	96.3	80	6	I96201	I96201 Sequence 38
3	22	81.5	22	6	AR086401	AR086401 Sequence 10
4	22	81.5	22	6	I44731	I44731 Sequence 10
5	22	81.5	22	6	I92877	I92877 Sequence 1
6	19	70.4	24	6	E16995	E16995 Primer. 7/1
7	19	70.4	24	6	A93183	A93183 Sequence 6
8	18	66.7	59	6	A93191	A93191 Sequence 14
9	18	63.0	51	6	AX115325	AX115325 Sequence
10	17	63.0	56	6	I12449	I12449 Sequence 19
11	17	63.0	56	6	I14511	I14511 Sequence 19
12	17	63.0	58	6	A93190	A93190 Sequence 13
13	17	63.0	76	3	SQDTRF506	SQDTRF506
14	17	63.0	76	3	SQDTRF152	SQDTRF152
15	16.8	62.2	71	9	ESL165N	ESL165N
16	16.4	60.7	28	6	E26953	E26953 Method for
17	16	59.3	54	10	AF224105	AF224105 Mus muscu
18	16	59.3	67	6	A93189	A93189 Sequence 12
19	16	59.3	75	9	F18552S11	F1855202 Homo sapi
20	15.8	58.5	20	6	I23911	I23911 Sequence 13
21	15.6	57.8	29	6	I27229	I27229 Sequence 35
22	15.2	56.3	29	6	A56950	A56950 Sequence 8
23	15.2	56.3	51	6	AX204128	AX204128 Sequence
24	15.2	56.3	64	6	F292317502	F2923178 Bos tauru
25	15	55.6	16	6	E13680	E13680 Substrate o
26	15	55.6	20	6	AR037942	AR037942 Sequence
27	15	55.6	40	6	AR037936	AR037936 Sequence
28	15	55.6	40	6	AR037937	AR037937 Sequence
29	15	55.6	66	6	A93188	A93188 Sequence 11
30	14.8	54.8	24	6	AX443608	AX443608 Sequence
31	14.8	54.8	25	6	AX447590	AX447590 Sequence
32	14.8	54.8	64	6	AX14972	AX14972 Sequence 13
33	14.8	54.8	67	6	AX436030	AX436030 Sequence
34	14.8	54.8	69	6	MS009943	MS009943 Morone saxa
35	14.8	54.8	69	6	AX435663	AX435663 Sequence
36	14.8	54.8	69	6	AX435978	AX435978 Sequence
37	14.8	54.8	76	1	BSNRNAK	V00103 Bacillus su
38	14.8	54.8	76	6	AX435959	AX435959 Sequence
39	14.8	54.8	76	6	AX435999	AX435999 Sequence
40	14.8	54.8	76	6	AX436011	AX436011 Sequence
41	14.8	54.8	76	6	AX436029	AX436029 Sequence
42	14.8	54.8	76	6	AX439994	AX439994 Sequence
43	14.8	54.8	76	6	AX440034	AX440034 Sequence
44	14.8	54.8	76	6	AX440046	AX440046 Sequence
45	14.8	54.8	76	6	AX440062	AX440062 Sequence

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	
158639	158639	Sequence 7 from patent US 5652222.	158639	158639.1	GI:2478787	unknown.	unknown.	Unclassified.	1 (bases 1 to 80)	Calderetta, B. and Gewirtz, A.M.	Selective inhibition of leukemic cell proliferation by bcr-abl antisense oligonucleotides	Patent: US 5652222-A 7 29-JUL-1997;

FEATURES
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Location/Qualifiers
BASE COUNT 16 a 22 c 27 g 15 t
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Query Match 96.3%; Score 26; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGCTCTGAG 26
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Db 55 TCTGACTTTGAGCCTCAGGCTCTGAG 80

RESULT 2
LOCUS 196201 80 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 38 from patent US 5734039.
ACCESSION 196201
VERSION 196201.1 GI:3940671
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 80)
AUTHORS Calabretta,B. and Skorski,T.
TITLE Antisense oligonucleotides targeting cooperating oncogenes
JOURNAL Patent: US 5734039-A 38 31-MAR-1998;
FEATURES Location/Qualifiers
source 1.80
/organism="unknown"

BASE COUNT 16 a 22 c 27 g 15 t
ORIGIN

Query Match 96.3%; Score 26; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGCTCTGAG 26
|||||
Db 55 TCTGACTTTGAGCCTCAGGCTCTGAG 80

RESULT 3
LOCUS AR086401/c 22 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from patent US 5985572.
ACCESSION AR086401
VERSION AR086401.1 GI:10013167
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Macfarlane,D.E.
TITLE Quaternary amine surfactant and methods of using same in isolation of RNA
JOURNAL Patent: US 5985572-A 1 16-NOV-1999;
FEATURES Location/Qualifiers
source 1.22
/organism="unknown"

BASE COUNT 6 a 7 c 5 g 4 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 22 GACTTTGAGCCTCAGGCTCTGA 1

RESULT 4
LOCUS 144731 22 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 10 from patent US 5635385.
ACCESSION 144731
VERSION 144731.1 GI:2469444
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 22)
AUTHORS Leopold,L.H., Shore,S.K., Reddy,M.V.R. and Reddy,E.Premkumar.
TITLE Multi-unit ribozyme inhibition of oncogene gene expression
JOURNAL Patent: US 5635385-A 10 03-JUN-1997;
FEATURES Location/Qualifiers
source 1.22
/organism="unknown"

BASE COUNT 6 a 7 c 5 g 4 t
ORIGIN

Query Match 81.5%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTTGAGCCTCAGGCTCTGA 25
|||||
Db 22 GACTTTGAGCCTCAGGCTCTGA 1

RESULT 5
LOCUS 192877 22 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 1 from patent US 5728822.
ACCESSION 192877
VERSION 192877.1 GI:3937347
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Macfarlane,D.E.
TITLE Quaternary amine surfactants and methods of using same in isolation of RNA
JOURNAL Patent: US 5728822-A 1 17-MAR-1998;
FEATURES Location/Qualifiers
source 1.22
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BASE COUNT 6 a 7 c 5 g 4 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 22 GACTTTGAGCCTCAGGCTCTGA 1

RESULT 6
LOCUS E16995 24 bp DNA linear PAT 28-JUL-1999
DEFINITION Primer.
ACCESSION E16995
VERSION E16995.1 GI:5711678
KEYWORDS JP 1998229899-A/10.
SOURCE unidentified.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 24)
AUTHORS Kobayashi,M., Kawaguchi,R., Segawa,M. and Takarada,Y.
TITLE PRIMER FOR DETECTING BCR/ABL TYPE CHIMERA MESSENGER RNA, AND

DETECTION OF BCR/ABL TYPE CHIMERA MESSENGER RNA AND USING THE SAME
 Patent: JP 199822899-A 10 02-SEP-1998;
 S R I.K.K. TOYORO CO LTD

COMMENT

OS None
 OC Artificial sequences.
 PN JP 199822899-A/10

PD 02-SEP-1998 JP 1997054092

PI KOBAYASHI MASARU, KAMAGUCHI RYUJI, SEGAWA MASAYA, PI

PC C12Q1/68,G01N33/50//C12N15/09;

CC strandedness: Single;

CC topology: Linear;

CC Key

FT source

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 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGG 19

DB 6 TCTGACTTTGAGCCTCAGG 24

RESULT 7
 LOCUS A93183 70 bp DNA linear PAT 22-JAN-2000
 DEFINITION Sequence 6 from Patent WO9746672.
 ACCESSION A93183
 VERSION A93183.1 GI:6741568
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.

REFERENCE 1 (bases 1 to 70)
 AUTHORS Sczakiel,G. and Haas,R.
 TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
 JOURNAL DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)

FEATURES
 source Location/Qualifiers
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 /organism="unidentified"
 /db_xref="taxon:32644"

BASE COUNT 15 a 18 c 22 g 15 t

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGG 19

DB 19 TCTGACTTTGAGCCTCAGG 1

RESULT 8
 LOCUS A93191 69 bp DNA linear PAT 22-JAN-2000
 DEFINITION Sequence 14 from Patent WO9746672.
 ACCESSION A93191
 VERSION A93191.1 GI:6741576
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified

REFERENCE 1 (bases 1 to 69)
 AUTHORS Sczakiel,G. and Haas,R.
 TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
 JOURNAL DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)

FEATURES

source Location/Qualifiers
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 /db_xref="taxon:32644"

BASE COUNT 15 a 17 c 22 g 15 t

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAG 18

DB 18 TCTGACTTTGAGCCTCAG 1

RESULT 9
 LOCUS AX115325 51 bp DNA linear PAT 11-MAY-2001
 DEFINITION Sequence 448 from Patent WO0129262.
 ACCESSION AX115325
 VERSION AX115325.1 GI:14032267
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 51)
 AUTHORS Picoult-Newburg,L. and Pohl,M.
 TITLE Genotyping reagents, kits and methods of use thereof
 JOURNAL Patent: WO 0129262-A 448 26-APR-2001;
 Orchid Biosciences, Inc. (US)

FEATURES
 source Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 6 a 5 c 21 g 19 t

ORIGIN

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 Best Local Similarity 80.0%; Pred. No. 3.6e+03;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 TGACTTTGAGCCTCAGGCTGTGAGT 27

DB 11 TGACTTTGAGCCTCAGGCTGTGAGT 35

RESULT 10
 LOCUS 112449 56 bp DNA linear PAT 26-JUL-1995
 DEFINITION Sequence 19 from patent US 5424413.
 ACCESSION 112449
 VERSION 112449.1 GI:909833
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 56)
 AUTHORS Hogan,J.J., Arnold,L.J. Jr., Nelson,N.C. and Bezerkov,R.
 TITLE Branched nucleic acid probes
 JOURNAL Patent: US 5424413-A 19 13-JUN-1995;
 LOCATION/Qualifiers
 1..56
 /organism="unknown"

BASE COUNT 13 a 14 c 15 g 14 t

ORIGIN

Query Match 63.0%; Score 17; DB 6; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
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QY 1 TCTGACTTGAGCCTCA 17
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 Db 40 TCTGACTTGAGCCTCA 56

RESULT 11
 LOCUS 114511 56 bp DNA linear PAT 26-SEP-1995
 DEFINITION Sequence 19 from patent US 5451503.
 ACCESSION 114511
 VERSION 114511.1 GI:996994
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 56)
 AUTHORS Hogan,J.J., Arnold,L.J., Jr., Nelson,N.C. and Bezyerkov,R.
 TITLE Method for use of branched nucleic acid probes
 JOURNAL Patent: US 5451503-A 19 19-SEP-1995;
 FEATURES
 source 1..56
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 ORIGIN
 BASE COUNT 13 a 14 c 15 g 14 t

Query Match 63.0%; Score 17; DB 6; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTGAGCCTCA 17
 |||||
 Db 40 TCTGACTTGAGCCTCA 56

RESULT 12
 LOCUS A93190 68 bp DNA linear PAT 22-JAN-2000
 DEFINITION Sequence 13 from Patent WO9746672.
 ACCESSION A93190
 VERSION A93190.1 GI:6741575
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 68)
 AUTHORS Sczakiel,G. and Haas,R.
 TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
 JOURNAL Patent: WO 9746672-A 13 11-DEC-1997;
 DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)
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 /organism="unidentified"
 /db_xref="taxon:332644"
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 BASE COUNT 15 a 16 c 22 g 15 t

Query Match 63.0%; Score 17; DB 6; Length 68;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTGAGCCTCA 17
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 Db 17 TCTGACTTGAGCCTCA 1

RESULT 13
 SODTRLXS06 76 bp tRNA linear INV 04-NOV-1999
 LOCUS SODTRLXS06

DEFINITION Squid tRNA-Lys(UUU).
 ACCESSION D50539
 VERSION D50539.1 GI:1256933
 KEYWORDS tRNA-Lys.
 SOURCE Loligo bleekeri tRNA.
 ORGANISM Loligo bleekeri
 Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Teuthoidea;
 Myopoda; Loliginidae; Loligo.
 REFERENCE 1 (bases 1 to 76)
 AUTHORS Matsuo,M., Abe,Y., Saruta,Y. and Okada,N.
 TITLE Mollusk genes encoding lysine tRNA (UUU) contain introns
 JOURNAL Gene 165 (2), 249-253 (1995)
 MEDLINE 96096530
 REFERENCE 2 (bases 1 to 76)
 AUTHORS Matsuo,M.
 TITLE Direct Submission
 JOURNAL Submitted (11-MAY-1995) Mami Matsuo, Tokyo Institute of Technology,
 Faculty of Bioscience and Biotechnology; Nagatsuta 4259, Yokohama,
 Kanagawa 226, Japan (Tel:045-923-1136, Fax:045-923-1136)
 FEATURES
 source 1..76
 /organism="Loligo bleekeri"
 /db_xref="taxon:6617"
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 /product="tRNA-Lys"
 /note="codon recognized: AAA"
 /anticodon="(pos:34..36,aa:Lys)"
 10
 /mod_base=m2g
 16
 /mod_base=d
 27
 /mod_base=p
 34
 /note="unidentified modified nucleotide"
 37
 /mod_base=OTHER
 46
 /note="unidentified modified nucleotide"
 /mod_base=OTHER
 47
 /mod_base=m7g
 48
 /mod_base=d
 54
 /mod_base=m5c
 55
 /mod_base=tm
 58
 /mod_base=p
 67
 /mod_base=m1a
 72
 /mod_base=m2g
 /mod_base=m5c
 20 c 22 g 19 t 1 others

BASE COUNT 14 a 20 c 22 g 19 t 1 others
 ORIGIN

Query Match 63.0%; Score 17; DB 3; Length 76;
 Best Local Similarity 76.9%; Pred. No. 3.3e+03;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCTGACTTGAGCCGAGGCTGCTGAG 26
 |||||
 Db 27 TCAGACTTTTANCTGAGGCTCTGGG 52

RESULT 14
 SODTRLXS2 76 bp tRNA linear INV 04-NOV-1999
 LOCUS SODTRLXS2
 DEFINITION Loligo bleekeri tRNA-Lys.
 ACCESSION D45191
 VERSION D45191.1 GI:1065614

KEYWORDS tRNA-Lys.
SOURCE Loligo bleekeri tRNA.
ORGANISM Loligo bleekeri
Euprymota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Teuthoidea;
Mysidacea; Loliginidae; Loligo.
REFERENCE 1 (bases 1 to 76)
AUTHORS Matsuo, M., Yokogawa, T., Nishikawa, K., Watanabe, K. and Okada, N.
TITLE Highly specific and efficient cleavage of squid tRNA(Lys) catalyzed by magnesium ions
JOURNAL U. Biol. Chem. 270 (17), 10097-10104 (1995)
MEDLINE 95247717
REFERENCE 2 (bases 1 to 76)
AUTHORS Matsuo, M.
TITLE Direct Submission
JOURNAL Submitted (18-JAN-1995) Mami Matsuo, Tokyo Institute of Technology,
Faculty of Bioscience and Biotechnology; Nagatsuta 4259, Yokohama,
Kanagawa 226, Japan (Tel:045-923-1136, Fax:045-923-1136)
LOCATION/Qualifiers

FEATURES
source 1..76
/organism="Loligo bleekeri"
/db_xref="taxon:6617"
1..76
/product="tRNA-Lys"
/note="codon recognized: AAA"
/anticodon=(pos:34..36,aa:Lys)
10
modified_base /mod_base=m2g
16
modified_base /mod_base=d
27
modified_base /mod_base=p
34
modified_base /note="derivative of U"
37
modified_base /mod_base=OTHER
46
modified_base /note="derivative of A"
47
modified_base /mod_base=OTHER
48
modified_base /mod_base=m7g
47
modified_base /mod_base=d
48
modified_base /mod_base=m5c
54
modified_base /mod_base=tm
55
modified_base /mod_base=p
58
modified_base /mod_base=m1a
67
modified_base /mod_base=m2g
72
modified_base /mod_base=m5c
14 a 20 c 22 g 19 t 1 others
BASE COUNT
ORIGIN

Query Match 63.0%; Score 17; DB 3; Length 76;
Best Local Similarity 76.9%; Pred. No. 3.5e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGCTCTGAG 26
||| ||||| ||| ||||| |||
DB 27 TCAGACTTTTANCTGAGGCTCTGG 52

RESULT 15
LOCUS HSA16SN 71 bp mRNA linear PRI 07-MAY-1999
DEFINITION H.sapiens mRNA for U56 small nuclear RNA.
ACCESSION X96653
VERSION X96653.1 GI:1321840
KEYWORDS small nuclear RNA.
SOURCE Homo sapiens.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 71)
AUTHORS Kiss-Iaszio, Z., Henry, Y., Bachellet, J.P., Calzergues-Ferrer, M.
and Kiss, T.
TITLE Site-specific ribose methylation of preribosomal RNA: a novel
function for small nuclear RNAs
JOURNAL Cell 85 (7), 1077-1088 (1996)
MEDLINE 96270510
PUBMED 8674114
REFERENCE 2 (bases 1 to 71)
AUTHORS Kiss, T.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-1996) T. Kiss, Iab. Biol. Mol. Enc. du CNRS,
Universit Paul Sabatier, 118, route de Narbonne, 31062 Toulouse
Cedex, France
LOCATION/Qualifiers

FEATURES
source 1..71
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HeLa"
/note="C and D boxes"
1..71
/gene="U56 small nuclear RNA"
1..71
/gene="U56 small nuclear RNA"
18 a 14 c 18 g 21 t
BASE COUNT
ORIGIN

Query Match 62.2%; Score 16.8; DB 9; Length 71;
Best Local Similarity 90.0%; Pred. No. 4.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 8 TTGAGCTCTGAGGCTCTGACT 27
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DB 50 TTGAGCTCTGAGGCTCTGACT 69

Search completed: December 21, 2002, 12:57:42
Job time : 391.596 secs

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:43:17 : Search time 386.596 Seconds

(Without alignments)
2032.551 Million cell updates/sec

Title: US-09-121-239-23

Perfect score: 27

Sequence: 1 UCUGACUUUGAGCCUAGGUCUGAGU 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0
Maximum DB seq length: 100
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: gb_da:*
2: gb_hlg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_jnu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlg_mus:*
34: em_hlg_pln:*
35: em_hlg_rtd:*
36: em_hlg_mam:*
37: em_hlg_vrt:*
38: em_sy:*
39: em_hlg_hum:*
40: em_hlg_mus:*
41: em_hlg_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	96.3	80	6	158639
2	26	96.3	80	6	196201
3	22	81.5	22	6	AR086401
4	22	81.5	22	6	144731
5	22	81.5	22	6	192877
6	19	70.4	24	6	E16995
7	19	70.4	20	6	A93183
8	18	66.7	69	6	A93191
9	17	63.0	51	6	AX115325
10	17	63.0	56	6	112449
11	17	63.0	56	6	114511
12	17	63.0	68	6	A93190
13	17	63.0	76	3	SQPRRLYS06
14	17	63.0	76	3	SQPRRLYS2
15	16.8	62.2	71	9	HSR16SN
16	16.4	60.7	28	6	E26953
17	16	59.3	54	10	AF224105
18	16	59.3	75	9	F185592S11
19	16	59.3	75	9	123911
20	15.8	58.5	67	6	127229
21	15.6	57.8	29	6	A56950
22	15.2	56.3	51	6	AX204128
23	15.2	56.3	64	4	F292317S02
24	15.2	56.3	16	6	E13680
25	15.2	56.3	20	6	AR037942
26	15	55.6	40	6	AR037936
27	15	55.6	40	6	AR037937
28	15	55.6	66	6	A93188
29	15	55.6	24	6	AX443608
30	14.8	54.8	25	6	AX447590
31	14.8	54.8	64	6	AX436030
32	14.8	54.8	67	5	MSU09943
33	14.8	54.8	69	5	AX435963
34	14.8	54.8	69	6	AX435978
35	14.8	54.8	76	1	BSRNRK
36	14.8	54.8	76	6	AX435959
37	14.8	54.8	76	6	AX435999
38	14.8	54.8	76	6	AX436011
39	14.8	54.8	76	6	AX436029
40	14.8	54.8	76	6	AX439994
41	14.8	54.8	76	6	AX440034
42	14.8	54.8	76	6	AX440046
43	14.8	54.8	76	6	AX440062
44	14.8	54.8	76	6	AX440062
45	14.8	54.8	76	6	AX440062

ALIGNMENTS

RESULT 1
158639
LOCUS 158639
DEFINITION Sequence 7 from patent US 5652222.
ACCESSION 158639
VERSION 158639.1 GI:2477877
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 80)
AUTHORS Calabretta,B. and Gewirtz,A.M.
TITLE Selective inhibition of leukemic cell proliferation by bcr-abl antisense oligonucleotides
JOURNAL Patent: US 5652222-A 7 29-JUL-1997;

80 bp. DNA linear PAT 07-OCT-1997

FEATURES Location/Qualifiers
source 1..80
BASE COUNT 16 a 22 c 27 g 15 t
ORIGIN

Query Match 96.3%; Score 26; DB 6; Length 80;
Best Local Similarity 69.2%; Pred. No. 0.21;
Matches 18; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

OY 1 UCUAGCUUUGAGCCUCAGGUCUGAG 26
Db 55 TCTGACTTGGAGCCTCAGGCTCTGAG 80

RESULT 2
LOCUS 196201
DEFINITION Sequence 38 from patent US 5734039.
ACCESSION 196201
VERSION 196201.1 GI:3940671
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 80)
AUTHORS Calabretta, B. and Skorski, T.
TITLE Antisense oligonucleotides targeting cooperating oncogenes
JOURNAL Patent: US 5734039-A 38 31-MAR-1998;
FEATURES Location/Qualifiers
source 1..80
BASE COUNT 16 a 22 c 27 g 15 t
ORIGIN

Query Match 96.3%; Score 26; DB 6; Length 80;
Best Local Similarity 69.2%; Pred. No. 0.21;
Matches 18; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

OY 1 UCUAGCUUUGAGCCUCAGGUCUGAG 26
Db 55 TCTGACTTGGAGCCTCAGGCTCTGAG 80

RESULT 3
LOCUS AR086401/c
DEFINITION Sequence 1 from patent US 5985572.
ACCESSION AR086401
VERSION AR086401.1 GI:10013167
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Macfarlane, D.E.
TITLE Quaternary amine surfactant and methods of using same in isolation of RNA
JOURNAL Patent: US 5985572-A 1 16-NOV-1999;
FEATURES Location/Qualifiers
source 1..22
BASE COUNT 6 a 7 c 5 g 4 t
ORIGIN

Query Match 81.5%; Score 22; DB 6; Length 22;
Best Local Similarity 72.7%; Pred. No. 17;
Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACUUGAGCCUCAGGUCUGA 25
Db 22 GACTTGGAGCCTCAGGCTCTGA 1

RESULT 4
LOCUS I44731/c
DEFINITION Sequence 10 from patent US 5635385.
ACCESSION I44731
VERSION I44731.1 GI:2469444
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 22)
AUTHORS Leopold, L.H., Shore, S.K., Reddy, M.V.R. and Reddy, E. Premkumar.
TITLE Multi-unit ribozyme inhibition of oncogene gene expression
JOURNAL Patent: US 5635385-A 10 03-JUN-1997;
FEATURES Location/Qualifiers
source 1..22
BASE COUNT 6 a 7 c 5 g 4 t
ORIGIN

Query Match 81.5%; Score 22; DB 6; Length 22;
Best Local Similarity 72.7%; Pred. No. 17;
Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACUUGAGCCUCAGGUCUGA 25
Db 22 GACTTGGAGCCTCAGGCTCTGA 1

RESULT 5
LOCUS I92877/c
DEFINITION Sequence 1 from patent US 5728822.
ACCESSION I92877
VERSION I92877.1 GI:3937347
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 22)
AUTHORS Macfarlane, D.E.
TITLE Quaternary amine surfactants and methods of using same in isolation of RNA
JOURNAL Patent: US 5728822-A 1 17-MAR-1998;
FEATURES Location/Qualifiers
source 1..22
BASE COUNT 6 a 7 c 5 g 4 t
ORIGIN

Query Match 81.5%; Score 22; DB 6; Length 22;
Best Local Similarity 72.7%; Pred. No. 17;
Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACUUGAGCCUCAGGUCUGA 25
Db 22 GACTTGGAGCCTCAGGCTCTGA 1

RESULT 6
LOCUS E16995
DEFINITION Primer.
ACCESSION E16995
VERSION E16995.1 GI:5711678
KEYWORDS JP 1998229899-A/10.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Kobayashi, M., Kawaguchi, R., Segawa, M. and Takarada, Y.
TITLE PRIMER FOR DETECTING BCR/ABL TYPE CHIMERA MESSENGER RNA, AND

JOURNAL
DETECTION OF BCR/ABL TYPE CHIMERA MESSENGER RNA AND USING THE SAME
Patent: JP 1998229899-A 10 02-SEP-1998;
S R I:KK, TOYOBO CO LTD

COMMENT

OS None
OC Artificial sequences.
PN JP 1998229899-A/10
PD 02-SEP-1998
PE 21-FEB-1997 JP 1997054092
PI KOBAYASHI MASARU, KAWACUCHI RYUJI, SEGAWA MASAYA, PI
TAKARADA YUTAKA
PC C1201/68, G01N33/50//C12N15/09;
CC strandedness: Single;
FH topology: Linear;
FH key Location/Qualifiers
FT source 1..24
Location/Qualifiers
1..24
/organism="unidentified"
/db_xref="taxon:32644"

FEATURES

BASE COUNT 5 a 6 c 6 g 7 t
ORIGIN

Query Match 70.4%; Score 19; DB 6; Length 24;
Best Local Similarity 68.4%; Pred. No. 4.2e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1 UCUGACUUUGAGCCUCAGG 19
Db 6 TCTGACTTTCAGCCTCAGG 24

RESULT 7
A93183/C A93183 70 bp DNA linear PAT 22-JAN-2000
LOCUS Sequence 6 from Patent WO974672.
DEFINITION A93183
ACCESSION A93183 GI:6741568
VERSION
KEYWORDS
SOURCE
ORGANISM
unclassified.
unclassified.
unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 70)
TITLE Sczakiel, G. and Haas, R.
JOURNAL ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)
location/Qualifiers
1..70
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 15 a 18 c 22 g 15 t
ORIGIN

Query Match 70.4%; Score 19; DB 6; Length 70;
Best Local Similarity 68.4%; Pred. No. 4.1e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1 UCUGACUUUGAGCCUCAGG 19
Db 19 TCTGACTTTCAGCCTCAGG 1

RESULT 8
A93191/C A93191 69 bp DNA linear PAT 22-JAN-2000
LOCUS Sequence 14 from Patent WO974672.
DEFINITION A93191
ACCESSION A93191 GI:6741576
VERSION
KEYWORDS
SOURCE
ORGANISM
unclassified.
unclassified.

unclassified.
1 (bases 1 to 69)
AUTHORS Sczakiel, G. and Haas, R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL
PATENT: WO 9746672-A 14 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)
location/Qualifiers
1..69
/organism="unidentified"
/db_xref="taxon:32644"

FEATURES

BASE COUNT 15 a 17 c 22 g 15 t
ORIGIN

Query Match 66.7%; Score 18; DB 6; Length 69;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1 UCUGACUUUGAGCCUCAGG 18
Db 18 TCTGACTTTCAGCCTCAGG 1

RESULT 9
AX115325 AX115325 51 bp DNA linear PAT 11-MAY-2001
LOCUS Sequence 448 from Patent WO0129262.
DEFINITION AX115325
ACCESSION AX115325 GI:14032267
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 51)
TITLE Picoult-Newburg, L. and Pohl, M.
JOURNAL Genotyping reagents, kits and methods of use thereof
PATENT: WO 0129262-A 448 26-APR-2001;
Orchid Biosciences, Inc. (US)
location/Qualifiers
1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 6 a 5 c 21 g 19 t
ORIGIN

Query Match 63.0%; Score 17; DB 6; Length 51;
Best Local Similarity 48.0%; Pred. No. 3.6e+03;
Matches 12; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

OY 3 UCUGACUUUGAGCCUCAGGUCUGAGU 27
Db 11 TGACTTTCAGGTCAGGTCGTGTGTGT 35

RESULT 10
112449 112449 56 bp DNA linear PAT 26-JUL-1995
LOCUS Sequence 19 from patent US 5424413.
DEFINITION 112449
ACCESSION 112449 GI:909833
VERSION
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 56)
Hogan, J.J., Arnold, L.J. Jr., Nelson, N.C. and Beazekov, R.
Branched nucleic acid probes
PATENT: US 5424413-A 19 13-JUN-1995;
location/Qualifiers
1..56
/organism="unknown"

BASE COUNT 13 a 14 c 15 g 14 t
ORIGIN

Query Match 63.0%; Score 17; DB 6; Length 56;
 Best Local Similarity 64.7%; Pred. No. 3.6e+03;
 Matches 11; Conservative 6; Mismatches 0; Indels 0;

QY 1 UCUGACUUUGAGCCUCA 17
 :|||||:|||||:|
 Db 40 TCTGACTTTGAGCCTCA 56

RESULT 11

LOCUS 114511 56 bp DNA linear PAT 26-SEP-1995
 DEFINITION Sequence 19 from patent US 5451503.
 ACCESSION 114511
 VERSION 114511.1 GI:996994
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 56)
 AUTHORS Hogan, J.J., Arnold, L.J., Jr., Nelson, N.C. and Bezverkov, R.
 TITLE Method for use of branched nucleic acid probes
 JOURNAL Patent: US 5451503-A 19 19-SEP-1995;
 FEATURES Location/Qualifiers
 source 1..56
 /organism="unknown"

BASE COUNT 13 a 14 c 15 g 14 t
 ORIGIN

Query Match 63.0%; Score 17; DB 6; Length 56;
 Best Local Similarity 64.7%; Pred. No. 3.6e+03;
 Matches 11; Conservative 6; Mismatches 0; Indels 0;

QY 1 UCUGACUUUGAGCCUCA 17
 :|||||:|||||:|
 Db 40 TCTGACTTTGAGCCTCA 56

RESULT 12

LOCUS A93190 68 bp DNA linear PAT 22-JAN-2000
 DEFINITION Sequence 13 from Patent WO9746672.
 ACCESSION A93190
 VERSION A93190.1 GI:6741575
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 68)
 AUTHORS Sczakiel, G. and Haas, R.
 TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
 JOURNAL Patent: WO 9746672-A 13 11-DEC-1997;
 DEUTSCHES KREBSFORSCH (DE); SZAKIEL GEORG (DE)
 FEATURES Location/Qualifiers
 source 1..68
 /organism="unidentified"
 /db_xref="taxon:32644"

BASE COUNT 15 a 16 c 22 g 15 t
 ORIGIN

Query Match 63.0%; Score 17; DB 6; Length 68;
 Best Local Similarity 64.7%; Pred. No. 3.5e+03;
 Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCA 17
 :|||||:|||||:|
 Db 17 TCTGACTTTGAGCCTCA 1

RESULT 13 76 bp tRNA linear INV 04-NOV-1999
 LOCUS SODTRLYS06
 SODTRLYS06

DEFINITION Squid tRNA-Lys(UUU).
 ACCESSION D50539
 VERSION D50539.1 GI:1256933
 KEYWORDS tRNA-Lys.
 SOURCE Loligo bleekeri tRNA.
 ORGANISM Loligo bleekeri
 Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Teuthoidea;
 Myopsida; Loliginidae; Loligo.

REFERENCE 1 (bases 1 to 76)
 AUTHORS Matsuo, M., Abe, Y., Saruta, Y. and Okada, N.
 TITLE Mollusk genes encoding lysine tRNA (UUU) contain introns
 JOURNAL Gene 165 (2), 249-253 (1995)
 MEDLINE 96096530
 REFERENCE 2 (bases 1 to 76)
 AUTHORS Matsuo, M.
 TITLE Direct Submission
 JOURNAL Submitted (11-MAY-1995) Mami Matsuo, Tokyo Institute of Technology,
 Faculty of Bioscience and Biotechnology, Nagatsuta 4259, Yokohama,
 Kanagawa 226, Japan (Tel:045-923-1136, Fax:045-923-1136)

FEATURES

source

tRNA

modified_base 1..76
 /organism="Loligo bleekeri"
 /db_xref="taxon:6617"
 1..76
 /product="tRNA-Lys"
 /note="codon recognized: AAA"
 /anticodon="(pos:34..36,aa:Lys)"
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 /mod_base=m2g
 16
 /mod_base=d
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 /mod_base=p
 34
 /note="unidentified modified nucleotide"
 /mod_base=OTHER
 37
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 46
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 /mod_base=d
 48
 /mod_base=m5c
 54
 /mod_base=tm
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 /mod_base=p
 58
 /mod_base=m1a
 67
 /mod_base=m2g
 72
 /mod_base=m5c
 20 c 22 g 19 t 1 others
 BASE COUNT 14 a 20 c 22 g 19 t 1 others
 ORIGIN

Query Match 63.0%; Score 17; DB 3; Length 76;
 Best Local Similarity 50.0%; Pred. No. 3.5e+03;
 Matches 13; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUGAG 26
 :|||||:|||||:|
 Db 27 TCAGACTTTTANCTGAGGCTGCGG 52

RESULT 14 76 bp tRNA linear INV 04-NOV-1999
 LOCUS SODTRLYS2
 SODTRLYS2
 DEFINITION Loligo bleekeri tRNA-Lys.
 ACCESSION D45191
 VERSION D45191.1 GI:1065614

KEYWORDS trna-lys.
SOURCE Loligo bleekeri trna.
ORGANISM Loligo bleekeri
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Teuthoidea;
Mysopoda; Loliginidae; Loligo.
REFERENCE Matsuo, M., Yokogawa, T., Nishikawa, K., Watanabe, K. and Okada, N.
AUTHORS 1 (bases 1 to 76)
TITLE Highly specific and efficient cleavage of squid trna(lys) catalyzed
by magnesium ions
JOURNAL J. Biol. Chem. 270 (17), 10097-10104 (1995)
MEDLINE 95247717
REFERENCE 2 (bases 1 to 76)
AUTHORS Matsuo, M.
TITLE Direct Submission
JOURNAL Submitted (18-JAN-1995) Mami Matsuo, Tokyo Institute of Technology,
Faculty of Bioscience and Biotechnology; Nagatsuta 4259, Yokohama,
Kanagawa 226, Japan (Tel:045-923-1136, Fax:045-923-1136)
LOCATION/Qualifiers
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Best Local Similarity 50.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
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RESULT 15
LOCUS HSA16SN 71 bp mRNA linear PRI 07-MAY-1999
DEFINITION H.sapiens mRNA for U56 small nuclear RNA.
ACCESSION X96655
VERSION X96655.1 GI:1321840
KEYWORDS small nuclear RNA.
SOURCE Homo sapiens.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Kiss, T., Bachelier, J.P., Calzergues-Ferrer, M.
AUTHORS 1 (bases 1 to 71)
TITLE Site-specific ribose methylation of preribosomal RNA: a novel
function for small nuclear RNAs
JOURNAL Cell 85 (7), 1077-1088 (1996)
MEDLINE 8674114
REFERENCE 2 (bases 1 to 71)
AUTHORS Kiss, T.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-1996) T. Kiss, Lab. Biol. Mol. Euc. du CNRS,
Universit Paul Sabatier, 118, route de Narbonne, 31062 Toulouse
Cedex, France
LOCATION/Qualifiers
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snRNA /gene="U56 small nuclear RNA"
BASE COUNT 18 a 14 c 18 g 21 t
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QY 8 UUGAGCCUCAGGUCUCAGU 27
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Db 50 TTGAGACTCTGCTGTGAGT 69

Search completed: December 21, 2002, 12:57:43
Job time : 387.596 secs

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

Title:	US-09-121-239-27
Perfect score:	26
Sequence:	1 CACTCAGCCACTGGATTTTAACGAG 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum	DB	seq	length:	0
Maximum	DB	seq	length:	100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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1:  gb_ba:*
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C 2	26	100.0	53	6	A93224 Sequence 47
C 3	26	100.0	54	6	A93225 Sequence 48
C 4	26	100.0	55	6	A93227 Sequence 50
C 5	26	100.0	56	6	A93228 Sequence 51
C 6	26	100.0	56	6	112446 Sequence 16
C 7	26	100.0	56	6	114508 Sequence 16
C 8	26	100.0	57	6	A93229 Sequence 52
C 9	26	100.0	57	6	A93230 Sequence 53
C 10	26	100.0	59	6	A93231 Sequence 54
C 11	26	100.0	90	9	HMMCRAT: AR1553123 Sequence
C 12	25	98.2	40	6	AR1553123 Sequence
C 13	25	98.2	58	6	BD0017111 Method fo
C 14	25	98.2	58	6	BD0017124 Method fo
C 15	25	96.2	59	6	BD0017120 Compositi
C 16	25	96.2	59	6	BD0017123 Method fo
C 17	25	96.2	60	6	A50294 Sequence 14
C 18	25	96.2	60	6	A50294 Sequence 14
C 19	25	96.2	66	6	112443 Sequence 13
C 20	25	96.2	66	6	114505 Sequence 13
C 21	21	82.3	40	6	AR037937 Sequence
C 22	21	80.8	44	6	AX280264 Sequence
C 23	20	76.9	44	6	AX280265 Sequence
C 24	20	76.9	47	6	AX280256 Sequence
C 25	20	76.9	47	6	AX280259 Sequence
C 26	19.4	74.6	91	6	AX280254 Sequence
C 27	19	73.1	41	6	AX280255 Sequence
C 28	19	73.1	41	6	AX280258 Sequence
C 29	18	69.2	18	6	AR037939 Sequence
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C 31	17.2	66.2	68	10	RR4240056 Rattus no
C 32	16.4	63.1	31	6	AX249334 Sequence
C 33	16	61.5	30	6	BD000491 Process f
C 34	16	61.5	50	6	AX199556 Sequence
C 35	16	61.5	50	6	AX199558 Sequence
C 36	16	61.5	51	6	AX199558 Sequence
C 37	16	61.5	51	6	AX8299 Sequence 33
C 38	16	61.5	88	6	AR193111 Sequence
C 39	15.8	60.8	88	6	AR193112 Sequence
C 40	15.8	60.8	21	6	AX092761 Sequence
C 41	15	57.7	21	6	AX059827 Sequence
C 42	15	57.7	22	6	AR153125 Sequence
C 43	15	57.7	22	6	AR153125 Sequence
C 44	15	57.7	22	6	AR163303 Sequence
C 45	14.8	56.9	18	6	AR163304 Sequence
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 43 CACTCAGCCACTGGATTAAACAGAG 18

RESULT 2
LOCUS A93224/c 53 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 47 from Patent WO9746672.
ACCESSION A93224
VERSION A93224.1 GI:6741609
KEYWORDS
SOURCE unclassified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 53)
AUTHORS Sczakiel,G. and Haas,R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL Patent: WO 9746672-A 47 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)

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Db 43 CACTCAGCCACTGGATTAAACAGAG 18

RESULT 3
LOCUS A93225/c 54 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 48 from Patent WO9746672.
ACCESSION A93225
VERSION A93225.1 GI:6741610
KEYWORDS
SOURCE unclassified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 54)
AUTHORS Sczakiel,G. and Haas,R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL Patent: WO 9746672-A 48 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)

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RESULT 4
LOCUS A93227/c 55 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 50 from Patent WO9746672.
ACCESSION A93227
VERSION A93227.1 GI:6741612
KEYWORDS
SOURCE unclassified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 55)
AUTHORS Sczakiel,G. and Haas,R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL Patent: WO 9746672-A 50 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)

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RESULT 5
LOCUS A93228 56 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 51 from Patent WO9746672.
ACCESSION A93228
VERSION A93228.1 GI:6741613
KEYWORDS
SOURCE unclassified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 56)
AUTHORS Sczakiel,G. and Haas,R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL Patent: WO 9746672-A 51 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)

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Db 43 CACTCAGCCACTGGATTAAACAGAG 18

RESULT 6
LOCUS 112446 56 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 16 from patent US 5424413.
ACCESSION 112446
VERSION 112446.1 GI:909830

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
1 (bases 1 to 56)
AUTHORS Hogan, J.J., Arnold, L.J., Jr., Nelson, N.C., and Bezerkov, R.
TITLE Branched nucleic acid probes
JOURNAL Patent: US 5424413-A 16 13-JUN-1995;
Location/Qualifiers

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BASE COUNT 16 a 17 c 9 g 14 t

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Query Match 100.0%; Score 26; DB 6; Length 56;
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAACAGAG 26
Db 10 CACTCAGCCACTGGATTAAACAGAG 35

RESULT 7
LOCUS 114508 56 bp DNA linear PAT 26-SEP-1995
DEFINITION Sequence 16 from patent US 5451503.
ACCESSION 114508
VERSION 114508.1 GI:996991
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
1 (bases 1 to 56)
AUTHORS Hogan, J.J., Arnold, L.J., Jr., Nelson, N.C., and Bezerkov, R.
TITLE Method for use of branched nucleic acid probes
JOURNAL Patent: US 5451503-A 16 19-SEP-1995;
Location/Qualifiers

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/organism="unknown"

BASE COUNT 16 a 17 c 9 g 14 t

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Query Match 100.0%; Score 26; DB 6; Length 56;
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DEFINITION Sequence 52 from Patent WO9746672.
ACCESSION A93229
VERSION A93229.1 GI:6741614
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE
1 (bases 1 to 57)
AUTHORS Sczakiel, G. and Haas, R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL Patent: WO 9746672-A 52 11-DEC-1997;
DEUTSCHES KREISFORSCH (DE); SCZAKIEL GEORG (DE)
Location/Qualifiers

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BASE COUNT 14 a 11 c 16 g 16 t

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Db 43 CACTCAGCCACTGGATTAAACAGAG 18

RESULT 9
LOCUS A93230 58 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 53 from Patent WO9746672.
ACCESSION A93230
VERSION A93230.1 GI:6741615
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE
1 (bases 1 to 58)
AUTHORS Sczakiel, G. and Haas, R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL Patent: WO 9746672-A 53 11-DEC-1997;
DEUTSCHES KREISFORSCH (DE); SCZAKIEL GEORG (DE)
Location/Qualifiers

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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 43 CACTCAGCCACTGGATTAAACAGAG 18

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LOCUS A93231 59 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 54 from Patent WO9746672.
ACCESSION A93231
VERSION A93231.1 GI:6741616
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE
1 (bases 1 to 59)
AUTHORS Sczakiel, G. and Haas, R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL Patent: WO 9746672-A 54 11-DEC-1997;
DEUTSCHES KREISFORSCH (DE); SCZAKIEL GEORG (DE)
Location/Qualifiers

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BASE COUNT 15 a 11 c 17 g 16 t

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Db 43 CACTCAGCCACTGGATTAAACAGAG 18

RESULT 11

HUMBCRA1
LOCUS HUMBCRA1 90 bp DNA linear PRI 27-APR-1993
DEFINITION Human chronic myelocytic leukemia c-abl oncogene breakpoint cluster
region (bcr) DNA, exon b3.
ACCESSION M25947
VERSION M25947.1 GI:1179381
KEYWORDS breakpoint cluster region; c-abl oncogene; chronic myelocytic
leukemia.
SEGMENT 1 of 3
SOURCE Human fibroblast cell line K562, cDNA to mRNA, clone pV1-3.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 90)
AUTHORS De Klein, A., Hermans, A., Bootsma, D., Grosveld, G., Heisterkamp, N.,
Stam, K. and Groffen, J.
TITLE The role of the Philadelphia translocation in chronic myelocytic
leukemia
JOURNAL Ann. Clin. Res. 18 (5-6), 278-283 (1986)
MEDLINE 87183193
PUBMED 3471171
FEATURES
SOURCE Location/Qualifiers
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OY 1 CACTGACCCACTGGATTAAACGAG 26
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Db 45 CACTGACCCACTGGATTAAACGAG 70
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AR153123/c 40 bp DNA linear PAT 08-AUG-2001
LOCUS AR153123
DEFINITION Sequence 125 from patent US 6235480.
ACCESSION AR153123
VERSION AR153123.1 GI:15120655
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 40)
AUTHORS Shultz, J. William., Lewis, M. K., Leippe, D., Mandrekar, M., Kephart, D.,
Rhodes, R. Byron., Andrews, C. Ann., Hartnett, J. Robert., Gu, T.,
Olson, R. J., Wood, K. V. and Welch, R.
TITLE Detection of nucleic acid hybrids
JOURNAL Patent: US 6235480-A 125 22-MAY-2001;
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source Location/Qualifiers
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AR153124/c 41 bp DNA linear PAT 08-AUG-2001
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DEFINITION Sequence 126 from patent US 6235480.
ACCESSION AR153124
VERSION AR153124.1 GI:15120656
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 41)
AUTHORS Shultz, J. William., Lewis, M. K., Leippe, D., Mandrekar, M., Kephart, D.,
Rhodes, R. Byron., Andrews, C. Ann., Hartnett, J. Robert., Gu, T.,
Olson, R. J., Wood, K. V. and Welch, R.
TITLE Detection of nucleic acid hybrids
JOURNAL Patent: US 6235480-A 126 22-MAY-2001;
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source Location/Qualifiers
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 41 ACTGAGCCACTGGATTAAACGAG 17
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BD001711 58 bp DNA linear PAT 31-JAN-2002
LOCUS BD001711
DEFINITION Compositions for homogeneous protection assay.
ACCESSION BD001711
VERSION BD001711.1 GI:18626270
KEYWORDS JP 2000350598-A/13.
SOURCE JP 2000350598-A/13.
ORGANISM
REFERENCE 1 (bases 1 to 58)
AUTHORS J. R. J. A. and Nelson, N. C.
TITLE Compositions for homogeneous protection assay
JOURNAL Patent: JP 2000350598-A 13 19-DEC-2000;
COMMENT GEN PROBE INC
OS Artificial sequence
PN JP 2000350598-A/13
PD 19-DEC-2000
PE 02-MAY-2000 JP 2000133493
PR 21-SEP-1987 US 099.392
PI RYLE JOHN ARNOLD JR, NORMAN C NELSON
PC C12Q1/68, C12N15/09, C12Q1/66, G01N31/78, G01N33/53, G01N33/58, PC
C12N15/00
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RESULT 15
BD001724

Mon Dec 23 08:48:03 2002

us-09-121-239-27.rge

Page 5

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DEFINITION	BD001724	Method for homogeneous protection assay.				
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KEYWORDS	JP 2000350599-A/13.					
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ORGANISM	artificial construct.					
REFERENCE	1 (bases 1 to 58)					
AUTHORS	Jr, R.J.A. and Nelson,N.C.					
TITLE	Method for homogeneous protection assay					
JOURNAL	Patent: JP 2000350599-A 13 19-DEC-2000;					
COMMENT	GEM PROBE INC					
CS	Artificial Sequence					
FN	JP 2000350599-A/13					
PD	19-DEC-2000 JP 2000133506					
PF	12-MAR-1987 US 5,099,392					
PR	21-SEP-1987 US 5,099,392					
PI	RYLEIGH ARNOLD JR NORMAN C NELSON					
PC	C12Q1/68;C12N15/09;C12Q1/66;G01N21/78;G01N33/53;G01N33/58, PC					
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Matches	25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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DB	1 ACTCAGCGACTGGATTAAACAAGAG 25					

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 02:43:17 : Search time 257.731 Seconds
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Title: US-09-121-239-26
Perfect score: 18
Sequence: 1 GCAATCATCGAGCATCG 18

Scoring table: IDENTITY_NDC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: gb_in:*

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14: gb_vi:*

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17: em_hum:*

18: em_in:*

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21: em_or:*

22: em_ov:*

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25: em_pl:*

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28: em_un:*

29: em_vi:*

30: em_hcg_hum:*

31: em_hcg_inv:*

32: em_hcg_mus:*

33: em_hcg_pin:*

34: em_hcg_rod:*

35: em_hcg_mam:*

36: em_hcg_vrt:*

37: em_sy:*

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39: em_hcg_mus:*

40: em_hcg_hum:*

41: em_hcg_other:*

pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	13.8	76.7	37	6	158617	158617 Sequence 3
3	13.8	76.7	37	6	163515	163515 Sequence 3
4	13.8	76.7	37	6	AR174784	AR174784 Sequence
5	13.4	74.4	50	6	AX162242	AX162242 Sequence
6	13.2	73.3	54	5	CHKIGHABD	M30369 Gallus gall
7	13.2	73.3	55	5	CHKIGHVAL	M30354 Gallus gall
8	13.2	73.3	57	5	CHKIGHVAL	M30351 Gallus gall
9	13.2	73.3	63	5	CHKIGHVAL	M30352 Gallus gall
10	13.2	73.3	66	5	CHKIGHABH	M30357 Gallus gall
11	13.2	73.3	69	5	CHKIGHABH	M30356 Gallus gall
12	13.2	73.3	69	5	CHKIGHABH	M30356 Gallus gall
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15	13.2	73.3	69	5	CHKIGHABH	M30356 Gallus gall
16	13.2	73.3	72	5	CHKIGHABH	M30356 Gallus gall
17	13.2	73.3	72	5	CHKIGHABH	M30356 Gallus gall
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20	12.8	71.1	20	6	AR031291	AR031291 Sequence
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22	12.8	71.1	20	6	AR102189	AR102189 Sequence
23	12.8	71.1	20	6	AR102200	AR102200 Sequence
24	12.8	71.1	20	6	AR106655	AR106655 Sequence
25	12.8	71.1	20	6	AR137590	AR137590 Sequence
26	12.8	71.1	20	6	AR154582	AR154582 Sequence
27	12.8	71.1	20	6	AR179852	AR179852 Sequence
28	12.8	71.1	20	6	164537	164537 Sequence 13
29	12.8	71.1	23	6	AR008076	AR008076 Sequence
30	12.8	71.1	23	6	AR031292	AR031292 Sequence
31	12.8	71.1	23	6	AR087477	AR087477 Sequence
32	12.8	71.1	23	6	AR102190	AR102190 Sequence
33	12.8	71.1	23	6	AR102201	AR102201 Sequence
34	12.8	71.1	23	6	AR110666	AR110666 Sequence
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36	12.8	71.1	23	6	AR154583	AR154583 Sequence
37	12.8	71.1	23	6	AR179853	AR179853 Sequence
38	12.8	71.1	23	6	164538	164538 Sequence 14
39	12.4	68.9	21	6	AX296863	AX296863 Sequence
40	12.4	68.9	21	6	AR1364	AR1364 Sequence 9
41	12.4	68.9	21	6	AX001584	AX001584 Sequence
C 42	12.4	68.9	24	6	AX292230	AX292230 Sequence
C 43	12.2	67.8	23	6	AX317694	AX317694 Sequence
C 44	12.2	67.8	23	6	AX402944	AX402944 Sequence
C 45	12.2	67.8	24	6	AR210302	AR210302 Sequence

ALIGNMENTS

RESULT 1	99 bp	uRNA	linear	INV 24-NOV-1992
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LOCUS	TTSNRNA			
DEFINITION	T.thermophila snRNA.			
ACCESSION	X65863			
VERSION	X65863.1 GI:10842			
KEYWORDS	small nuclear RNA.			
SOURCE	Tetrahymena thermophila.			
ORGANISM	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;			
REFERENCE	Hymenostomatida; Tetrahymena; Tetrahymena.			
AUTHORS	I (bases 1 to 99)			
TITLE	Engberg, J.			
JOURNAL	Submitted (27-APR-1992) J. Engberg, The Royal Danish School of			

Pharmacy, Dept of Biological Sciences, 2 Universitetsparken, 2100
Copenhagen, DENMARK

REFERENCE 2 (bases 1 to 99)
AUTHORS Orum, H., Nielsen, H. and Engberg, J.
TITLE Sequence of a new snRNA from the ciliate *Tetrahymena thermophila*
JOURNAL Nucleic Acids Res. 20 (13), 3518 (1992)
MEDLINE 9235014
PUBMED 1630929

FEATURES
SOURCE Location/Qualifiers
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/organism="Tetrahymena thermophila"
/strain="B186VIT"
/db_xref="taxon:5911"

snRNA 32 a 22 c 19 g 25 t 1 others
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ORIGIN

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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGCATGG 18
Db 82 GGAATCATCGAGCATGG 65

RESULT 2
LOCUS 158617 158617 37 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 3 from patent US 5652210.
ACCESSION 158617
VERSION 158617.1 GI:2477855
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 37)
AUTHORS Barr, P.J., Shapiro, J.P. and Kiefer, M.C.
TITLE Soluble splice variant of the Fas (Apo-1) antigen, Fas. DELTA. TM
JOURNAL Patent: US 5652210-A 3 29-JUL-1997;
FEATURES Location/Qualifiers
1..37
/organism="unknown"

BASE COUNT 12 a 8 c 8 g 9 t

Query Match 76.7%; Score 13.8; DB 6; Length 37;
Best Local Similarity 88.2%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGCATG 17
Db 14 GGAATCATCGAGCATG 30

RESULT 3
LOCUS 163515 163515 37 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 3 from patent US 5663070.
ACCESSION 163515
VERSION 163515.1 GI:2481088
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 37)
AUTHORS Barr, P.J., Shapiro, J.P. and Kiefer, M.C.
TITLE Recombinant production of a soluble splice variant of the Fas (Apo-1) antigen, fas TM
JOURNAL Patent: US 5663070-A 3 02-SEP-1997;
FEATURES Location/Qualifiers
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/organism="unknown"

BASE COUNT 12 a 8 c 8 g 9 t

Query Match 76.7%; Score 13.8; DB 6; Length 37;
Best Local Similarity 88.2%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGCATG 17
Db 14 GGAATCATCGAGCATG 30

RESULT 4
LOCUS AR174784 AR174784 73 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 36 from patent US 6307037.
ACCESSION AR174784
VERSION AR174784.1 GI:17915104
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 73)
AUTHORS Gaffney, T. Deane, J., Flavler, A., Cloyd Kirksey, M.M., Philippsen, P., Dietrich, F., Wendland, J., Bernasconi, P., White, K. and Filipowicz, W.
TITLE Fungal target genes and methods
JOURNAL Patent: US 6307037-A 36 23-OCT-2001;
FEATURES Location/Qualifiers
1..73
/organism="unknown"

BASE COUNT 23 a 16 c 17 g 17 t

Query Match 76.7%; Score 13.8; DB 6; Length 73;
Best Local Similarity 88.2%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGCATG 17
Db 44 GGAATCATCGAGCATG 60

RESULT 5
LOCUS AX162242 AX162242 50 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 5570 from Patent WO0140521.
ACCESSION AX162242
VERSION AX162242.1 GI:14543573
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 50)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 5570 07-JUN-2001;
FEATURES Curagen Corporation (US)
Location/Qualifiers
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"

misc.feature 25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number c94400660"

misc.feature

BASE COUNT 13 a 14 c 13 g 10 t
/note="2 of 2 allelic variants (5569 is other entry)"

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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 ATCATCGAGCATGG 18
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Db 17 ATCATCGAGCATGG 31

RESULT 6
CHRGVHAAO 54 bp mRNA linear VRT 12-OCT-1994
LOCUS Gallus gallus (clone 3W-101) Ig rearranged heavy chain D region
DEFINITION mRNA, partial cds.
ACCESSION M30369
VERSION M30369.1 GI:557505
KEYWORDS Ig heavy chain; Igm; diversity region; immunoglobulin;
SOURCE immunoglobulin heavy chain; mu-immunoglobulin; processed gene;
Gallus gallus (strain CB inbred line) 21 day old neonate cDNA to
mRNA.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 54)
AUTHORS Reynaud,C.A., Dahan,A., Anguez,V. and Weill,J.C.
TITLE Somatic hyperconversion diversifies the single Vh gene of the
JOURNAL chicken with a high incidence in the D region
MEDLINE Cell 59 (1), 171-183 (1989)
PUBMED 90003227
FEATURES
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                    /strain="CB inbred line"
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                    /clone="3W-101"
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                    /dev_stage="21 day old neonate"
                    <1..>54
BASE COUNT 9 a 10 c 20 g 15 t
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Best Local Similarity 83.3%; Pred. No. 2.4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGATTCATCGAGCATGG 18
    |||||||
Db 37 GGTAGCATCGAGCATGG 54

RESULT 7
CHRGVHAAO 55 bp mRNA linear VRT 12-OCT-1994
LOCUS Gallus gallus (clone 18D-5) Ig rearranged heavy chain D region
DEFINITION mRNA, partial.
ACCESSION M30354
VERSION M30354.1 GI:557529
KEYWORDS Ig heavy chain; Ig variable region; Igm; diversity region;
immunoglobulin; immunoglobulin heavy chain; mu-immunoglobulin;
processed gene; rearranged.
SOURCE Gallus gallus (strain CB inbred line) 18 day old embryo cDNA to
mRNA.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 55)
AUTHORS Reynaud,C.A., Dahan,A., Anguez,V. and Weill,J.C.
TITLE Somatic hyperconversion diversifies the single Vh gene of the
JOURNAL chicken with a high incidence in the D region
MEDLINE Cell 59 (1), 171-183 (1989)
PUBMED 90003227
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                    <1..>57
BASE COUNT 10 a 11 c 21 g 15 t
D.segment
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Query Match 73.3%; Score 13.2; DB 5; Length 57;
Best Local Similarity 83.3%; Pred. No. 2.4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGATTCATCGAGCATGG 18
    |||||||
Db 40 GGTAGCATCGAGCATGG 57

RESULT 9
CHRGVHAAO 63 bp mRNA linear VRT 12-OCT-1994
LOCUS Gallus gallus (clone 18D-2) Ig rearranged heavy chain D region
DEFINITION mRNA, partial.
ACCESSION M30352
VERSION M30352.1 GI:557527
KEYWORDS Ig heavy chain; Ig variable region; Igm; diversity region;

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FEATURES
source
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BASE COUNT
ORIGIN

Query Match
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGCGATCG 18
||| ||||| |||||
Db 52 GGTACATCGACGCGATCG 69

RESULT 13
CHRGHAB
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
FEATURES
source

CHRGHAB
Gallus gallus (clone 3W-1) Ig Rearranged heavy chain D region mRNA,
partial cds.
M30358.1 GI:557494
Ig heavy chain; IGM; diversity region; immunoglobulin;
immunoglobulin heavy chain; mu-immunoglobulin; processed gene.
Gallus gallus (strain CB Inbred line) 21 day old neonate cDNA to
mRNA.
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 69)
Reynaud C.A., Dahan A., Anguez V. and Weill J.C.
Somatic hyperconversion diversifies the single Vh gene of the
chicken with a high incidence in the D region
Cell 59 (1), 171-183 (1989)
90003227
2507167
Location/Qualifiers
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BASE COUNT
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Query Match
Best Local Similarity 73.3%; Score 13.2; DB 5; Length 69;
Pred. No. 2.3e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGCGATCG 18
||| ||||| |||||
Db 52 GGTACATCGACGCGATCG 69

RESULT 14
CHRGHAB
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
FEATURES
source

CHRGHAB
Gallus gallus (clone 3W-21) Ig rearranged heavy chain D region
mRNA, partial cds.
M30364.1 GI:557500
Ig heavy chain; IGM; diversity region; immunoglobulin;
immunoglobulin heavy chain; mu-immunoglobulin; processed gene.
Gallus gallus (strain CB Inbred line) 21 day old neonate cDNA to
mRNA.
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 69)
Reynaud C.A., Dahan A., Anguez V. and Weill J.C.
Somatic hyperconversion diversifies the single Vh gene of the
chicken with a high incidence in the D region
Cell 59 (1), 171-183 (1989)
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/clone="3W-21"
/cell_type="bursal"
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ORIGIN

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 5; Length 69;
Pred. No. 2.3e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGCGATCG 18

SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
FEATURES
source

Gallus gallus (strain CB Inbred line) 21 day old neonate cDNA to
mRNA
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 69)
Reynaud C.A., Dahan A., Anguez V. and Weill J.C.
Somatic hyperconversion diversifies the single Vh gene of the
chicken with a high incidence in the D region
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BASE COUNT
ORIGIN

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 5; Length 69;
Pred. No. 2.3e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGCGATCG 18
||| ||||| |||||
Db 52 GGTACATCGACGCGATCG 69

RESULT 15
CHRGHAB
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
FEATURES
source

CHRGHAB
Gallus gallus (clone 3W-93) Ig rearranged heavy chain D region
mRNA, partial cds.
M30368.1 GI:557504
Ig heavy chain; IGM; diversity region; immunoglobulin;
immunoglobulin heavy chain; mu-immunoglobulin; processed gene.
Gallus gallus (strain CB Inbred line) 21 day old neonate cDNA to
mRNA.
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 69)
Reynaud C.A., Dahan A., Anguez V. and Weill J.C.
Somatic hyperconversion diversifies the single Vh gene of the
chicken with a high incidence in the D region
Cell 59 (1), 171-183 (1989)
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2507167
Location/Qualifiers
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/strain="CB Inbred line"
/db_xref="taxon:9031"
/clone="3W-93"
/cell_type="bursal"
/dev_stage="21 day old neonate"
D_segment 11 a 11 c 23 g 24 t
BASE COUNT
ORIGIN

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 5; Length 69;
Pred. No. 2.3e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGAATCATCGAGCGATCG 18

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Db 52 GGTAGCATCGACCATGG 69

Search completed: December 21, 2002, 12:57:47
Job time : 261.731 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:21:10 ; Search time 38.1306 Seconds
(without alignments)
562.024 Million cell updates/sec

Title: US-09-121-239-1
Perfect score: 54
Sequence: 1 TAAATTAATAGACTACTACTA.....CCCTGAGCTCAAGTCACA 54

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 214544

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31.8	58.9	51	10	US-09-944-036-40
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5	29.4	54.4	49	10	US-09-944-036-42
6	28.2	52.2	53	10	US-09-944-036-42
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13	28	51.9	35	10	US-09-944-036-45
14	28	51.9	37	10	US-09-944-036-45
15	28	51.9	41	10	US-09-944-036-45
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17	28	51.9	52	10	US-09-944-036-45
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21	28	51.9	53	10	US-09-944-036-36	Sequence 36, Appl
22	28	51.9	53	10	US-09-944-036-37	Sequence 37, Appl
23	28	51.9	53	10	US-09-944-036-38	Sequence 38, Appl
24	28	51.9	53	10	US-09-944-036-42	Sequence 42, Appl
25	28	51.9	54	10	US-09-944-036-42	Sequence 42, Appl
26	28	51.9	54	10	US-09-944-036-42	Sequence 42, Appl
27	28	51.9	54	10	US-09-944-036-42	Sequence 42, Appl
28	28	51.9	55	10	US-09-944-036-42	Sequence 42, Appl
29	28	51.9	55	10	US-09-944-036-42	Sequence 42, Appl
30	28	51.9	57	9	US-10-001-407-18	Sequence 18, Appl
31	28	51.9	57	10	US-09-738-972-13	Sequence 13, Appl
32	28	51.9	57	10	US-09-738-972-13	Sequence 13, Appl
33	28	51.9	58	9	US-10-001-407-19	Sequence 19, Appl
34	28	51.9	59	10	US-09-738-972-11	Sequence 11, Appl
35	28	51.9	59	10	US-09-738-972-11	Sequence 11, Appl
36	28	51.9	61	10	US-09-738-972-12	Sequence 12, Appl
37	28	51.9	61	10	US-09-738-972-12	Sequence 12, Appl
38	28	51.9	63	10	US-09-953-321-5	Sequence 5, Appl
39	28	51.9	63	10	US-09-953-321-5	Sequence 5, Appl
40	27.6	50.7	51	10	US-09-866-408-56	Sequence 46, Appl
41	27.4	50.4	47	10	US-09-975-479-56	Sequence 56, Appl
42	27.2	50.4	47	10	US-09-975-479-56	Sequence 56, Appl
43	27	50.0	35	10	US-09-202-972-18	Sequence 18, Appl
44	27	50.0	35	10	US-09-202-972-18	Sequence 18, Appl
45	27	50.0	54	12	US-10-075-479-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-09-944-036-40
Sequence 40, Application US/09944036
Patent No. US2002005095A1
GENERAL INFORMATION:
APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: VERRET, Guy
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
FILE REFERENCE: G114-02.0T
CURRENT APPLICATION NUMBER: US/09/944,036
PRIORITY FILING DATE: 2001-08-31
PRIORITY FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 40
LENGTH: 51
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
NAME/KEY: promoter
LOCATION: (1)..(29)
US-09-944-036-40

Query Match 58.9% Score 31.8; DB 10; Length 51;
Best Local Similarity 76.5%; Pred. No. 0.00064;
Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
DB 1 TAAATTAATAGACTACTACTAAGTCAGACCTCAAGTCGA 52
1 TAAATTAATAGACTACTACTAAGTCAGACCTCAAGTCGA 51
RESULT 2
US-09-944-036-45

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; Sequence 45, Application US/09944036
; Patent No. US2002005095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO Steven T.
; APPLICANT: BABOLA Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNER, Guy
; TITLE OF INVENTION: APPLICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: G9114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 45
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; US-09-944-036-45
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Query Match 55.6%; Score 30; DB 10; Length 55;
Best Local Similarity 86.8%; Pred. No. 0.0034;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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OY 2 AAATTATACGACTACTATAGGAGAGCTCAGACCTG 39
Db 2 AAATTATACGACTACTATAGGAGAGACCAATCCCTG 39
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RESULT 3
US-09-202-972-11
; Sequence 11, Application US/09202972
; Patent No. US2002002518A1
; GENERAL INFORMATION:
; APPLICANT: Hirose, Minoru
; APPLICANT: Hashimoto, Junko
; APPLICANT: Yoshimura, Tadashi
; TITLE OF INVENTION: METHOD FOR THE DETECTION OF TELOMERASE ACTIVITY
; FILE REFERENCE: sequence listing for 382,1024
; CURRENT APPLICATION NUMBER: US/09/202,972
; EARLIER FILING DATE: 1998-12-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02251
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 11
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; US-09-202-972-11
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Query Match 54.8%; Score 29.6; DB 10; Length 53;
Best Local Similarity 79.5%; Pred. No. 0.0049;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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OY 2 AAATTATACGACTACTATAGGAGAGCTCAGACCTGAGGCTC 45
Db 1 AAATTATACGACTACTATAGGAGAGCTCTCTCTCTCTC 44
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RESULT 4
US-09-975-408-1

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; Sequence 1, Application US/09975408
; Patent No. US20020150917A1
; GENERAL INFORMATION:
; APPLICANT: Nanogen, Inc.
; APPLICANT: Weidenhammer, Elaine M.
; APPLICANT: Xu, Xiao
; APPLICANT: Kahl, Brenda F.
; TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC
; FILE REFERENCE: 267/174 Patrick S. Bagleman
; CURRENT APPLICATION NUMBER: US/09/975,408
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 09/710,200
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 1
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(1)
; OTHER INFORMATION: Biotinylated
; US-09-975-408-1
```

```
Query Match 54.4%; Score 29.4; DB 10; Length 49;
Best Local Similarity 84.6%; Pred. No. 0.0058;
Matches 33; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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```
OY 6 TAATACGACTCAGTATAGGAGAGCTCAGACCCCTGAGGCT 44
Db 1 TAATACGACTCAGTATAGGAGAGACAGACAGTGGATGTT 39
```

```
RESULT 5
US-10-075-579-1
; Sequence 1, Application US/10075579
; Patent No. US20020119484A1
; GENERAL INFORMATION:
; APPLICANT: Nanogen, Inc.
; APPLICANT: Weidenhammer, Elaine M.
; APPLICANT: Wang, Ling
; APPLICANT: Xu, Xiao
; APPLICANT: Heller, Michael J.
; APPLICANT: Kahl, Brenda F.
; TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC
; FILE REFERENCE: 256/262 Patrick S. Bagleman
; CURRENT APPLICATION NUMBER: US/10/075,579
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/710,200
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 1
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(1)
; OTHER INFORMATION: Biotinylated
; US-10-075-579-1
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Query Match 54.4%; Score 29.4; DB 12; Length 49;
Best Local Similarity 84.6%; Pred. No. 0.0058;
Matches 33; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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```
OY 6 TAATACGACTCAGTATAGGAGAGCTCAGACCCCTGAGGCT 44
Db 1 TAATACGACTCAGTATAGGAGAGACAGACAGTGGATGTT 39
```

RESULT 6

US-09-975-408-13
Sequence 13, Application US/09975408
Patent No. US20020150917A1
GENERAL INFORMATION:
APPLICANT: Nanogen, Inc.
APPLICANT: Weidenhammer, Elaine M.
APPLICANT: Xu, Xiao
APPLICANT: Kahl, Brenda F.
TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC MIC
FILE REFERENCE: 267/174 Patrick S. Eagelman
CURRENT APPLICATION NUMBER: US/09/975,408
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/710,200
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 13
LENGTH: 53
TYPE: DNA
ORGANISM: Homo sapiens
US-09-975-408-13

Query Match 52.2%; Score 28.2; DB 10; Length 53;
Best Local Similarity 80.5%; Pred. No. 0.018; 8; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 8;

OY 2 AAATTATAGACTCTACTATAGGAGAGCTGAGG 42
DB 2 AAATTATAGACTCTACTATAGGAGAGCTGAGG 42

RESULT 7
US-10-075-579-13
Sequence 13, Application US/10075579
Patent No. US20020119484A1
GENERAL INFORMATION:
APPLICANT: Nanogen, Inc.
APPLICANT: Weidenhammer, Elaine M.
APPLICANT: Wang, Ling
APPLICANT: Xu, Xiao
APPLICANT: Heller, Michael J.
APPLICANT: Kahl, Brenda F.
TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC MIC
FILE REFERENCE: 256/262 Patrick S. Eagelman
CURRENT APPLICATION NUMBER: US/10/075,579
CURRENT FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: US/09/710,200
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 13
LENGTH: 53
TYPE: DNA
ORGANISM: Homo sapiens
US-10-075-579-13

Query Match 52.2%; Score 28.2; DB 12; Length 53;
Best Local Similarity 80.5%; Pred. No. 0.018; 8; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 8;

OY 2 AAATTATAGACTCTACTATAGGAGAGCTGAGG 42
DB 2 AAATTATAGACTCTACTATAGGAGAGCTGAGG 42

RESULT 8
US-09-876-527-29
Sequence 29, Application US/09876527
Patent No. US20020102816A1
GENERAL INFORMATION:
APPLICANT: Kindsvogel, Wayne
APPLICANT: Jelinek, Laura J.
APPLICANT: Sheppard, Paul O.

Hagopian, William A.
Lagasse, James M.
TITLE OF INVENTION: ISLET CELL ANTIGEN 1851
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/876,527
FILING DATE: 07-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/811,481
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Langenfelter, Susan
REGISTRATION NUMBER: P-41,156
REFERENCE/DOCKET NUMBER: 95-36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6675
TELEFAX: 206-442-6678
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: ZC11197

US-09-876-527-29
SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Query Match 51.9%; Score 28; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.018; 0; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0;

OY 2 AAATTATAGACTCTACTATAGGAGAG 29
DB 1 AAATTATAGACTCTACTATAGGAGAG 28

RESULT 9
US-10-001-407-29
Sequence 29, Application US/10001407
Patent No. US20020177127A1
GENERAL INFORMATION:
APPLICANT: Yang, Yeasing
APPLICANT: Bartell, Terrie
TITLE OF INVENTION: Compositions and Methods for Detecting
FILE REFERENCE: GP17-03.07
TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
CURRENT APPLICATION NUMBER: US/10/001,407
CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/242,620
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/280,058
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 29
LENGTH: 33
TYPE: DNA

ORGANISM: HIV-2
US-10-001-407-29

Query Match
Best Local Similarity 51.9%; Score 28; DB 9; Length 33;
Pred. No. 0.019;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AATTAATACGACTCATTATAGGAGAC 29
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DB 2 AATTAATACGACTCATTATAGGAGAC 29

RESULT 10
US-09-738-972-10

Sequence 10, Application US/09738972
Patent No. US20020012918A1
GENERAL INFORMATION:
APPLICANT: BRENTANO, Steven T.
APPLICANT: LANKFORD, Roger L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
FILE REFERENCE: GP119-02.UT
CURRENT APPLICATION NUMBER: US/09/738,972
CURRENT FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: 60/171,202
PRIOR FILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: promoter
US-09-738-972-10

Query Match
Best Local Similarity 51.9%; Score 28; DB 10; Length 33;
Pred. No. 0.019;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AATTAATACGACTCATTATAGGAGAC 29
|||||
DB 2 AATTAATACGACTCATTATAGGAGAC 29

RESULT 11
US-09-944-036-4

Sequence 4, Application US/09944036
Patent No. US2002005095A1
GENERAL INFORMATION:
APPLICANT: YANG, Yeasien Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
TITLE OF INVENTION: APPLICATION OF HIV-1 SEQUENCES FOR DETECTION OF
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/09/944,036
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: T7 promoter
NAME/KEY: promoter
LOCATION: (1)..(33)

US-09-944-036-4

Query Match
Best Local Similarity 51.9%; Score 28; DB 10; Length 33;
Pred. No. 0.019;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AATTAATACGACTCATTATAGGAGAC 29
|||||
DB 2 AATTAATACGACTCATTATAGGAGAC 29

RESULT 12

US-09-202-972-15
Sequence 15, Application US/09202972
Patent No. US20020025518A1
GENERAL INFORMATION:
APPLICANT: Hirose, Minoru
APPLICANT: Yoshimura, Tadashi
TITLE OF INVENTION: METHOD FOR THE DETECTION OF TELOMERASE ACTIVITY
FILE REFERENCE: sequence listing for 382.1024
CURRENT APPLICATION NUMBER: US/09/202,972
CURRENT FILING DATE: 1998-12-23
EARLIER APPLICATION NUMBER: PCT/JP97/02251
EARLIER FILING DATE: 1997-06-27
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 35
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-202-972-15

Query Match
Best Local Similarity 51.9%; Score 28; DB 10; Length 35;
Pred. No. 0.019;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAATACGACTCATTATAGGAGAC 28
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DB 6 TAAATTAATACGACTCATTATAGGAGAC 33

RESULT 13

US-09-202-972-17
Sequence 17, Application US/09202972
Patent No. US20020025518A1
GENERAL INFORMATION:
APPLICANT: Hirose, Minoru
APPLICANT: Yoshimura, Tadashi
TITLE OF INVENTION: METHOD FOR THE DETECTION OF TELOMERASE ACTIVITY
FILE REFERENCE: sequence listing for 382.1024
CURRENT APPLICATION NUMBER: US/09/202,972
CURRENT FILING DATE: 1998-12-23
EARLIER APPLICATION NUMBER: PCT/JP97/02251
EARLIER FILING DATE: 1997-06-27
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 35
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-202-972-17

Query Match
Best Local Similarity 51.9%; Score 28; DB 10; Length 35;
Pred. No. 0.019;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AATTAATACGACTCATTATAGGAGAC 29

DB 7 AAATTAATACGACTCCTACTATAGGAGAC 34

RESULT 14
US-09-944-036-2

Sequence 2, Application US/09944036
Patent No. US2002005095A1
GENERAL INFORMATION:
APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
FILE REFERENCE: GP114-02.UF
CURRENT APPLICATION NUMBER: US/09/944,036
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 37
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: T7 promoter
NAME/KEY: Promoter
LOCATION: (1)...(29)
US-09-944-036-2

Query Match
Best local Similarity 51.9%; Score 28; DB 10; Length 37;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

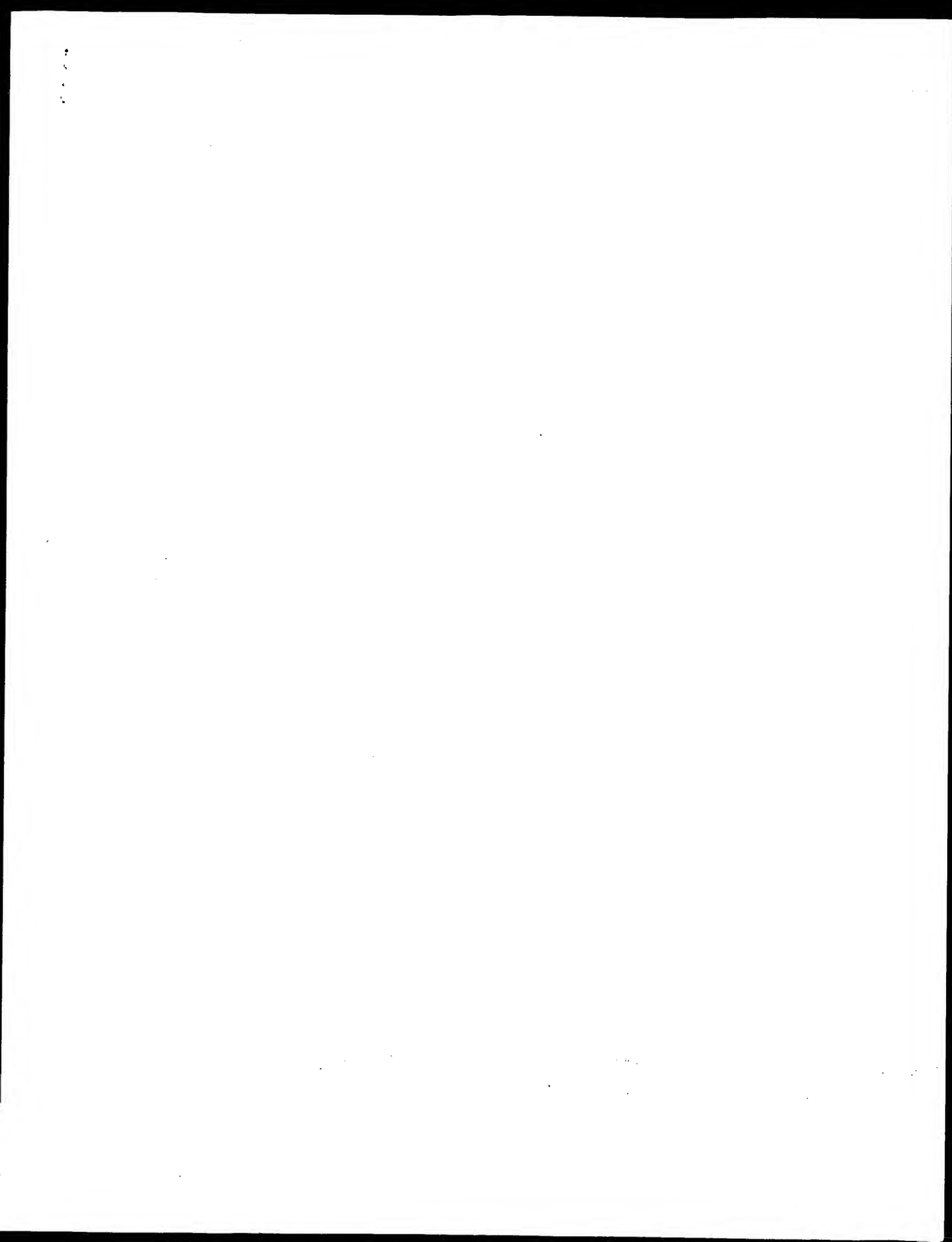
OY 2 AAATTAATACGACTCCTACTATAGGAGAC 29
DB 2 AAATTAATACGACTCCTACTATAGGAGAC 29

RESULT 15
US-09-953-321-15
Sequence 15, Application US/09953321
Patent No. US20020115083A1
GENERAL INFORMATION:
APPLICANT: PLOCKHON, ANDREAS
APPLICANT: HANES, JOZEF
APPLICANT: JERMOTUS, LOTY
TITLE OF INVENTION: NOVEL METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: (POLY) PEPTIDES THAT INTERACT WITH TARGET MOLECULES
FILE REFERENCE: PLOCK/1 CON2
CURRENT APPLICATION NUMBER: US/09/953,321
CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 09/425,585
PRIOR FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 41
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide T7B
US-09-953-321-15

Query Match
Best local Similarity 51.9%; Score 28; DB 10; Length 41;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AAATTAATACGACTCCTACTATAGGAGAC 29
DB 6 AAATTAATACGACTCCTACTATAGGAGAC 33

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Mon Dec 23 08:48:06 2002

us-09-121-239-5.rnpb

Page 1

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OM nucleic - nucleic search, using sw model

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Searched: 356696 seqs, 198428768 residues

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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

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and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	13.4	55.8	95	10	US-09-853-263-53
C 4	13.2	55.0	30	9	US-09-811-3678-17
C 5	13.2	55.0	31	9	US-09-811-3678-16
C 6	13.2	55.0	32	10	US-09-894-6334-50
C 7	13	54.2	20	10	US-09-895-382-17
C 8	12.8	53.3	35	10	US-09-780-929-115
C 9	12.8	53.3	77	10	US-09-878-574-10313
C 10	12.8	53.3	86	9	US-10-040-497-57
C 11	12.8	53.3	91	10	US-09-864-761-33030
C 12	12.6	52.5	48	9	US-09-864-785-3282
C 13	12.6	52.5	78	10	US-09-864-761-32336
C 14	12.4	51.7	22	8	US-09-983-605-347
C 15	12.4	51.7	24	9	US-09-966-8804-20
C 16	12.4	51.7	32	9	US-09-925-664-39
C 17	12.4	51.7	32	10	US-09-921-992-63
C 18	12.4	51.7	32	10	US-09-987-025-11
C 19	12.2	50.8	57	12	US-10-153-064-82

C 20	12.2	50.8	58	12	US-10-153-064-10	Sequence 10, Appl
C 21	12.2	50.8	58	12	US-10-153-064-83	Sequence 83, Appl
C 22	12.2	50.8	59	12	US-10-153-064-11	Sequence 11, Appl
C 23	12	50.0	24	9	US-09-905-2914-129	Sequence 129, Appl
C 24	12	50.0	24	10	US-09-920-920-77	Sequence 77, Appl
C 25	12	50.0	24	10	US-09-909-320-129	Sequence 129, Appl
C 26	12	50.0	24	10	US-09-909-0888-129	Sequence 129, Appl
C 27	12	50.0	24	10	US-09-565-233-16	Sequence 16, Appl
C 28	12	50.0	48	9	US-09-864-785-3011	Sequence 3011, Appl
C 29	12	50.0	48	9	US-09-864-785-3173	Sequence 3173, Appl
C 30	12	50.0	48	9	US-09-864-785-3203	Sequence 3203, Appl
C 31	12	50.0	48	9	US-09-864-785-3267	Sequence 3267, Appl
C 32	12	50.0	63	10	US-09-745-605-41	Sequence 41, Appl
C 33	12	50.0	73	10	US-09-888-280-53	Sequence 53, Appl
C 34	12	50.0	86	10	US-09-878-574-14526	Sequence 14526, A
C 35	12	50.0	100	10	US-09-878-446-597	Sequence 997, Appl
C 36	11.8	49.2	25	10	US-09-866-108-5107	Sequence 5107, Appl
C 37	11.8	49.2	25	10	US-09-866-108-5108	Sequence 5108, Appl
C 38	11.8	49.2	27	10	US-09-828-108-5109	Sequence 5109, Appl
C 39	11.8	49.2	31	10	US-09-753-436-8	Sequence 8, Appl
C 40	11.8	49.2	31	10	US-09-801-274-757	Sequence 757, Appl
C 41	11.8	49.2	31	10	US-09-882-246-58	Sequence 58, Appl
C 42	11.8	49.2	32	10	US-09-757-992-2	Sequence 2, Appl
C 43	11.8	49.2	37	10	US-09-882-246-25	Sequence 25, Appl
C 44	11.8	49.2	49	10	US-09-882-246-61	Sequence 61, Appl
C 45	11.8	49.2	49	10	US-09-882-246-61	Sequence 61, Appl

ALIGNMENTS

RESULT 1
US-10-025-380-53/c
Sequence 53, Application US/10025380
Publication No. US20020182191A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
APPLICANT: Meagher, Madeline Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tonglong
APPLICANT: Jiang, Yugu
APPLICANT: Smith, Carole L.
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick Thomas S.
APPLICANT: Carter, Darick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLOR CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.47C14
CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 53
LENGTH: 95
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: 37, 60, 73, 76, 92
OTHER INFORMATION: n = A,T,C or G
US-10-025-380-53
Query Match 55.8%; Score 13.4; DB 9; Length 95;
Best Local Similarity 73.9%; Pred. NO. 7.8e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Query Match	55.08;	Score 13.2;	DB 9;	Length 31;
Best Local Similarity	83.38;	Pred. No. 8.1e+02;		
Matches 15; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0

Query Match	54.28;	Score 13;	DB 10;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 9.4e+02;		
Matches 13;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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RESULT 9
US-09-878-574-10313
; Sequence 10313, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ. ID NOS: 15775
; SEQ. ID NO. 10313
; LENGTH: 77
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701103536H1
US-09-878-574-10313

Query Match          53.3%   Score 12.8;   DB 10:   Length 77;
Best Local Similarity 70.8%;   Pred. No.1.5e+03;
Matches 17;   Conservative 0;   Mismatches 7;   Indels 0;   Gaps 0;

QY      1  GACCACTGCTGTGTGGAACGCCA 24
        ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB      44  GATCATAGGTGTGTCACTACCA 67

RESULT 10
US-10-040-497-57
; Sequence 57, Application US/10040497

```

Patent No. US20020172962A1
GENERAL INFORMATION:
APPLICANT: GOLD, LARRY
TIERK, CRAIG
TITLE OF INVENTION: METHODS OF PRODUCING NUCLEIC ACID LIGANDS
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/5 inch, 1.44 MB
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/040,497
FILING DATE: 07-Jan-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/748,697
FILING DATE: 13-NOVEMBER-1996
APPLICATION NUMBER: 08/442,062
FILING DATE: 16-MAY-1995
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX05/DC-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-040-497-57
Query Match 53.3%; Score 12.8; DB 9; Length 86;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 16; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
QY 1 GACCAACTCGTGTGTAATCGA 24
DB 21 GACCAACUCCAUCCAGAAACGCA 44
RESULT 11
US-09-864-761-33030
Sequence 33030, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 33030
LENGTH: 91
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL078623.21
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
OTHER INFORMATION: EST_HUMAN HIT: A1201676.1, EVALU8 1.10e+00
US-09-864-761-33030
Query Match 53.3%; Score 12.8; DB 10; Length 91;
Best Local Similarity 87.5%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 ACCAACTCGTGTGTA 17
DB 26 ACCAACTCGTGTGTA 41
RESULT 12
US-09-864-785-3282
Sequence 3282, Application US/09864785
Patent No. US20020177568A1
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Stinchcomb, Dan
APPLICANT: Draper, Ken
APPLICANT: McSwigen, Jim
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel
FILE REFERENCE: 400/022 (RHE00-812-D)
CURRENT APPLICATION NUMBER: US/09/864,785
CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 3929
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3282
LENGTH: 48

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; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; US-09-864-761-3282

Query Match          52.5%; Score 12.6; DB 9; Length 48;
Best Local Similarity 63.2%; Pred. No. 1.7e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 AACGTGTGTGAACCTCC 23
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DB 2 AACDCAUGAGGAGAAACUCC 20

RESULT 13
US-09-864-761-32336/c
; Sequence 32336, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Weisheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEOTIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-R-1
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32336
; LENGTH: 78
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC003677.1

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
; OTHER INFORMATION: NT HIT: AF096872.1, EVALUATE 2.40e+00
; OTHER INFORMATION: EST_HUMAN HIT: R67876.1, EVALUATE 3.60e+00
; US-09-864-761-32336

Query Match          52.5%; Score 12.6; DB 10; Length 78;
Best Local Similarity 78.9%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 ACTGTGTGTGAACCTCCA 24
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DB 44 ACTGTGTGTGAACCTCCA 26

RESULT 14
US-08-983-605-347/c
; Sequence 347, Application US/08983605A
; Patent No. US20020066118A1
; GENERAL INFORMATION:
; APPLICANT: Roder, Marion
; TITLE OF INVENTION: Microsatellite Markers for Plants of the Species
; FILE REFERENCE: 2936.10400
; CURRENT FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: DE 195 25 284.5
; EARLIER FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 347
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Triticum aestivum
; US-08-983-605-347

Query Match          51.7%; Score 12.4; DB 8; Length 22;
Best Local Similarity 92.9%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TCGTGTGTGAACCT 21
    |||:|:| |||||:|
DB 15 TCTGTGTGAACCT 2

RESULT 15
US-09-966-880A-20/c
; Sequence 20, Application US/09966880A
; Patent No. US20020164743A1
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Muramatsu, Masamichi
; TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
; FILE REFERENCE: 06501-088001
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/966,880A
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: PCT/JP00/01918
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: JP 11-371382
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: JP 11-178999
; PRIOR FILING DATE: 1999-06-24
; PRIOR APPLICATION NUMBER: JP 11-87192
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially synthesized primer sequence, p3
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Mon Dec 23 08:48:06 2002

us-09-121-239-5.rnpb

Page 6

US-09-966-880A-20

Query Match 51.7%; Score 12.4; DB 9; Length 24;
Best Local Similarity 72.7%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY	1	GACCAACTCGTGTGAACTC	22
Db	22	GTCCAACTGTACTCAACTC	1

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Job time : 18.9469 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:21:10 ; Search time 17.6511 Seconds
(without alignments)
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Title: US-09-121-239-9
Perfect score: 25
Sequence: 1 GACTGTCACAGCATTCGCGTACC 25

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 356696 seqs, 198428768 residues

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Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/PCRUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	16	64.0	28	10	US-09-779-881-2
2	15.6	62.4	82	10	US-09-864-761-26163
3	14.4	57.6	100	10	US-09-983-965-1713
4	14	56.0	16	10	US-09-068-817-9
5	14	56.0	100	10	US-09-864-761-26368
6	13.8	55.2	34	10	US-09-772-120-4
7	13.8	55.2	80	10	US-09-864-761-21132
8	13.8	55.2	80	10	US-09-783-590-6697
9	13.8	55.2	89	10	US-09-741-669-78
10	13.2	52.8	77	10	US-09-815-242-2240
11	13	52.0	22	12	US-10-028-415-38
12	13	52.0	66	10	US-09-766-113-20
13	12.8	51.2	21	10	US-09-104-654-8
14	12.8	51.2	39	9	US-09-733-042-48
15	12.8	51.2	65	10	US-09-783-590-6219
16	12.8	51.2	94	10	US-09-294-0938-3985
17	12.8	51.2	96	10	US-09-864-761-23371
18	12.8	51.2	97	10	US-09-864-761-19961
19	12.6	50.4	29	10	US-09-828-303-49

20	12.6	50.4	67	10	US-09-783-590-1116	Sequence 1116, Ap
21	12.6	50.4	90	12	US-10-051-843-7	Sequence 7, Appl
22	12.4	49.6	25	10	US-09-866-108-13884	Sequence 13884, A
23	12.4	49.6	25	10	US-09-866-108-13885	Sequence 13885, A
24	12.4	49.6	25	10	US-09-866-108-13886	Sequence 13886, A
25	12.4	49.6	25	10	US-09-866-108-13887	Sequence 13887, A
26	12.4	49.6	64	10	US-09-766-113-4	Sequence 4, Appl
27	12.4	49.6	75	10	US-09-983-965-5804	Sequence 5804, Ap
28	12.4	49.6	90	10	US-09-917-330-3	Sequence 3, Appl
29	12.4	49.6	96	10	US-09-864-761-17595	Sequence 17595, A
30	12.2	48.8	17	10	US-09-866-108-10265	Sequence 10265, A
31	12.2	48.8	25	10	US-09-866-108-15157	Sequence 15157, A
32	12.2	48.8	25	10	US-09-866-108-15158	Sequence 15158, A
33	12.2	48.8	25	10	US-09-866-108-15159	Sequence 15159, A
34	12.2	48.8	25	10	US-09-866-108-15160	Sequence 15160, A
35	12.2	48.8	25	10	US-09-866-108-15161	Sequence 15161, A
36	12.2	48.8	25	10	US-09-866-108-15162	Sequence 15162, A
37	12.2	48.8	25	10	US-09-866-108-15163	Sequence 15163, A
38	12.2	48.8	25	10	US-09-866-108-15164	Sequence 15164, A
39	12.2	48.8	25	10	US-09-866-108-15165	Sequence 15165, A
40	12.2	48.8	30	10	US-09-752-110A-21	Sequence 21, Appl
41	12.2	48.8	47	10	US-09-264-468B-5	Sequence 4, Appl
42	12.2	48.8	66	10	US-09-572-365-6	Sequence 6, Appl
43	12.2	48.8	66	10	US-09-572-365-6	Sequence 6, Appl
44	12.2	48.8	66	10	US-09-573-465-6	Sequence 6, Appl
45	12.2	48.8	85	10	US-09-864-761-30027	Sequence 30027, A

ALIGNMENTS

```

RESULT 1
US-09-779-881-2/c
; Sequence 2, Application US/09779881
; Patent No. US20020081749A1
; GENERAL INFORMATION: Sakari
; APPLICANT: Kunitama, Taro
; APPLICANT: Aia Kieme, Taro
; APPLICANT: Eskola, Jari
; TITLE OF INVENTION: ELECTRICAL EXCITATION OF LABEL SUBSTANCES AT COATED
; FILE REFERENCE: TUR-080
; CURRENT APPLICATION NUMBER: US/09/779,881
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/341,955
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/F198/00114
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 2
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide containing an amino group
US-09-779-881-2
Query Match 64.0%; Score 16; DB 10; Length 28;
Best Local Similarity 100.0%; Pred No. 73;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 CAGCATTCGCGTGACC 25
DB 28 CAGCATTCGCGTGACC 13
RESULT 2
US-09-864-761-26163/c
; Sequence 26163, Application US/09864761
; Patent No. US20020048763A1

```

RESULT 3

Query Match	57.68;	Score 14.4;	DB 10;	Length 100;
Best Local Similarity	75.08;	Pred. No. 5e+02;		
Matches	18;	Conservative	0;	Mismatches 6.
			Totals	0.

RESULT 4

APPLICANT: MCIVOR, R.S.

PRIOR APPLICATION NUMBER: PCT/US96/18273

PRIOR FILING DATE: 1995-11-14

```

; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9

```

TYPE: DNA
ORGANISM: Homo sapiens

Query Match	62.4%;	Score 15.6;	DB 10;	Length 82;
Best Local Similarity	81.8%;	Pred. No. 1.3e+02;		
Matches	18;	Conservative	0;	Mismatches 4;
				Indels 0;
				Caps 0;

QY 2 ACTGTCACAGATTCCGCTGA 23
|||||
Db 50 ACTGTCACACAGACCCCGGTTA 29

RESULT 3

; GENERAL INFORMATION:

RESULT 5

Query Match	56.0%	Score 14;	DB 10;	Length 16;
Best Local Similarity	100.0%	Pred. No.	5 Re+02.	

RESULT 5

; GENERAL INFORMATION:


```

; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 21132
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC012122.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: NT HIT: 914758563, EVALUATE 3.00e-06
; OTHER INFORMATION: EST HUMAN HIT: AW293349.1, EVALUATE 4.00e-33
; OTHER INFORMATION: SWISSPROT HIT: P35820, EVALUATE 5.40e+00
US-09-864-761-21132

Query Match      55.2%; Score 13.8; DB 10; Length 80;
Best Local Similarity 72.0%; Pred. No. 9.3e+02;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 GACTGTCACGACATTCGGCTGAC 25
DB 68 GCCTCTCTCAGCCATCAGCTGATC 44
```

```

RESULT 8
US-09-783-590-6697/c
; Sequence 6697, Application US/09783590
```

```

; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16,2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 6697
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (72)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-6697

Query Match      55.2%; Score 13.8; DB 10; Length 80;
Best Local Similarity 88.2%; Pred. No. 9.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

OY 5 GTCACGACATTCGGCT 21
DB 62 GTCACGACATTCGGCT 46
```

```

RESULT 9
US-09-741-669-78/c
; Sequence 78, Application US/09741669
; Patent No. US2002022718A1
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; TITLE OF INVENTION: Genes identified as required for
; FILE REFERENCE: ELITRA.009A
; CURRENT APPLICATION NUMBER: US/09/741,669
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 60/173005
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 89
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-741-669-78
```

```

Query Match      55.2%; Score 13.8; DB 10; Length 89;
Best Local Similarity 88.2%; Pred. No. 9.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 7 CCACGACATTCGGCTGA 23
DB 88 CCACGACATTCGGCTGA 72
```

```

RESULT 10
US-09-815-242-2240
```

```
Sequence 2240, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlson, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2240
LENGTH: 77
TYPE: DNA
ORGANISM: Staphylococcus aureus
US-09-815-242-2240

Query Match      52.8%; Score 13.2; DB 10; Length 77;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 TGTCACAGACATTCGGCT 21
      ||||| |||||
DB      44 TGTCACGCAATGCGCT 61

RESULT 11
US-10-028-415-38/c
Sequence 38, Application US/10028415
Patent No. US20020151063A1
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Methods for Modulating Apoptotic Cell
FILE REFERENCE: 1100.1004c3
CURRENT APPLICATION NUMBER: US/10/028,415
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: PCT/NZ01/00286
PRIOR FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: US 09/724,809
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/036,004
PRIOR FILING DATE: 1998-03-04
PRIOR APPLICATION NUMBER: US 08/713,557
PRIOR FILING DATE: 1996-08-30
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 38
LENGTH: 22
TYPE: DNA
ORGANISM: Human
```

```
US-10-028-415-38
Query Match      52.0%; Score 13; DB 12; Length 22;
Best Local Similarity 76.2%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      5 GTCCACAGACATTCGCTGACC 25
      ||||| ||||| |||||
DB      22 GGCACAGACATTCGCTGCC 2

RESULT 12
US-09-766-113-20
Sequence 20, Application US/09766113
Patent No. US20010047525A1
GENERAL INFORMATION:
APPLICANT: Bruce, Wesley B.
APPLICANT: Niu, Xiping
TITLE OF INVENTION: No. US20010047525A1 Root-Preferred Promoter Elements
FILE REFERENCE: 1166
CURRENT APPLICATION NUMBER: US/09/766,113
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/177,473
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 66
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic sequences flanking a random
US-09-766-113-20

Query Match      52.0%; Score 13; DB 10; Length 66;
Best Local Similarity 76.2%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 ACTGTCACAGACATTCGCTG 22
      ||||| ||||| |||||
DB      46 ACTGCTACAGACATTCAGCTG 66

RESULT 13
US-09-104-654-8/c
Sequence 8, Application US/09104654
Patent No. US2001008026A1
GENERAL INFORMATION:
APPLICANT: Schneider, Michael D.
APPLICANT: Overbeek, Paul
APPLICANT: Frenkel, Peter
TITLE OF INVENTION: System for Tissue-Restricted Gene
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,654
FILING DATE: 25-JUN-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
```

NAME: MacKnight, Kamrin T.
 REGISTRATION NUMBER: 38,230
 REFERENCE/DOCKET NUMBER: BCM-02973
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "DNA"
 US-09-104-654-8

Query Match 51.2%; Score 12.8; DB 10; Length 21;
 Best Local Similarity 87.5%; Pred. No. 2.2e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 TCACAGCATTCGCT 21
 ||||| |||||
 Db 19 TCACACATTCGCT 4

RESULT 14
 US-09-733-042-48/c
 ; Sequence 48, Application US/09733042
 ; Patent No. US20020168709A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hennecke, Frank
 ; APPLICANT: Renner, Wolfgang A.
 ; TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes
 ; FILE REFERENCE: 1700.0100001
 ; CURRENT APPLICATION NUMBER: US/09/733,042
 ; CURRENT FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: US 60/169,988
 ; PRIOR FILING DATE: 1999-12-10
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 48
 ; LENGTH: 39
 ; TYPE: DNA
 ; ORGANISM: 5'SV40 PUR
 ; US-09-733-042-48

Query Match 51.2%; Score 12.8; DB 9; Length 39;
 Best Local Similarity 70.8%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GACTGTCACAGCATTCGCTGAC 24
 ||||| ||||| |||||
 Db 36 GACTTCCACACCCCTACGCGGCC 13

RESULT 15
 US-09-783-590-6219/c
 ; Sequence 6219, Application US/09783590
 ; Patent No. US20020110850A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dillon, Patrick J.
 ; APPLICANT: Haseltine, William A.
 ; APPLICANT: Li, Haodong
 ; APPLICANT: Rosen, Craig A.
 ; APPLICANT: Ruben, Steven M.
 ; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
 ; FILE REFERENCE: PO-16.2C1
 ; CURRENT APPLICATION NUMBER: US/09/783,590
 ; CURRENT FILING DATE: 2000-02-15
 ; PRIOR APPLICATION NUMBER: 08/420,856
 ; PRIOR FILING DATE: 1995-04-12
 ; PRIOR APPLICATION NUMBER: 08/346,731
 ; PRIOR FILING DATE: 1994-11-21

NUMBER OF SEQ ID NOS: 12485
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6219
 ; LENGTH: 65
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (15)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (45)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; US-09-783-590-6219

Query Match 51.2%; Score 12.8; DB 10; Length 65;
 Best Local Similarity 68.0%; Pred. No. 2.6e+03;
 Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GACTGTCACAGCATTCGCTGACC 25
 ||||| ||||| |||||
 Db 38 GTCAATCAACAGCATTCGCGCAANC 14

Search completed: December 21, 2002, 19:28:13
 Job time : 18.6531 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:21:10 : Search time 14.1224 Seconds
(without alignments)
562.024 Million cell updates/sec

Title: US-09-121-239-13

Sequence: 1 CAAGAGCAGGAGAGAGAG 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 214544

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_PCT_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.4	87.0	96	12	US-10-078-777-8
2	15.2	76.0	23	10	US-09-814-777A-82
3	14.8	74.0	84	12	US-10-078-777-7
4	14.8	74.0	87	12	US-10-078-777-9
5	14.2	71.0	45	12	US-10-002-278-14
6	14.2	71.0	91	10	US-09-864-761-19573
7	13.8	69.0	31	10	US-09-801-274-1776
8	13.8	69.0	84	10	US-09-864-761-26118
9	13.6	68.0	89	10	US-09-772-719-42
10	13.2	66.0	23	9	US-09-966-546-52
11	13.2	66.0	23	9	US-09-966-546-52
12	13.2	66.0	59	10	US-09-426-548-84
13	13.2	66.0	87	10	US-09-864-761-21662
14	12.8	64.0	19	9	US-09-963-875-14
15	12.8	64.0	21	10	US-09-918-203-3
16	12.8	64.0	32	10	US-09-885-478-20
17	12.8	64.0	32	10	US-09-885-478-21
18	12.8	64.0	97	10	US-09-864-761-19704
19	12.6	63.0	24	10	US-09-754-997A-41

20	12.6	63.0	43	9	US-10-027-806-90	Sequence 90, Appl
21	12.6	63.0	75	10	US-09-864-761-23841	Sequence 23841, A
22	12.6	63.0	94	10	US-09-864-761-22644	Sequence 22644, A
23	12.6	63.0	97	10	US-09-864-761-24367	Sequence 24367, A
24	12.6	62.0	18	10	US-09-789-556A-32	Sequence 32, Appl
25	12.4	62.0	20	10	US-09-789-556A-31	Sequence 31, Appl
26	12.4	62.0	22	10	US-09-789-556A-30	Sequence 30, Appl
27	12.4	62.0	26	10	US-09-789-556A-29	Sequence 29, Appl
28	12.4	62.0	31	10	US-09-801-274-1190	Sequence 1190, Appl
29	12.4	62.0	38	12	US-10-036-342-48	Sequence 48, Appl
30	12.4	62.0	80	10	US-09-864-761-1767	Sequence 1767, A
31	12.2	61.0	21	10	US-09-955-380-13	Sequence 13, Appl
32	12.2	61.0	30	9	US-09-48-297-48	Sequence 48, Appl
33	12.2	61.0	30	9	US-10-033-297-48	Sequence 48, Appl
34	12.2	61.0	30	10	US-09-777-430A-3	Sequence 3, Appl1
35	12.2	61.0	30	10	US-09-777-430A-4	Sequence 4, Appl1
36	12.2	61.0	31	10	US-09-801-274-571	Sequence 571, Appl
37	12.2	61.0	43	12	US-10-001-344-8	Sequence 8, Appl1
38	12.2	61.0	50	10	US-09-504-231A-2965	Sequence 2965, Ap
39	12.2	61.0	50	10	US-09-274-553D-2965	Sequence 2965, Ap
40	12.2	61.0	61	9	US-09-946-807-1332	Sequence 1332, Ap
41	12.2	61.0	61	10	US-09-795-668-1332	Sequence 1332, Ap
42	12.2	61.0	61	10	US-09-795-668-1332	Sequence 1332, Ap
43	12.2	61.0	78	10	US-09-864-761-24659	Sequence 24659, A
44	12.2	61.0	90	10	US-09-864-761-28450	Sequence 28450, A
45	12.2	61.0	91	10	US-09-783-590-2439	Sequence 2439, Ap

ALIGNMENTS

RESULT 1
US-10-078-777-8
Sequence 8, Appl
Patent No. US2002013785A1
GENERAL INFORMATION:
APPLICANT: REDEI, Eva
TITLE OF INVENTION: CORTICOTROPIN RELEASE INHIBITING FACTOR AND METHODS OF
FILE REFERENCE: 0054-103
CURRENT APPLICATION NUMBER: US/10/078,777
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/366,627
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 08/523,125
PRIOR FILING DATE: 1995-09-08
PRIOR APPLICATION NUMBER: 08/304,383
PRIOR FILING DATE: 1994-09-12
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 8
LENGTH: 96
TYPE: DNA
ORGANISM: Homo sapiens
US-10-078-777-8
Query Match 87.0%; Score 17.4; DB 12; Length 96;
Best local similarity 94.7%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAAGAGCAGGAGAGAG 19
DB 37 CAAGAGCAGGAGAGAG 55
RESULT 2
US-09-814-777A-82
Sequence 82, Appl
Patent No. US20020142415A1
GENERAL INFORMATION:
APPLICANT: KOOPMAN, Peter Anthony
APPLICANT: MOSCAT, George Eugene Orlando


```

; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: US 09/774,203
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 19573
; LENGTH: 91
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011416.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.98
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN NT HIT: X94232.1, EVALUATE 1.60e-01
; US-09-864-761-19573

Query Match          71.0%; Score 14.2; DB 10; Length 91;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1776
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-801-274-1776

Query Match          69.0%; Score 13.8; DB 10; Length 31;
Best Local Similarity 78.9%; Pred. No. 1.2e+03;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

QY 2 AAAGGAGGAGGAGGAGGAGG 20
 DB 31 AAAGGAGGAGGAGGAGGAGG 13

```

; US-09-864-761-26118
; Sequence 26118, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Bank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aesomica-X-1
; CURRENT FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: US 09/774,203
; NUMBER OF SEQ ID NOS: 49117

```

SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 26118
LENGTH: 84
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL022318.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.8
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 43
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.6
OTHER INFORMATION: NT HIT: AL163210.2, EVALU2 2.00e-35
OTHER INFORMATION: EST_HUMAN HIT: BE150340.1, EVALU2 1.00e-34
US-09-864-761-26118

Query Match
Best Local Similarity 69.0%; Score 13.8; DB 10; Length 84;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 AGGACGACGAGGAGAGG 20
DB 56 AGGACGACGAGGAGAGG 72

RESULT 9
US-09-772-719-42

Sequence 42, Application US/09772719
Patent No. US20020137910A1

GENERAL INFORMATION:

APPLICANT: Zavada, Jan

APPLICANT: Pastorekova, Silvia

APPLICANT: Pastorek, Jaromir

TITLE OF INVENTION: MN Gene and Protein

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leona L. Lauder

STREET: 369 Pine Street

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/772,719

FILING DATE: 30-JAN-2001

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/485,049

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/260,190

FILING DATE: 15-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Lauder, Leona L.

REGISTRATION NUMBER: 30,863

REFERENCE/DOCKET NUMBER: D-0021.3E

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-981-2034

TELEFAX: 415-981-0332

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 89 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
DESCRIPTION: 4th MN intron
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-772-719-42

Query Match
Best Local Similarity 68.0%; Score 13.6; DB 10; Length 89;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CAAGGACGCGGCGGAGG 20
DB 27 CAAGGACGCGGCGGAGG 46

RESULT 10
US-09-966-546-52

Sequence 52, Application US/09966546
Patent No. US20020168716A1

GENERAL INFORMATION:

APPLICANT: Fernandes, Elma

APPLICANT: Vernet, Corine

APPLICANT: Shimkets, Richard A.

TITLE OF INVENTION: Them

FILE REFERENCE: Cura-46 (15966-546)

CURRENT APPLICATION NUMBER: US/09/966,546

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 09/544,511

PRIOR FILING DATE: 2000-04-06

NUMBER OF SEQ ID NOS: 57

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 52

LENGTH: 23

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Oligo Primer

US-09-966-546-52

Query Match
Best Local Similarity 66.0%; Score 13.2; DB 9; Length 23;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 AAAGGACGAGGAGAGG 19
DB 1 AAAGGACGAGGAGAGG 18

RESULT 11
US-09-966-545-52

Sequence 52, Application US/09966545
Patent No. US20020172999A1

GENERAL INFORMATION:

APPLICANT: Fernandes, Elma

APPLICANT: Vernet, Corine

APPLICANT: Shimkets, Richard A.

TITLE OF INVENTION: Them

FILE REFERENCE: Cura-46 (15966-546)

CURRENT APPLICATION NUMBER: US/09/966,545

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 09/544,511

PRIOR FILING DATE: 2000-04-06

NUMBER OF SEQ ID NOS: 57

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 52

LENGTH: 23

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Oligo Primer

US-09-966-545-52

Query Match 66.0%; Score 13.2; DB 9; Length 23;
Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGACGAGGAGAG 19
DB 1 AAAGGACGAGGAGAG 18

RESULT 12
US-09-426-548-84/c
; Sequence 84, Application US/09426548
; Patent No. US20010044936A1
; GENERAL INFORMATION:
; APPLICANT: Robbins, David
; APPLICANT: Lin-Goeke, Jull L.
; TITLE OF INVENTION: No. US20010044936A1 Mutations in Human MLH1 and MSH2 Genes Used
; FILE REFERENCE: DEX-0054
; CURRENT APPLICATION NUMBER: US/09/426,548
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-426-548-84

Query Match 66.0%; Score 13.2; DB 10; Length 59;
Best Local Similarity 83.3%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGACGAGGAGAG 19
DB 46 AAAGGACGAGGAGAG 29

RESULT 13
US-09-864-761-21662
; Sequence 21662, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEOTIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 21662
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL034399.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EST HUMAN HIT: BF337932.1, EVALUATE 2.70e-01
; OTHER INFORMATION: NT HIT: AL161560.2, EVALUATE 1.50e-01
US-09-864-761-21662

Query Match 66.0%; Score 13.2; DB 10; Length 87;
Best Local Similarity 83.3%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAGGACGAGGAGAG 18
DB 19 CTAAGGAGGAGAGAG 36

RESULT 14
US-09-963-875-14
; Sequence 14, Application US/09963875
; Patent No. US20020164307A1
; GENERAL INFORMATION:
; APPLICANT: Massachusetts General Hospital
; TITLE OF INVENTION: Stem Cells of the Islets of Langerhans and Their Use in Treati
; FILE REFERENCE: 17633/1235
; CURRENT APPLICATION NUMBER: US/09/963,875
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US60/169082
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/215109
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: US 60/238880
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/731261
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: oligonucleotide
US-09-963-875-14

Query Match 64.0%; Score 12.8; DB 9; Length 19;
Best Local Similarity 87.5%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGGAGCGAGGAG 16
|| |||||
DB 3 CACTGAGCGAGGAG 18

RESULT 15

US-09-918-203-3/c
; Sequence 3, Application US/09918203
; Patent No. US2002002530A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Affourtit, Jason
; APPLICANT: Seymour, Albert
; TITLE OF INVENTION: A PCR-BASED MULTIPLEX ASSAY FOR DETERMINING HAPLOTYPE
; FILE REFERENCE: PC10704DAM
; CURRENT APPLICATION NUMBER: US/09/918,203
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-203-3

Query Match 64.0%; Score 12.8; DB 10; Length 21;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGCAGGAGGAGG 20
||| |||||
DB 21 GGAGCAGGAGGATCG 6

Search completed: December 21, 2002, 19:28:15
Job time : 16.1224 secs


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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 29032
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL121908.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.92
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: NT HIT: D17760.1, EVALUO 7.90e-01
; OTHER INFORMATION: EST_HUMAN HIT: AW629605.1, EVALUO 7.40e-02
US-09-864-761-29032
```

```
Query Match
Best Local Similarity 65.0%; Score 15.6; DB 10; Length 95;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY 1 GTGAACATGAAGCCCTTCAGC 22
Db 51 GGGAGAGATGAAGCCCTTCATC 72
```

```
RESULT 2
US-09-946-807-1334
; Sequence 1334, Application US/09946807
; Patent No. US20020165144A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreln
; APPLICANT: Steinhorsdottir, Valgerdur
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/946,807
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US/09/795,668
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1334
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-946-807-1334
```

```
Query Match
Best Local Similarity 63.3%; Score 15.2; DB 9; Length 61;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 2 TGAACATGAAGCCCTTCAG 21
Db 37 TGAATATGAAGCATTTTCAG 56
```

```
RESULT 3
US-09-795-668-1334
; Sequence 1334, Application US/09795668
; Patent No. US20020045577A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Stefansson, Hreln
; APPLICANT: Steinhorsdottir, Valgerdur
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/795,668
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1334
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-668-1334
```

```
Query Match
Best Local Similarity 63.3%; Score 15.2; DB 10; Length 61;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 2 TGAACATGAAGCCCTTCAG 21
Db 37 TGAATATGAAGCATTTTCAG 56
```

```
RESULT 4
US-09-795-668-1334
; Sequence 1334, Application US/09795668
; Patent No. US2002004954A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreln
; APPLICANT: Steinhorsdottir, Valgerdur
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2005-001
; CURRENT APPLICATION NUMBER: US/09/795,686
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,715
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1334
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-668-1334
```

```
Query Match
Best Local Similarity 63.3%; Score 15.2; DB 10; Length 61;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 2 TGAACATGAAGCCCTTCAG 21
Db 37 TGAATATGAAGCATTTTCAG 56
```

```
RESULT 5
US-09-792-793A-47
; Sequence 47, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggin, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
; FILE REFERENCE: 25020-601D
; CURRENT APPLICATION NUMBER: US/09/792,793A
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 38
```

```

;
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: forward primer (SDF-1-Beta)
US-09-792-793A-47
Query Match
Best Local Similarity 60.8%; Score 14.6; DB 9; Length 38;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 TGGAACATGAAGCCCTTCAGC 22
DB 7 TAGCATATGAAGCCCTTCAGC 27
RESULT 6
US-09-801-274-652
; Sequence 652, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825-2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; NUMBER OF SEQ ID NOS: 2000-05-22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 652
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-652
Query Match
Best Local Similarity 59.2%; Score 14.2; DB 10; Length 31;
Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 2 TGGAACATGAAGCCCTTCAGC 22
DB 10 TGGAACATGAAGCCCTTCAGC 30
RESULT 7
US-09-779-881-1/C
; Sequence 1, Application US/09779881
; Patent No. US20020081749A1
; GENERAL INFORMATION:
; APPLICANT: Kultima, Sakari
; APPLICANT: Ala-Kleme, Timo
; APPLICANT: Eskola, Jarkko
; APPLICANT: Kotkola, Jukka
; TITLE OF INVENTION: ELECTRICAL EXCITATION OF LABEL SUBSTANCES AT COATED
; FILE REFERENCE: IOR-080
; CURRENT APPLICATION NUMBER: US/09/779,881
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US/09/7341,955
; PRIOR FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: PCT/FI98/00114
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```

; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide containing amino groups
US-09-779-881-1
Query Match
Best Local Similarity 58.3%; Score 14; DB 10; Length 26;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 11 AAGCCCTTCAGCG 24
DB 26 AAGCCCTTCAGCG 13
RESULT 8
US-09-263-689-57
; Sequence 57, Application US/09263689
; Patent No. US20020150970A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein, & Fox P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,689
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/946,914
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488,0560001/EKS/SGW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-263-689-57
Query Match
Best Local Similarity 58.3%; Score 14; DB 10; Length 32;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 GGACATGAAGCCCTTCAGCG 24
DB 8 GGACATGAAGCCCTTCAGCG 29
RESULT 9
US-09-864-761-22792/C
; Sequence 22792, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
```

APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aecmiga-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 22792
LENGTH: 96
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC002458.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
OTHER INFORMATION: NT HIT: D14547.1, EVALUATE 2.00e-10
OTHER INFORMATION: EST_HUMAN HIT: A1392964.1, EVALUATE 9.00e-17
US-09-864-761-22792

Query Match 58.3%; Score 14; DB 10; Length 96;
Best Local Similarity 77.3%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTGACATGAGCCCTTCAGC 22
DB 82 GTGAACATAAAGCTCTCATC 61

RESULT 10
US-09-828-366-28
Sequence 28, Application US/09828366
Patent No. US20020010137A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Klein, Robert D.
APPLICANT: Napier, Mary
APPLICANT: Wood, William I.
APPLICANT: Yuan, Jean
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITTING NEOPLASTIC
FILE REFERENCE: P1694R1C1
CURRENT APPLICATION NUMBER: US/09/828,366
CURRENT FILING DATE: 2001-04-05
Prior filing data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 28
LENGTH: 40
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-828-366-28

Query Match 57.5%; Score 13.8; DB 10; Length 40;
Best Local Similarity 88.2%; Pred. No. 8.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAACATGAGCCCTTC A 20
DB 18 GAACATGAGCCCTTC A 34

RESULT 11
US-09-990-080-20
Sequence 20, Application US/09990080
Patent No. US20020102686A1
GENERAL INFORMATION:
APPLICANT: Morlin, Gregg B.
APPLICANT: Geron Corporation
TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
FILE REFERENCE: 018/258c
CURRENT APPLICATION NUMBER: US/09/990,080
CURRENT FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: US 09/052,864
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 20
LENGTH: 60
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: RT6 oligo
US-09-990-080-20

Query Match 56.7%; Score 13.6; DB 10; Length 60;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GAACATGAGCCCTTCAGCG 23
DB 21 GAACATGAGCCCTTCAGCG 40

RESULT 12
US-09-783-590-2448/c
Sequence 2448, Application US/09783590
Patent No. US20020110850A1

```

GENERAL INFORMATION:
APPLICANT: DILLON, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Steven A.
TITLE OF INVENTION: Polynucleotide sequences, and expression products 16.2
FILE REFERENCE: P1-1201
CURRENT APPLICATION NUMBER: US/09/783,590
PRIORITY FILING DATE: 2000-02-15
PRIORITY FILING DATE: 1995-04-12
PRIORITY FILING DATE: 1995-04-12
PRIORITY FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: Patent Ver. 2.0
SEQ ID NO: 2448
LENGTH: 65
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: misc feature
LOCATION: 127
OTHER INFORMATION: n equals a, t, g, or c
US-09-783-590-2448

Query Match
Best Local Similarity 56.7%; Score 13.6; DB 10; Length 65;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

4 GAACATGAAGCCCTTCAGCG 23
DB 54 GACACGAGTCCCTTCAGCG 35

RESULT 13
US-10-084-206-9/C
Sequence 9, Application US/10084206
Patent No. US20020106741A1
GENERAL INFORMATION:
APPLICANT: Li et al.
TITLE OF INVENTION: G-protein Receptor HTMD29
FILE REFERENCE: P191D1C1
CURRENT APPLICATION NUMBER: US/10/084,206
PRIORITY FILING DATE: 2002-02-28
PRIORITY FILING DATE: 1995-06-06
PRIORITY FILING DATE: 1995-06-06
PRIORITY FILING DATE: 1995-06-06
PRIORITY FILING DATE: 1995-06-06
PRIORITY FILING DATE: 1999-09-20
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patent Version 3.1
SEQ ID NO: 9
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Contains the cleavage site for the restriction
OTHER INFORMATION: endonuclease BamHI
US-10-084-206-9

Query Match
Best Local Similarity 55.8%; Score 13.4; DB 12; Length 32;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

2 TGGAACATGAAGCCCTTCAGCG 24
DB 30 TGGAATTAAGAGCTCTTCAGCG 8

RESULT 14
US-09-923-876-1514/C

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```

Sequence 1514, Application US/09923876
Patent No. US20020013958A1
GENERAL INFORMATION:
APPLICANT: Laligudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: P1-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
PRIORITY FILING DATE: 2001-08-06
PRIORITY FILING DATE: 09/298,329
PRIORITY FILING DATE: 1999-04-21
PRIORITY FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program
SEQ ID NO: 1514
LENGTH: 82
TYPE: DNA
ORGANISM: Zea mays
NAME/KEY: misc feature
OTHER INFORMATION: incyte ID No. US20020013958A1 700158952H1
LOCATION: 2, 12-13, 37, 51, 58, 65, 67, 81
OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-1514

Query Match
Best Local Similarity 55.0%; Score 13.2; DB 10; Length 82;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

4 GAACATGAAGCCCTTCAGCG 23
DB 28 GAACAGATGCCCGTNNCG 9

RESULT 15
US-09-882-246-51
Sequence 51, Application US/09882246
Patent No. US20020106652A1
GENERAL INFORMATION:
APPLICANT: GOLD, LARRY
APPLICANT: WILLIS, MICHAEL
APPLICANT: KOCH, TAD
APPLICANT: RINGQUIST, STEVEN
APPLICANT: JENSEN, KIRK
APPLICANT: ATKINSON, BRENT
TITLE OF INVENTION: SYSTEMATIC EVOLUTION
OF
LIGANDS BY EXPONENTIAL
ENRICHMENT: PHOTOSELECTION
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESS: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
storage
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/882,246
FILING DATE: 14-Jun-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/093,293
FILING DATE: <Unknown>

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APPLICATION NUMBER: PCT/US94/10542
FILING DATE: 18 September 1994
APPLICATION NUMBER: 08/123,935
FILING DATE: 17 September 1993
APPLICATION NUMBER: 08/143,564
FILING DATE: 25 October 1993
APPLICATION NUMBER: 07/714,131
FILING DATE: 10 JUNE 1991
APPLICATION NUMBER: 07/536,428
FILING DATE: 11 JUNE 1990
APPLICATION NUMBER: 07/931,473
FILING DATE: 17 AUGUST 1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX10/US-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-882-246-51

Query Match 54.2% Score 13; DB 10; Length 37;
Best Local Similarity 61.9%; Pred. No. 1.9e+03;
Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 GTGGAACATGAAAGCCCTTCAG 21
I:|||||:|||||:||
Db 3 GUGGAACCTCAATCCCGUAG 23

Search completed: December 21, 2002, 19:28:16
Job time: 17.9469 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:21:10 : Search time 19.0653 Seconds
(without alignments)
562.024 Million cell updates/sec

Title: US-09-121-239-22

Perfect score: 27
Sequence: 1 TCTGACTTGAGCCTCAGGCTGAGT 27

Scoring table: IDENTITY_NDC
Gapop 10.0, Gapext 1.0

Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 214544

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications, NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCT06_PUBCOMB.seq:*
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- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22	81.5	22	10	US-09-995-912-4
C 2	14.8	54.8	67	10	US-09-974-300-4445
C 3	14.8	54.8	69	10	US-09-974-300-4378
C 4	14.8	54.8	69	10	US-09-974-300-4373
C 5	14.8	54.8	76	10	US-09-974-300-4374
C 6	14.8	54.8	76	10	US-09-974-300-4414
C 7	14.8	54.8	76	10	US-09-974-300-4426
C 8	14.8	54.8	76	10	US-09-974-300-4444
C 9	14.8	54.8	76	10	US-09-974-300-8449
C 10	14.8	54.8	76	10	US-09-974-300-8461
C 11	14.8	54.8	76	10	US-09-974-300-8477
C 12	14.8	54.8	76	10	US-09-974-300-8477
C 13	14.8	54.8	84	10	US-09-864-761-17329
C 14	14.8	54.8	87	10	US-09-864-761-19502
C 15	14.6	54.1	79	10	US-09-864-761-28857
C 16	14.4	53.3	36	10	US-09-504-231A-2483
C 17	14.4	53.3	36	10	US-09-504-231A-2660
C 18	14.4	53.3	36	10	US-09-504-231A-2816
C 19	14.4	53.3	36	10	US-09-274-553D-2483

C 20	14.4	53.3	36	10	US-09-274-553D-2660	Sequence 2660, Ap
C 21	14.4	53.3	36	10	US-09-274-553D-2816	Sequence 2816, Ap
C 22	14.2	52.6	96	12	US-10-078-777-8	Sequence 8, Appl
C 23	14	51.9	42	10	US-09-286-240-9	Sequence 9, Appl
C 24	14	51.9	42	10	US-09-765-272-353	Sequence 353, App
C 25	13.8	51.1	36	10	US-09-504-231A-2517	Sequence 2517, Ap
C 26	13.8	51.1	36	10	US-09-504-231A-2514	Sequence 2514, Ap
C 27	13.8	51.1	36	10	US-09-504-231A-2740	Sequence 2740, Ap
C 28	13.8	51.1	36	10	US-09-504-231A-2807	Sequence 2807, Ap
C 29	13.8	51.1	36	10	US-09-504-231A-2815	Sequence 2815, Ap
C 30	13.8	51.1	36	10	US-09-504-231A-2830	Sequence 2830, Ap
C 31	13.8	51.1	36	10	US-09-504-231A-2879	Sequence 2879, Ap
C 32	13.8	51.1	36	10	US-09-274-553D-2517	Sequence 2517, Ap
C 33	13.8	51.1	36	10	US-09-274-553D-2534	Sequence 2534, Ap
C 34	13.8	51.1	36	10	US-09-274-553D-2740	Sequence 2740, Ap
C 35	13.8	51.1	36	10	US-09-274-553D-2807	Sequence 2807, Ap
C 36	13.8	51.1	36	10	US-09-274-553D-2815	Sequence 2815, Ap
C 37	13.8	51.1	36	10	US-09-274-553D-2830	Sequence 2830, Ap
C 38	13.8	51.1	36	10	US-09-274-553D-2879	Sequence 2879, Ap
C 39	13.8	51.1	36	10	US-09-864-761-26264	Sequence 26264, A
C 40	13.6	50.4	31	10	US-09-801-274-1152	Sequence 1152, Ap
C 41	13.4	49.6	36	10	US-09-504-231A-22080	Sequence 22080, Ap
C 42	13.4	49.6	36	10	US-09-504-231A-2279	Sequence 2279, Ap
C 43	13.4	49.6	36	10	US-09-504-231A-2515	Sequence 2515, Ap
C 44	13.4	49.6	36	10	US-09-504-231A-2709	Sequence 2709, Ap
C 45	13.4	49.6	36	10	US-09-274-553D-2090	Sequence 2090, Ap

ALIGNMENTS

RESULT 1
US-09-995-912-4/c
Sequence 4, Application US/0995912
Patent No. US2002013706A1
GENERAL INFORMATION:
APPLICANT: Shultz, John W.
APPLICANT: Andrews, Martin K.
TITLE OF INVENTION: RNA Polymers and Uses Thereof
FILE REFERENCE: PRNG-06684
CURRENT APPLICATION NUMBER: US/09/995,912
PRIOR FILING DATE: 2001-11-28
PRIORITY APPLICATION NUMBER: 60/253,451
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 4
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-995-912-4

Query Match: 81.5%; Score 22; DB 10; Length 22;
Best Local Similarity: 100.0%; Pred. No. 0.53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTGAGCCTCAGGCTGTA 25
DB 22 GACTTGAGCCTCAGGCTGTA 1

RESULT 2
US-09-974-300-4445
Sequence 4445, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
Expression

FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974.300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4445
LENGTH: 67
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4445

Query Match 54.8%; Score 14.8; DB 10; Length 67;
Best Local Similarity 73.1%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGCTCTGAG 26
||||| | | | | | | |
Db 20 TCTGACTTTTATCATCAGAGGCTCGAAG 45

RESULT 3
US-09-974-300-4378
Sequence 4378, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974.300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4378
LENGTH: 69
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4378

Query Match 54.8%; Score 14.8; DB 10; Length 69;
Best Local Similarity 73.1%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGCTCTGAG 26
||||| | | | | | | |
Db 20 TCTGACTTTTATCATCAGAGGCTCGAAG 45

RESULT 4
US-09-974-300-4393
Sequence 4393, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974.300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4393
LENGTH: 69
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4393

Query Match 54.8%; Score 14.8; DB 10; Length 69;
Best Local Similarity 73.1%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGCTCTGAG 26
||||| | | | | | | |
Db 20 TCTGACTTTTATCATCAGAGGCTCGAAG 45

RESULT 5
US-09-974-300-4374
Sequence 4374, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974.300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4374
LENGTH: 76
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4374

Query Match 54.8%; Score 14.8; DB 10; Length 76;
Best Local Similarity 73.1%; Pred. No. 8.2e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGCTCTGAG 26
||||| | | | | | | |
Db 27 TCTGACTTTTATCATCAGAGGCTCGAAG 52

RESULT 6
US-09-974-300-4414
Sequence 4414, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974.300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4414
LENGTH: 76
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4414

Query Match	54.8%;	Score 14.8;	DB 10;	Length 76;
Best Local Similarity	73.1%;	Pred. No. 8.2e+02;		
Matches 19; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0

Qy 1 TCTGACTTTGAGCCTCAGGGTCTGAG 26
 ||||| | | ||||| ||
 Db 27 TCTGACTTTTATCAGAGGGTCGAAG 52

```

RESULT 7
US-09-974-300-4426
Sequence 4426, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groh
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085, 500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/27'9,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4426
LENGTH: 76
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4426

```

Query Match	54.8%;	Score 14.8;	DB 10;	Length 76;
Best Local Similarity	73.1%;	Pred. No. 8.2e+02;		
Matches 19; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0;

Oy 1 TCTGACTTTGAGCCTCAGGGTCTGAG 26
||| |||
Db 27 TCTGACTTTAATCAGAGGGTCGAAG 52

```

RESULT 8
US-09-974-300-4444
Sequence 4444, Application US/05974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berkta, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085, 500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ. ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4444
LENGTH: 76
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4444

```

Query Match	54.8%	Score 14.8	DB 10	Length 76
Best Local Similarity	73.1%	Pred. No. 8.2e+02		
Matches 19	Conservative	0	Mismatches 7	Indels 0
			Gaps	0
QY	1	TGTGACTTTGAGCCTCAGGCTCGAG	26	

1 TCTGACTTTGAGCCTCAGGGTCTGAG 26

Db 27 TCTGACTTTTAATCAGAGGGTCCGAAG 52

```

RESULT 9
US-09-974-300-8409
Sequence 8409, Application US/09974300
Patent No. US20020146731A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods for Monitoring Multiple Gene
FILE REFERENCE: 10085,500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: PASTESD for Windows Version 4.0
SEQ ID NO 8409
LENGTH: 76
TYPE: DNA
ORGANISM: Bacillus clausii
US-09-974-300-8409

```

Query Match	54.8%;	Score 14.8;	DB 10;	Length 76;
Best Local Similarity	73.1%;	Pred. No. 8.2e+02;		
Matches 19; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGGTCTGAG 26
 ||||| | | ||||| ||
 Db 27 TCTGACTTTTAATCAGAGGGTCTGAG 52

```

; RESULT 10
; US-09-974-300-8449
; Sequence 8449, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berkta, Randy M.
; TITLE OF INVENTION: Methods for Monitoring Multiple Genes
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085, 500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIORITY FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,558
; PRIORITY FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIORITY FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
; SEQ ID NO 8449
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Bacillus clausii
US-09-974-300-8449

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Query Match.	54.8%;	Score 14.8;	DB 10;	Length 76;
Best Local Similarity	73.1%;	Pred. No. 8.2e+02;		
Matches 19; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGGTCTGAG 26
||||| - - ||||| - -
Db 27 TCTGACTTTTAATCAGAGGGTCTGAAG 52

RESULT 11
US-09-974-300-8461
; Sequence 8461, Application US/09974300
; Patent No. US20020146721A1

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GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085,500-US
CURRENT APPLICATION NUMBER: US/09/974,300
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8461
LENGTH: 76
TYPE: DNA
ORGANISM: Bacillus clausii
US-09-974-300-8461
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```
Query Match          54.8%; Score 14.8; DB 10; Length 76;
Best Local Similarity 73.1%; Pred. No. 8.2e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 1 TCTGACTTTGAGCCTCAGGCTGTAG 26
||||| 1 | ||||| 11
Db 27 TCTGACTTTATCATCAGAGGCTCGAAG 52
```

```
RESULT 12
US-09-974-300-8477
Sequence 8477, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085,500-US
CURRENT APPLICATION NUMBER: US/09/974,300
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8477
LENGTH: 76
TYPE: DNA
ORGANISM: Bacillus clausii
US-09-974-300-8477
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```
Query Match          54.8%; Score 14.8; DB 10; Length 76;
Best Local Similarity 73.1%; Pred. No. 8.2e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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```
QY 1 TCTGACTTTGAGCCTCAGGCTGTAG 26
||||| 1 | ||||| 11
Db 27 TCTGACTTTATCATCAGAGGCTCGAAG 52
```

```
RESULT 13
US-09-864-761-17329
Sequence 17329, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
GENE EXPRESSION ANALYSIS BY MICROARRAY
```

```
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 17329
LENGTH: 84
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC008166.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.3
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4.9
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 5.6
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.3
OTHER INFORMATION: NT HIT: AL163248.2, EVALUATE 3.00e-12
OTHER INFORMATION: EST_HUMAN HIT: AV721403.1, EVALUATE 1.00e-18
US-09-864-761-17329
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Query Match          54.8%; Score 14.8; DB 10; Length 84;
Best Local Similarity 73.1%; Pred. No. 8.3e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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```
QY 2 CTGACTTTGAGCCTCAGGCTGTAGT 27
||||| 1 | ||||| 11
Db 2 CTGCTTGTGACATCGAGCTGTAGT 27
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```
RESULT 14
US-09-864-761-19502
Sequence 19502, Application US/09864761
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Query Match 54.1%; Score 14.6; DB 10; Length 79;
 Best Local Similarity 81.0%; Pred. No. 1e+03; 4; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ACTTTGAGGCTCAGGGCTCTGA 25
 ||| ||||| || |||||
 Db 50 ACTTGAGGCCACACAGGCTCTGA 30

Search completed: December 21, 2002, 19:28:18
 Job time : 21.0653 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:21:10 ; Search time 19.0653 Seconds
(without alignments)
562.024 Million cell updates/sec

Title: US-09-121-239-23
Perfect score: 27
Sequence: 1 UCUGACUUGAGCCUCCAGGUCUGAGU 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 356696 seqs, 198428768 residues
Total number of hits satisfying chosen parameters: 214544

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCRN_NPW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NPW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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- 6: /cgn2_6/ptodata/2/pubpna/PCRN_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NPW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NPW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NPW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	81.5	22	10	US-09-995-912-4
C 2	14.8	54.8	67	10	US-09-974-300-4445
C 3	14.8	54.8	69	10	US-09-974-300-4378
C 4	14.8	54.8	69	10	US-09-974-300-4393
C 5	14.8	54.8	76	10	US-09-974-300-4374
C 6	14.8	54.8	76	10	US-09-974-300-4414
C 7	14.8	54.8	76	10	US-09-974-300-4426
C 8	14.8	54.8	76	10	US-09-974-300-4444
C 9	14.8	54.8	76	10	US-09-974-300-8409
C 10	14.8	54.8	76	10	US-09-974-300-8449
C 11	14.8	54.8	76	10	US-09-974-300-8461
C 12	14.8	54.8	76	10	US-09-974-300-8477
C 13	14.8	54.8	84	10	US-09-864-761-17329
C 14	14.8	54.8	87	10	US-09-864-761-19502
C 15	14.6	54.1	79	10	US-09-864-761-28857
C 16	14.4	53.3	36	10	US-09-504-231A-2483
C 17	14.4	53.3	36	10	US-09-504-231A-2660
C 18	14.4	53.3	36	10	US-09-504-231A-2816
C 19	14.4	53.3	36	10	US-09-274-553D-2483

C 20	14.4	53.3	36	10	US-09-274-553D-2660	Sequence 2660, Ap
C 21	14.4	53.3	36	10	US-09-274-553D-2816	Sequence 2816, Ap
C 22	14.2	52.6	36	12	US-10-078-277-8	Sequence 8, Appl
C 23	14.2	51.9	42	10	US-09-286-240-9	Sequence 353, App
C 24	14.1	51.9	42	10	US-09-765-272-353	Sequence 2517, Ap
C 25	13.8	51.1	36	10	US-09-504-231A-2517	Sequence 2534, Ap
C 26	13.8	51.1	36	10	US-09-504-231A-2534	Sequence 2760, Ap
C 27	13.8	51.1	36	10	US-09-504-231A-2760	Sequence 2807, Ap
C 28	13.8	51.1	36	10	US-09-504-231A-2807	Sequence 2815, Ap
C 29	13.8	51.1	36	10	US-09-504-231A-2815	Sequence 2830, Ap
C 30	13.8	51.1	36	10	US-09-504-231A-2830	Sequence 2879, Ap
C 31	13.8	51.1	36	10	US-09-504-231A-2879	Sequence 2930, Ap
C 32	13.8	51.1	36	10	US-09-274-553D-2517	Sequence 2517, Ap
C 33	13.8	51.1	36	10	US-09-274-553D-2534	Sequence 2534, Ap
C 34	13.8	51.1	36	10	US-09-274-553D-2740	Sequence 2740, Ap
C 35	13.8	51.1	36	10	US-09-274-553D-2807	Sequence 2807, Ap
C 36	13.8	51.1	36	10	US-09-274-553D-2815	Sequence 2815, Ap
C 37	13.8	51.1	36	10	US-09-274-553D-2830	Sequence 2830, Ap
C 38	13.8	51.1	36	10	US-09-274-553D-2879	Sequence 2879, Ap
C 39	13.8	51.1	36	10	US-09-864-761-26264	Sequence 1152, Ap
C 40	13.6	50.4	31	10	US-09-504-231A-2090	Sequence 2090, Ap
C 41	13.4	49.6	36	10	US-09-504-231A-2279	Sequence 2279, Ap
C 42	13.4	49.6	36	10	US-09-504-231A-2515	Sequence 2515, Ap
C 43	13.4	49.6	36	10	US-09-504-231A-2709	Sequence 2709, Ap
C 44	13.4	49.6	36	10	US-09-504-231A-2709	Sequence 2090, Ap
C 45	13.4	49.6	36	10	US-09-274-553D-2090	

ALIGNMENTS

RESULT 1
US-09-995-912-4/c
Sequence 4, Appl
Patent No. US20020137076A1
GENERAL INFORMATION:
APPLICANT: Spultz, John W.
APPLICANT: Lewis, Martin K.
TITLE OF INVENTION: RNA Polymers and Uses Thereof
FILE REFERENCE: PRMG-06684
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 60/235,451
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-995-912-4

Query Match
Best Local Similarity 81.5%
Matches 16, Conservative 6; Mismatches 0; Indels 0; Gaps 0;
CY 4 GACUUGAGCCUCCAGGUCUGA 25
DB 22 GACUUGAGCCUCCAGGUCUGA 1
RESULT 2
US-09-974-300-4445
Sequence 4445, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression

```
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4445
LENGTH: 67
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4445
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```
Query Match          54.8%; Score 14.8; DB 10; Length 67;
Best Local Similarity 50.0%; Pred. No. 8.1e+02;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
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Qy      1 UCUGACUUGAGCCUCAGGUCUGAG 26
Db      20 TCTGACTTTTATCATCAGAGGTCGAG 45
```

```
RESULT 3
US-09-974-300-4378
Sequence 4378, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4378
LENGTH: 69
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4378
```

```
Query Match          54.8%; Score 14.8; DB 10; Length 69;
Best Local Similarity 50.0%; Pred. No. 8.1e+02;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy      1 UCUGACUUGAGCCUCAGGUCUGAG 26
Db      20 TCTGACTTTTATCATCAGAGGTCGAG 45
```

```
RESULT 4
US-09-974-300-4393
Sequence 4393, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
```

```
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4393
LENGTH: 69
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4393
```

```
Query Match          54.8%; Score 14.8; DB 10; Length 69;
Best Local Similarity 50.0%; Pred. No. 8.1e+02;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy      1 UCUGACUUGAGCCUCAGGUCUGAG 26
Db      20 TCTGACTTTTATCATCAGAGGTCGAG 45
```

```
RESULT 5
US-09-974-300-4374
Sequence 4374, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4374
LENGTH: 76
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4374
```

```
Query Match          54.8%; Score 14.8; DB 10; Length 76;
Best Local Similarity 50.0%; Pred. No. 8.2e+02;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy      1 UCUGACUUGAGCCUCAGGUCUGAG 26
Db      27 TCTGACTTTTATCATCAGAGGTCGAG 52
```

```
RESULT 6
US-09-974-300-4414
Sequence 4414, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4414
LENGTH: 76
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-4414
```



```
Query Match          54.8%; Score 14.8; DB 10; Length 76;
Best Local Similarity 50.0%; Pred. No. 8.2e+02;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 UCUGACUUGAGCCUCAGGUCUGAG 26
:|||||:| | | | | | | |
Db 27 TCTGACTTTTATCATCAGAGGTCGAG 52

RESULT 7
US-09-974-300-4426
; Sequence 4426, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4426
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-4426

Query Match          54.8%; Score 14.8; DB 10; Length 76;
Best Local Similarity 50.0%; Pred. No. 8.2e+02;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 UCUGACUUGAGCCUCAGGUCUGAG 26
:|||||:| | | | | | | |
Db 27 TCTGACTTTTATCATCAGAGGTCGAG 52

RESULT 8
US-09-974-300-4444
; Sequence 4444, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4444
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-4444

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; Patent No. US20020146721A1
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; APPLICANT: Berka, Randy M.
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
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; ORGANISM: Bacillus clausii
US-09-974-300-8409

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; APPLICANT: Berka, Randy M.
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
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; ORGANISM: Bacillus clausii
US-09-974-300-8449

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Mon Dec 23 08:48:02 2002

us-09-121-239-26.rmpb

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Published Applications, NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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8	11.6	63.3	90	10	US-09-974-300-4057
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23	10.8	60.0	31	10	US-09-801-274-803	Sequence 803, App
24	10.8	60.0	35	9	US-09-993-164-19	Sequence 19, Appl
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35	10.6	58.9	33	10	US-09-790-417-122	Sequence 3, Appl1
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ALIGNMENTS

RESULT 1
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Sequence 294, Application us/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Boistein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Oliang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paonl, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William T.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2860PCL1
CURRENT APPLICATION NUMBER: US/09/978, 295A
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249

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? APPLICANT: Baker Kevin P.
? APPLICANT: Botstein, David
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? APPLICANT: Wood, William T.
? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
? FILE REFERENCE: P2630PIC27
? CURRENT APPLICATION NUMBER: US/09/978,697
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PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
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PRIOR FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 82.2% Score 14.8; DB 9; Length 50;
Best Local Similarity 88.9%; Pred. No. 35;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGAATCATCGAGCATGG 18
DB 5 GGAATCATCGATCGAGG 22

RESULT 3
US-09-978-192A-294
Sequence 294, Application US/09978192A
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Flvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/074450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791

Mon Dec 23 08:48:02 2002

us-09-121-239-26.rnpb

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6	PRIOR FILING DATE: 1998-04-22
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59	PRIOR APPLICATION NUMBER: 60/085699
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61	PRIOR APPLICATION NUMBER: 60/085579
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64	PRIOR FILING DATE: 1998-05-15
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66	PRIOR FILING DATE: 1998-05-15
67	PRIOR APPLICATION NUMBER: 60/085704
68	PRIOR FILING DATE: 1998-05-15
69	PRIOR APPLICATION NUMBER: 60/085697

Query Match 82.2%; Score 14.8; DB 9; Length 50;
Best Local Similarity 88.9%; Pred. No. 35;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 5 GAATCATCGATGCAGG 22

RESULT 4

US-09-799-946-1
; Sequence 1, Application US/09799946
; Patent No. US2002009028A1

GENERAL INFORMATION:

APPLICANT: Gudkov, Andrei
Kazarov, Alexander
Mazo, Ilya

Roinson, Igor B

TITLE OF INVENTION: Methods for Identifying Genetic
Suppressor Elements and Genes Associated with Malignant
Growth in Cancer Cells

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Aligretti & Witcoff, Ltd.
STREET: 10 S. Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,946
FILING DATE: 06-Mar-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/204,740
FILING DATE: 04-MAR-1994

ATTORNEY/AGENT INFORMATION:
NAME: No. US2002009028A1man, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-C

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-799-946-1

Query Match 71.1%; Score 12.8; DB 10; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AATCATCGAGCATGG 18
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DB 1 AATCATCGATGATGG 16

US-09-799-946-2/c
; Sequence 2, Application US/09799946
; Patent No. US2002009028A1

GENERAL INFORMATION:
APPLICANT: Gudkov, Andrei
Kazarov, Alexander
Mazo, Ilya

Roinson, Igor B

TITLE OF INVENTION: Methods for Identifying Genetic
Suppressor Elements and Genes Associated with Malignant
Growth in Cancer Cells

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Aligretti & Witcoff, Ltd.
STREET: 10 S. Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,946
FILING DATE: 06-Mar-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/204,740
FILING DATE: 04-MAR-1994

ATTORNEY/AGENT INFORMATION:
NAME: No. US2002009028A1man, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-C

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-923-876-2188/c

Query Match 71.1%; Score 12.8; DB 10; Length 23;
Best Local Similarity 87.5%; Pred. No. 3.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AATCATCGAGCATGG 18
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DB 20 AATCATCGATGATGG 5

US-09-923-876-2188/c
; Sequence 2188, Application US/09923876
; Patent No. US20020013958A1

GENERAL INFORMATION:
APPLICANT: Laligudi, Raghunath V.
Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/085,331
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program


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; SEQ ID NO 41
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-879-257A-41
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Best Local Similarity 81.2%; Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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RESULT 10
US-09-796-088-6
; Sequence 6, Application US/09796088
; Patent No. US20020119573A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Karen
; APPLICANT: Kenny, Terry
; APPLICANT: Shimer Jr., George H.
; TITLE OF INVENTION: Footprinting Plasmid
; FILE REFERENCE: 1034/0H284
; CURRENT APPLICATION NUMBER: US/09/796,088
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer Sequence
US-09-796-088-6
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Best Local Similarity 81.2%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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RESULT 11
US-09-854-302-6
; Sequence 6, Application US/09854302
; Patent No. US20020165228A1
; GENERAL INFORMATION:
; APPLICANT: Rybczynski, Philip
; APPLICANT: et al.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE 4H-BENZOL(1,4)OXAZIN-3-ONES
; FILE REFERENCE: PM431, Patent 2.1
; CURRENT APPLICATION NUMBER: US/09/854,302
; CURRENT FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-854-302-6
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Best Local Similarity 81.2%; Pred. No. 3.1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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OY 3 AATCATCGAGGCATGG 18
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DB 24 AATCATTTAGGCATAG 39
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RESULT 12
US-09-853-798-6
; Sequence 6, Application US/09853798
; Patent No. US20020103193A1
; GENERAL INFORMATION:
; APPLICANT: Rybczynski, Philip
; APPLICANT: et al.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE 4H-BENZOL(1,4)OXAZIN-3-ONES
; FILE REFERENCE: PM431, Patent 2.1
; CURRENT APPLICATION NUMBER: US/09/853,798
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-853-798-6
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Best Local Similarity 81.2%; Pred. No. 3.1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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OY 3 AATCATCGAGGCATGG 18
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DB 24 AATCATTTAGGCATAG 39
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RESULT 13
US-09-764-877-3299
; Sequence 3299, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3299
; LENGTH: 83
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3299
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Best Local Similarity 81.2%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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DB 11 AATTAGCCAGGCATGG 26
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RESULT 14
US-09-764-869-2041/C
; Sequence 2041, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
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; Prior application data removed - refer to PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 2442
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2041
 ; LENGTH: 87
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-869-2041

Query Match 62.2%; Score 11.2; DB 10; Length 87;
 Best Local Similarity 81.2%; Pred. No. 3.3e+03;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 Db 52 AATTAACCGCATGG 37

RESULT 15
 US-09-969-373-47
 ; Sequence 47, Application US/09969373
 ; Patent No. US20020133852A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Efferitz, Roger J.
 ; APPLICANT: Hauge, Brian M.
 ; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
 ; FILE REFERENCE: 38-1052679A
 ; CURRENT APPLICATION NUMBER: US/09/969,373
 ; CURRENT FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: US 09/754,853
 ; PRIOR FILING DATE: 2001-01-05
 ; PRIOR APPLICATION NUMBER: US 09/760,427
 ; PRIOR FILING DATE: 2001-01-13
 ; PRIOR APPLICATION NUMBER: US 09/855,768
 ; PRIOR FILING DATE: 2001-05-15
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 ; ORGANISM: Glycine max
 US-09-969-373-47

Query Match 62.2%; Score 11.2; DB 10; Length 94;
 Best Local Similarity 81.2%; Pred. No. 3.3e+03;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 Db 5 GGAATCATCGAGCAT 20

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 Job time : 14.7102 secs

Mon Dec 23 08:48:04 2002

us-09-121-239-27.rmpb

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2002, 11:21:10 : Search time 18.3592 Seconds
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Title: US-09-121-239-27

Perfect score: 26

Sequence: 1 CACTGACCCACTGATTTAAGCAGAG 26

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Searched: 356696 segs, 198428768 residues

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4: /cgn2_6/p/odata2/pub/pna/US06_PUBCOMB.seq:*
5: /cgn2_6/p/odata2/pub/pna/US07_NEM_PUB.seq:*
6: /cgn2_6/p/odata2/pub/pna/PC07_PUBCOMB.seq:*
7: /cgn2_6/p/odata2/pub/pna/US08_NEM_PUB.seq:*
8: /cgn2_6/p/odata2/pub/pna/US08_PUBCOMB.seq:*
9: /cgn2_6/p/odata2/pub/pna/US09_NEM_PUB.seq:*
10: /cgn2_6/p/odata2/pub/pna/US09_PUBCOMB.seq:*
11: /cgn2_6/p/odata2/pub/pna/US10_NEM_PUB.seq:*
12: /cgn2_6/p/odata2/pub/pna/US10_PUBCOMB.seq:*
13: /cgn2_6/p/odata2/pub/pna/US60_NEM_PUB.seq:*
14: /cgn2_6/p/odata2/pub/pna/US60_PUBCOMB.seq:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	25	96.2	40	10	US-09-790-417-125
2	25	96.2	41	10	US-09-790-417-126
3	16.4	63.1	31	10	US-09-801-274-1413
4	16	61.5	88	9	US-09-909-363-17
5	15	61.5	88	9	US-09-909-363-18
6	15	57.7	22	10	US-09-790-417-127
7	15	57.7	22	10	US-09-790-417-128
8	14.4	55.4	25	10	US-09-866-108-14228
9	14.4	55.4	25	10	US-09-866-108-14229
10	14.4	55.4	28	10	US-09-766-095-12
11	14.4	55.4	28	10	US-09-766-095-64
12	14.4	55.4	28	10	US-09-766-095-78
13	14.4	55.4	28	10	US-09-766-095-92
14	14.4	55.4	42	9	US-09-991-003B-19
15	14.4	55.4	80	10	US-09-864-761-23997
16	14.4	55.4	83	10	US-09-864-761-27487
17	13.4	51.5	25	10	US-09-866-108-14227
18	13.4	51.5	25	10	US-09-866-108-14230
19	13.2	50.8	36	10	US-09-738-968-15

20	13	50.0	90	10	US-09-753-436-47	Sequence 47, Appl
21	13	50.0	98	9	US-09-924-400-282	Sequence 282, Appl
22	13	50.0	98	10	US-09-810-936-282	Sequence 282, Appl
23	13	50.0	98	10	US-09-429-755-282	Sequence 282, Appl
24	12.8	49.2	21	10	US-09-853-986-145	Sequence 145, Appl
25	12.6	48.5	69	10	US-09-775-743A-10	Sequence 10, Appl
26	12.6	48.5	26	10	US-09-911-935A-17	Sequence 17, Appl
27	12.6	48.5	78	10	US-09-374-671-56	Sequence 56, Appl
28	12.4	47.7	25	10	US-09-866-108-14226	Sequence 14226, A
29	12.4	47.7	25	10	US-09-866-108-14231	Sequence 14231, A
30	12.4	47.7	28	10	US-09-812-216-8	Sequence 8, Appl
31	12.4	47.7	51	10	US-09-917-265-96	Sequence 96, Appl
32	12.4	47.7	78	10	US-09-777-564-1563	Sequence 1563, Appl
33	12.4	47.7	78	10	US-09-983-965-3131	Sequence 3131, Appl
34	12.4	47.7	79	10	US-09-783-590-1166	Sequence 1166, Appl
35	12.4	47.7	92	10	US-09-864-761-31467	Sequence 31467, A
36	12.4	47.7	100	10	US-09-728-446-1353	Sequence 1353, Appl
37	12.2	46.9	45	9	US-09-905-291A-337	Sequence 337, Appl
38	12.2	46.9	45	10	US-09-909-280-337	Sequence 337, Appl
39	12.2	46.9	45	10	US-09-909-088B-337	Sequence 337, Appl
40	12.2	46.9	79	9	US-09-870-753-75	Sequence 75, Appl
41	12.2	46.9	84	10	US-09-864-761-17357	Sequence 17357, A
42	12.2	46.9	88	10	US-09-864-761-26014	Sequence 26014, A
43	12	46.2	20	9	US-09-966-955A-17	Sequence 17, Appl
44	12	46.2	23	10	US-09-910-635-2	Sequence 2, Appl
45	12	46.2	23	10	US-09-956-412-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-790-417-125/c
Sequence 125, Application US/09790417
Patient No US0010031470A1
GENERAL INFORMATION: John W
APPLICANT: Shultz, John W
APPLICANT: Lewis, Martin K.
APPLICANT: Liepp, Donna
APPLICANT: Mandrekar, Michelle
APPLICANT: Kephart, Daniel
APPLICANT: Rhodes, Richard B.
APPLICANT: Andrews, Christine A.
APPLICANT: Hartnett, James R.
APPLICANT: Gu, Trent
APPLICANT: Olson, Ryan J.
APPLICANT: Wood, Keith W.
APPLICANT: Welch, Roy
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: Pro-103 6868/75528
CURRENT APPLICATION NUMBER: US/09/790,417
CURRENT FILING DATE: 2001-02-22
PRIORITY FILING DATE: 1999-07-21
PRIORITY APPLICATION NUMBER: 09/042,287
PRIORITY FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 290
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 125
LENGTH: 40
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: native bcr
US-09-790-417-125
Query Match 96.2% Score 25; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 40 ACTGACCCACTGATTTAAGCAGAG 26
OY 2 ACTGACCCACTGATTTAAGCAGAG 26
DB 40 ACTGACCCACTGATTTAAGCAGAG 16

RESULT 2

US-09-790-417-126/c
; Sequence 126, Application US/09790417
; Patent No. US20010031470A1
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W.
; APPLICANT: Lewis, Martin K.
; APPLICANT: Lieppe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J.
; APPLICANT: Wood, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Nucleic Acid Detection
; FILE REFERENCE: Pro-103 6868/75528
; CURRENT APPLICATION NUMBER: US/09/790,417
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/358,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 09/042,287
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 126
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: bcr/abl translocation
US-09-790-417-126

Query Match 96.2%; Score 25; DB 10; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ACTCAGCCACTGATTTAAGCAGAG 26
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Db 41 ACTCAGCCACTGATTTAAGCAGAG 17

RESULT 3

US-09-801-274-1413
; Sequence 1413, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825,2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1413
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-1413

Query Match 63.1%; Score 16.4; DB 10; Length 31;
Best Local Similarity 85.0%; Pred. No. 47;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 GCCACTGATTTAAGCAGAG 26
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Db 2 GCCACTGATTTAAGCAGAG 21

RESULT 4

US-09-909-363-17
; Sequence 17, Application US/09909363
; Patent No. US20020164783A1
; GENERAL INFORMATION:
; APPLICANT: Feldhaus, Andrew
; TITLE OF INVENTION: TRANSCRIPTIONALLY-ACTIVATED
; AAV INVERTED TERMINAL REPEATS (ITRS) FOR USE WITH RECOMB
; AAV VECTORS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/909,363
; FILING DATE: 19-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/171,759
; FILING DATE: 20-OCT-1998
; APPLICATION NUMBER: PCT/US98/21937
; FILING DATE: 20-OCT-1998
; APPLICATION NUMBER: 08/955,400
; FILING DATE: 27-OCT-1997
; APPLICATION NUMBER: 60/108,162
; FILING DATE: 21-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Polizzi, Catherine M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 226272003802
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 88 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-909-363-17

Query Match 61.5%; Score 16; DB 9; Length 88;
Best Local Similarity 79.2%; Pred. No. 93;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CTCAGCCACTGATTTAAGCAGAG 26
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Db 43 CCCACCCCTGATTTAAGCAGAG 66

RESULT 5

US-09-909-363-18/c
; Sequence 18, Application US/09909363
; Patent No. US20020164783A1
; GENERAL INFORMATION:
; APPLICANT: Feldhaus, Andrew

TITLE OF INVENTION: TRANSCRIPTIONALLY-ACTIVATED
AAV INVERTED TERMINAL REPEATS (ITRS) FOR USE WITH RECOMBINANT
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/909,363
APPLICATION NUMBER: 19-JUL-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/171,759
FILING DATE: 20-OCT-1998
APPLICATION NUMBER: PCT/US98/21937
FILING DATE: 20-OCT-1998
APPLICATION NUMBER: 08/955,400
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: 60/108,162
FILING DATE: 21-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Polizzi, Catherine M.
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 226272003802
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-909-363-18
Query Match 61.5%; Score 16; DB 9; Length 88;
Best Local Similarity 79.2%; Pred. No. 93;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
CY 3 CTCAGCAGCTGATTTAGCAGAG 26
DB 50 CCCACCCCTGTATATACAGAG 27
RESULT 6
US-09-790-417-127
Sequence 127, Application US/09790417
Patent No. US20010031470A1
GENERAL INFORMATION:
APPLICANT: Shultz, John W.
APPLICANT: Lewis, Martin K.
APPLICANT: Lieppe, Donna
APPLICANT: Mandrekar, Michelle
APPLICANT: Kephart, Daniel
APPLICANT: Rhodes, Richard B.
APPLICANT: Andrews, Christine A.
APPLICANT: Hartnett, James R.
APPLICANT: Gu, Trent
APPLICANT: Olson, Ryan J.
APPLICANT: Wood, Keith W.
APPLICANT: Welch, Roy
TITLE OF INVENTION: Nucleic Acid Detection

FILE REFERENCE: PRO-103 6868/75528
CURRENT APPLICATION NUMBER: US/09/790,417
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 09/358,972
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: 09/042,287
PRIOR FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 290
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 127
LENGTH: 22
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: probe for native bcr
US-09-790-417-127
Query Match 57.7%; Score 15; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 12 TGGATTTAGCAGAG 26
DB 1 TGGATTTAGCAGAG 15
RESULT 7
US-09-790-417-128
Sequence 128, Application US/09790417
Patent No. US20010031470A1
GENERAL INFORMATION:
APPLICANT: Shultz, John W.
APPLICANT: Lewis, Martin K.
APPLICANT: Lieppe, Donna
APPLICANT: Mandrekar, Michelle
APPLICANT: Kephart, Daniel
APPLICANT: Rhodes, Richard B.
APPLICANT: Andrews, Christine A.
APPLICANT: Hartnett, James R.
APPLICANT: Gu, Trent
APPLICANT: Olson, Ryan J.
APPLICANT: Wood, Keith W.
APPLICANT: Welch, Roy
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: PRO-103 6868/75528
CURRENT APPLICATION NUMBER: US/09/790,417
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 09/358,972
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: 09/042,287
PRIOR FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 290
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 128
LENGTH: 22
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: probe for bcr/abl translocation
US-09-790-417-128
Query Match 57.7%; Score 15; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 12 TGGATTTAGCAGAG 26
DB 1 TGGATTTAGCAGAG 15
RESULT 8
US-09-866-108-14228
Sequence 14228, Application US/09866108

```
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aecmca Sequence Listing Engine
SEQ ID NO 14228
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-14228

Query Match      55.4%; Score 14.4; DB 10; Length 25;
Best Local Similarity 75.0%; Pred. No. 4e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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3 CTCAGCCACTGGATTAAAGAGAG 26
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2 CTCAGCCCCCAGATTAACGAGAG 25
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RESULT 9

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US-09-866-108-14229
Sequence 14229, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
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FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aecmca Sequence Listing Engine
SEQ ID NO 14229
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-14229

Query Match      55.4%; Score 14.4; DB 10; Length 25;
Best Local Similarity 75.0%; Pred. No. 4e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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3 CTCAGCCACTGGATTAAAGAGAG 26
111111111111111111111111
1 CTCAGCCCCCAGATTAACGAGAG 24
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RESULT 10

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US-09-766-095-12/c
Sequence 12, Application US/09766095
Patent No. US20020062016A1
GENERAL INFORMATION:
APPLICANT: Sheriol H. McDonough, Thomas B. Ryder,
yeasing yang
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
OLIGONUCLEOTIDES AND PROBES
TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PS/2 Model 50x or 55sx
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
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Mon Dec 23 08:48:04 2002

us-09-121-239-27.rnpb

Page 5

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,095
FILING DATE: 18-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/013,406
FILING DATE: 26-Jan-01
APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/550,837
FILING DATE: 10-Jul-90
APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/379,501
FILING DATE: 11-Jul-89
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION/DOCKET NUMBER: 32,327
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-766-095-12
Query Match 55.4%; Score 14.4; DB 10; Length 28;
Best Local Similarity 75.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CACTGACCCAGTCGATTAACGAC 24
Db 28 CCCTCAGATCTCGCATATACGAC 5

RESULT 11
US-09-766-095-64
Sequence 64, Application US/09766095
Patent No. US20020062016A1
GENERAL INFORMATION:
APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,
Yeastling Yang
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
OLIGONUCLEOTIDES AND PROBES
TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (version 3.30)
SOFTWARE: Wordperfect (version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,095
FILING DATE: 18-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/013,406
FILING DATE: 26-Jan-01
APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/550,837
FILING DATE: 10-Jul-90
APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/379,501
FILING DATE: 11-Jul-89
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION/DOCKET NUMBER: 32,327
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-766-095-12
```

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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 196/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-09-766-095-64
Query Match 55.4%; Score 14.4; DB 10; Length 28;
Best Local Similarity 75.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CACTGACCCAGTCGATTAACGAC 24
Db 1 CCCTCAGATCTCGCATATACGAC 24

RESULT 12
US-09-766-095-78/C
Sequence 78, Application US/09766095
Patent No. US20020062016A1
GENERAL INFORMATION:
APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,
Yeastling Yang
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
OLIGONUCLEOTIDES AND PROBES
TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (version 3.30)
SOFTWARE: Wordperfect (version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,095
FILING DATE: 18-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/013,406
FILING DATE: 26-Jan-01
APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/550,837
FILING DATE: 10-Jul-90
APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/379,501
FILING DATE: 11-Jul-89
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION/DOCKET NUMBER: 32,327
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 78:
US-09-766-095-78
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US-09-766-095-78

Query Match 55.4%; Score 14.4; DB 10; Length 28;
Best Local Similarity 75.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CACTCAGCCACTGGATTAGACG 24
1 ||||| ||||| ||||| |||||
Db 28 CCTCAGATCCTGCATATAGCAG 5

RESULT 13

US-09-766-095-92
Sequence 92, Application US/09766095
Patent No. US20020062016A1

GENERAL INFORMATION:

APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,

Yeasting Yang

TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION

OLIGONUCLEOTIDES AND PROBES

TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSER: Lyon & Lyon

STREET: 611 West Sixth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90017

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM PS/2 Model 502 or 55SX

OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

SOFTWARE: Wordperfect (Version 5.0)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/766,095

FILING DATE: 18-Jan-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/013,406

FILING DATE: 26-Jan-01

APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/550,837

FILING DATE: 10-Jul-90

APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/379,501

FILING DATE: 11-Jul-89

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 196/189

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 92:

SEQUENCE CHARACTERISTICS:

LENGTH: 28

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 92:

US-09-766-095-92

Query Match 55.4%; Score 14.4; DB 10; Length 28;

Best Local Similarity 58.3%; Pred. No. 4.1e+02;

Matches 14; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CACTCAGCCACTGGATTAGACG 24

1 ||||| ||||| ||||| |||||

Db 1 CCTCAGATCCTGCATATAGCAG 24

RESULT 14

US-09-991-003B-19/c

Sequence 19, Application US/09991003B

Patent No. US20020177125A1

GENERAL INFORMATION:

APPLICANT: KAMB, Carl Alexander

APPLICANT: KAMITZ, Mark Aaron

APPLICANT: TENG, David Heng-Fai

TITLE OF INVENTION: Human Rhinovirus Assays, and Compositions Therefrom

FILE REFERENCE: 29345/36971A

CURRENT APPLICATION NUMBER: US/09/991,003B

CURRENT FILING DATE: 2002-11-16

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn version 3.0

SEQ ID NO 19

LENGTH: 42

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: rh2B.F1 primer

US-09-991-003B-19

Query Match 55.4%; Score 14.4; DB 9; Length 42;

Best Local Similarity 93.8%; Pred. No. 4.6e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CACTCAGCCACTGGAT 16

1 ||||| ||||| ||||| |||||

Db 26 CACTCAGCCCTGGAT 11

RESULT 15

US-09-864-761-23997

Sequence 23997, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO

FILE REFERENCE: Aeomla-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263,6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23997
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC022392.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
; OTHER INFORMATION: EST_HUMAN HIT: AW861102.1, EVALU9.50e-01
US-09-864-761-23997

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Query Match      55.4%: Score 14.4; DB 10; Length 80;
Best Local Similarity 75.0%: Pred. No. 5.3e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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OY 2 ACTCAGCCACTGATTTAAGCAGA 25
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Db 3 ATTATCCATGATGATTTATCAGA 26

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Search completed: December 21, 2002, 19:28:21
 Job time : 19:3592 secs

